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(54) Title: NUCLEIC ACIDS INCLUDING OPEN READING FRAMES ENCODING POLYPEPTIDES; "ORFX"			
(57) Abstract The present invention provides open reading frames ORFX, encoding isolated polypeptides, as well as polynucleotides encoding ORFX and antibodies that immunospecifically bind to ORFX or any derivative, variant, mutant, or fragment of the ORFX polypeptides, polynucleotides or antibodies. The invention additionally provides methods in which the ORFX polypeptide, polynucleotide and antibody are used in detection and treatment of a broad range of pathological states, as well as to other uses.			

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NOVEL POLYNUCLEOTIDES AND POLYPEPTIDES ENCODED THEREBY

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BACKGROUND OF THE INVENTION

The invention relates generally to nucleic acids and polypeptides encoded thereby, and methods of using these nucleic acids and polypeptides.

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SUMMARY OF THE INVENTION

The invention is based in part on the discovery of nucleic acids that include open reading frames encoding novel polypeptides, and on the polypeptides encoded thereby. The nucleic acids and polypeptides are collectively referred to herein as "ORFX".

Accordingly, in one aspect, the invention provides an isolated nucleic acid molecule (SEQ ID NO:2*n*-1, wherein *n* is an integer between 1-3161), that encodes novel polypeptide, or a fragment, homolog, analog or derivative thereof. The nucleic acid can include, *e.g.*, a nucleic acid sequence encoding a polypeptide at least 85% identical to a polypeptide comprising the amino acid sequences of SEQ ID NO:2*n*, wherein *n* is an integer between 1-3161. The nucleic acid can be, *e.g.*, a genomic DNA fragment, or a cDNA molecule.

Also included in the invention is a vector containing one or more of the nucleic acids described herein, and a cell containing the vectors or nucleic acids described herein.

The invention is also directed to host cells transformed with a recombinant expression vector comprising any of the nucleic acid molecules described above.

In another aspect, the invention includes a pharmaceutical composition that includes an ORFX nucleic acid and a pharmaceutically acceptable carrier or diluent.

In a further aspect, the invention includes a substantially purified ORF polypeptide, *e.g.*, any of the ORFX polypeptides encoded by an ORFX nucleic acid, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition that includes a ORFX polypeptide and a pharmaceutically acceptable carrier or diluent.

5 In a still a further aspect, the invention provides an antibody that binds specifically to an ORFX polypeptide. The antibody can be, *e.g.*, a monoclonal or polyclonal antibody, and fragments, homologs, analogs, and derivatives thereof. The invention also includes a pharmaceutical composition including ORFX antibody and a pharmaceutically acceptable carrier or diluent. The invention is also directed to isolated antibodies that bind to an epitope on a
10 polypeptide encoded by any of the nucleic acid molecules described above.

The invention also includes kits comprising any of the pharmaceutical compositions described above.

The invention further provides a method for producing an ORFX polypeptide by providing a cell containing a ORFX nucleic acid, *e.g.*, a vector that includes a ORFX nucleic
15 acid, and culturing the cell under conditions sufficient to express the ORFX polypeptide encoded by the nucleic acid. The expressed ORFX polypeptide is then recovered from the cell. Preferably, the cell produces little or no endogenous ORFX polypeptide. The cell can be, *e.g.*, a prokaryotic cell or eukaryotic cell.

The invention is also directed to methods of identifying an ORFX polypeptide or nucleic
20 acids in a sample by contacting the sample with a compound that specifically binds to the polypeptide or nucleic acid, and detecting complex formation, if present.

The invention further provides methods of identifying a compound that modulates the activity of a ORFX polypeptide by contacting ORFX polypeptide with a compound and determining whether the ORFX polypeptide activity is modified.

25 The invention is also directed to compounds that modulate ORFX polypeptide activity identified by contacting a ORFX polypeptide with the compound and determining whether the compound modifies activity of the ORFX polypeptide, binds to the ORFX polypeptide, or binds to a nucleic acid molecule encoding a ORFX polypeptide.

30 In a another aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a sample from the subject and measuring the amount of ORFX polypeptide in the subject sample.

The amount of ORFX polypeptide in the subject sample is then compared to the amount of ORFX polypeptide in a control sample. An alteration in the amount of ORFX polypeptide in the subject protein sample relative to the amount of ORFX polypeptide in the control protein sample indicates the subject has a tissue proliferation-associated condition. A control sample is preferably taken from a matched individual, *i.e.*, an individual of similar age, sex, or other general condition but who is not suspected of having a tissue proliferation-associated condition. Alternatively, the control sample may be taken from the subject at a time when the subject is not suspected of having a tissue proliferation-associated disorder. In some embodiments, the ORFX is detected using a ORFX antibody.

In a further aspect, the invention provides a method of determining the presence of or predisposition of an ORFX-associated disorder in a subject. The method includes providing a nucleic acid sample, *e.g.*, RNA or DNA, or both, from the subject and measuring the amount of the ORFX nucleic acid in the subject nucleic acid sample. The amount of ORFX nucleic acid sample in the subject nucleic acid is then compared to the amount of an ORFX nucleic acid in a control sample. An alteration in the amount of ORFX nucleic acid in the sample relative to the amount of ORFX in the control sample indicates the subject has a tissue proliferation-associated disorder.

In a still further aspect, the invention provides method of treating or preventing or delaying a ORFX-associated disorder. The method includes administering to a subject in which such treatment or prevention or delay is desired a ORFX nucleic acid, a ORFX polypeptide, or an ORFX antibody in an amount sufficient to treat, prevent, or delay a tissue proliferation-associated disorder in the subject.

Unless otherwise defined, all technical and scientific terms used herein have the same meaning as commonly understood by one of ordinary skill in the art to which this invention belongs. Although methods and materials similar or equivalent to those described herein can be used in the practice or testing of the present invention, suitable methods and materials are described below. All publications, patent applications, patents, and other references mentioned herein are incorporated by reference in their entirety. In the case of conflict, the present specification, including definitions, will control. In addition, the materials, methods, and examples are illustrative only and not intended to be limiting.

Other features and advantages of the invention will be apparent from the following detailed description and claims.

DETAILED DESCRIPTION OF THE INVENTION

The invention provides novel polypeptides and nucleotides encoded thereby. The polynucleotides and their encoded polypeptides can be grouped according to the functions played by their gene products. Such functions include, structural proteins, proteins from which associated with metabolic pathways fatty acid metabolism, glycolysis, intermediary metabolism, calcium metabolism, proteases, and amino acid metabolism, etc.

Included in the invention are 3161 novel nucleic acid sequences and their encoded polypeptides. The sequences are collectively referred to as "ORFX nucleic acids" or ORFX polynucleotides" and the corresponding encoded polypeptide is referred to as a "ORFX polypeptide" or ORFX protein". For example, an ORFX nucleic acid according to the invention is a nucleic acid including an ORF1 nucleic acid, and an ORF polypeptide according to the invention is a polypeptide that includes the amino acid sequence of an ORF1 polypeptide. Unless indicated otherwise, "ORFX" is meant to refer to any of the ORF1-3161 sequences disclosed herein.

Table 1 provides a summary of the ORFX nucleic acids and their encoded polypeptides are summarized in Table 1. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention is provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 1 of Table 1, entitled "ORF #", denotes an ORF number assigned to a nucleic acid containing an open reading frame according to the invention.

Column 2 of Table 1, entitled "Internal Identification number (Nucleic Acid Sequence Identification Number, Polypeptide Sequence Identification Number), provides an internal identification number for the indicated ORF, along with sequence identification numbers (SEQ ID NOs.) corresponding to the indicated ORF. In general, for an ORF_n according to the invention (wherein *n* is any integer from 1 to 3161), a nucleic acid corresponding to the ORF is SEQ ID NO:2*n*-1, and an amino acid sequence encoded by the ORF is SEQ ID NO:2*n*. For example, a nucleic acid sequence corresponding to an ORF1 nucleic acid is SEQ ID NO:1, and a polypeptide sequence corresponding to an ORF1 polypeptide is SEQ ID NO:2. Similarly, a

nucleic acid sequence corresponding to an ORF4 nucleic acid is SEQ ID NO:7, and a polypeptide sequence corresponding to an ORF4 polypeptide is SEQ ID NO:8; a nucleic acid sequence corresponding to an ORF198 nucleic acid sequence is SEQ ID NO:395, and a polypeptide sequence corresponding to an ORF198 polypeptide is SEQ ID NO:396. Nucleic acid sequences and polypeptide sequences for ORFX nucleic acids according to the invention are provided in the section of the specification entitled "Disclosed Sequences of ORFX Nucleic Acid and Polypeptide Sequences."

Column 2 of Table 1, entitled "Protein Similarity", lists previously described proteins that are related to polypeptides encoded by the ORFs. Genbank identifiers for the previously described proteins are provided. These can be retrieved from <http://www.ncbi.nlm.nih.gov/>.

To determine similarity to previously described proteins, polypeptides encoded by ORFX DNA sequences were tested using the Framesearch Algorithm against a nonredundant version of the GenPept Database from NCBI/Genbank. DNA sequences that had a score of '90' or above (Framesearch algorithm score, Edelman et. al. GCG Genetics) to a known protein were selected.

Open reading frames were extended beyond the region of the protein matched using standard DNA translation and codon tables. Novel proteins that lacked a protein match were translated against the standard genetic codons and proteins with an ORF at least 80 amino acids and containing a Methionine start are included in the Table.

Column 3 of Table 3, entitled "Protein Domains", lists previously described protein domains, designated by pfam entries, that are present in polypeptides encoded by the ORFs. Also included in column 3 are proteins in which these domains are present. The pfam entries can be retrieved from <http://pfam.wustl.edu/>. DNA sequences were translated in all six frames and tested using the Hmmer Algorithm against the Pfam Database (References to the algorithm and Pfam database can be found at <http://pfam.wustl.edu>). Translated DNA sequences that matched a protein domain entry in the Pfam database AND had a score of '7.5' were selected.

Column 4 of Table 3, entitled "Protein Classification", lists the type of classification assigned for the protein, based on its homology. Examples of proteins in the classification include the following proteins:

Amylases

Amylase is responsible for endohydrolysis of 1,4-alpha-glucosidic linkages in oligosaccharides and polysaccharides. Variations in amylase gene may be indicative of delayed maturation and of various amylase producing neoplasms and carcinomas.

5 **Amyloid**

The serum amyloid A (SAA) proteins comprise a family of vertebrate proteins that associate predominantly with high density lipoproteins (HDL). The synthesis of certain members of the family is greatly increased in inflammation. Prolonged elevation of plasma SAA levels, as in chronic inflammation, 15 results in a pathological condition, called amyloidosis, which affects the liver, kidney and spleen and which is characterized by the highly insoluble accumulation of SAA in these tissues. Amyloid selectively inhibits insulin-stimulated glucose utilization and glycogen deposition in muscle, while not affecting adipocyte glucose metabolism. Deposition of fibrillar amyloid proteins intraneuronally, as neurofibrillary tangles, extracellularly, as plaques and in blood vessels, is characteristic of both Alzheimer's disease and aged Down's syndrome. 15 Amyloid deposition is also associated with type II diabetes mellitus.

Angiopoeitin

Members of the angiopoietin/fibrinogen family have been shown to stimulate the generation of new blood vessels, inhibit the generation of new blood vessels, and perform several roles in blood clotting. This generation of new blood vessels, called angiogenesis, is also an 20 essential step in tumor growth in order for the tumor to get the blood supply it needs to expand. Variation in these genes may be predictive of any form of heart disease, numerous blood clotting disorders, stroke, hypertension and predisposition to tumor formation and metastasis. In particular, these variants may be predictive of the response to various antihypertensive drugs and chemotherapeutic and anti-tumor agents.

25 **Apoptosis-related proteins**

Active cell suicide (apoptosis) is induced by events such as growth factor withdrawal and toxins. It is controlled by regulators, which have either an inhibitory effect on programmed cell

death (anti-apoptotic) or block the protective effect of inhibitors (pro-apoptotic). Many viruses have found a way of countering defensive apoptosis by encoding their own anti-apoptosis genes preventing their target-cells from dying too soon. Variants of apoptosis related genes may be useful in formulation of anti-aging drugs.

5 **Cadherin, Cyclin, Polymerase, Oncogenes, Histones, Kinases**

Members of the cell division/cell cycle pathways such as cyclins, many transcription factors and kinases, DNA polymerases, histones, helicases and other oncogenes play a critical role in carcinogenesis where the uncontrolled proliferation of cells leads to tumor formation and eventually metastasis. Variation in these genes may be predictive of predisposition to any form of cancer, from increased risk of tumor formation to increased rate of metastasis. In particular, these variants may be predictive of the response to various chemotherapeutic and anti-tumor agents.

Colony-stimulating factor-related proteins

Granulocyte/macrophage colony-stimulating factors are cytokines that act in hematopoiesis by controlling the production, differentiation, and function of 2 related white cell populations of the blood, the granulocytes and the monocytes-macrophages.

Complement-related proteins

Complement proteins are immune associated cytotoxic agents, acting in a chain reaction to exterminate target cells to that were opsonized (primed) with antibodies, by forming a membrane attack complex (MAC). The mechanism of killing is by opening pores in the target cell membrane. Variations in 20 complement genes or their inhibitors are associated with many autoimmune disorders. Modified serum levels of complement products cause edemas of various tissues, lupus (SLE), vasculitis, glomerulonephritis, renal failure, hemolytic anemia, thrombocytopenia, and arthritis. They interfere with mechanisms of ADCC (antibody dependent cell cytotoxicity), severely impair immune competence and reduce phagocytic ability. Variants of complement genes may also be indicative of type I diabetes mellitus, meningitis neurological disorders such as nemaline myopathy, neonatal hypotonia, muscular disorders such as congenital myopathy and other diseases.

Cytochrome

The respiratory chain is a key biochemical pathway which is essential to all aerobic cells. There are five different cytochromes involved in the chain. These are heme bound proteins which serve as electron carriers. Modifications in these genes may be predictive of ataxia areflexia, dementia and myopathic and neuropathic changes in muscles. Also, association with various types of solid tumors.

Kinesins

Kinesins are tubulin molecular motors that function to transport organelles within cells and to move chromosomes along microtubules during cell division. Modifications of these genes may be indicative of neurological disorders such as Pick disease of the brain, tuberous sclerosis.

Cytokines, Interferon, Interleukin

Members of the cytokine families are known for their potent ability to stimulate cell growth and division even at low concentrations. Cytokines such as erythropoietin are cell-specific in their growth stimulation; erythropoietin is useful for the stimulation of the proliferation of erythroblasts. Variants in cytokines may be predictive for a wide variety of diseases, including cancer predisposition.

G-protein coupled receptors

G-protein coupled receptors (also called R7G) are an extensive group of hormones, neurotransmitters, odorants and light receptors which transduce extracellular signals by interaction with guanine nucleotide-binding (G) proteins. Alterations in genes coding for G-coupled proteins may be involved in and indicative of a vast number of physiological conditions. These include blood pressure regulation, renal dysfunctions, male infertility, dopamine associated cognitive, emotional, and endocrine functions, hypercalcemia, chondrodysplasia and osteoporosis, pseudohypoparathyroidism, growth retardation and dwarfism.

Thioesterases

Eukaryotic thiol proteases are a family of proteolytic enzymes which contain an active site cysteine. Catalysis proceeds through a thioester intermediate and is facilitated by a nearby histidine side chain; an asparagine completes the essential catalytic triad. Variants of thioester associated genes may be predictive of neuronal disorders and mental illnesses such as Ceroid Lipoffiscinosis, Neuronal 1, Infantile, Santavuori disease and more.

The key to the molecule type is as follows:

10	Abbrev:	Title:
	amylase	amylase protein
	amylaseinhib	amylase inhibitor
	amyloid	amyloid protein
15	apoptosis	apoptosis associated protein
	apoptosisinhib	apoptosis inhibitors
	apoptosisrecep	apoptosis receptors
	ATPase_associated	ATPase associated protein
	biotindep	biotin dependent enzyme/protein
20	cadherin	cadherin protein
	calcium_channel	calcium channel protein
	carboxylase	carboxylase protein
	cathepsin	cathepsin/carboxypeptidases
	cathepsininhib	cathepsin/carboxypeptidase inhibitor
25	chloride_channel	chloride channel protein
	collagen	collagen
	complement	complement protein
	complementrecept	complement receptor protein
	complementinhib	complement inhibitor
30	csf	colony stimulating factor
	csfrecept	colony stimulating factor receptor
	cyclin	cyclin protein
	cyto450	cytochrome p450 protein
	cytochrome	cytochrome related protein
35	deaminase	deaminase
	dehydrogenase	dehydrogenase
	desaturase	desaturase
	dna_ma_bind	DNA/RNA binding protein/factor
	dna_ma_inhib	DNA/RNA binding protein/factor inhibitor
40	dynein	dynein

	elastase	elastase
	elastaseinhib	elastase inhibitor
	eph	EPH family of tyrosine kinases
	esterase	esterase
5	esteraseinhib	esterase inhibitor
	fgf	fibroblast growth factor
	fgfreceptor	fibroblast growth factor receptor
	gaba	GABA receptor
	glucoamylase	glucoamylase
10	glucoronidase	glucoronidase
	glycoprotein	glycoprotein
	Guanylyl	guanylylate cyclase
	helicase	helicase
	histone	histone
15	HOM	homologous
	homeobox	homeobox protein
	hydrolase	hydrolase
	hydroxysteroid	hydroxysteroid associated protein
	hypoxanthine	hypoxanthine associated protein
20	immunoglob	immunoglobulin
	immunoglobrecept	immunoglobulin receptor
	interferon	interferon
	interleukin	interleukin
	interleukinrecept	interleukin receptor
25	isomerase	isomerase
	isomeraseinhibitor	isomerase inhibitor
	isomerasereceptor	isomerase receptor
	kinase	kinase
	kinaseinhibitor	kinase inhibitor
30	kinasereceptor	kinase receptor
	kinesin	kinesin
	laminin	laminin associated protein
	lipase	lipase
	metallothionein	metallothionein
35	MHC	major histocompatibility complex
	misc_channel	miscellaneous channel
	ngf	nerve growth factor
	nuci_recpt	nuclear receptor
	nuclease	nuclease
40	oncogene	oncogene associated protein
	oxidase	oxidase
	oxygenase	oxygenase
	peptidase	peptidase
	peroxidase	peroxidase
45	phosphatase	phosphatase
	phosphataseinhib	phosphatase inhibitor

	phosphorylase	phosphorylase
	PIR	PIR DATABASE (release 56, 29-OCT-1998)
5	polymerase	polymerase
	potassium_channel	potassium channel protein
	prostaglandin	prostaglandin
	protease	protease
	proteaseinhib	protease inhibitor
10	reductase	reductase
	ribosomalprot	ribosomal associated protein
	RTR	EMBLDATABASE translated entries not to be incorporated into SWISS-PROT (20-JUL-1998)
15	SIM	similar
	SPTR	EMBL DATABASE translated entries to be incorporated into SWISS-PROT (20-JUL-1998)
	struct	structural associated protein
20	sulfotransferase	sulfotransferase
	SWP	SWISS-PROT DATABASE (release 18-OCT-1998)
	SWPN	SWISS-PROT Update (release 11-NOV-98)
	synthase	synthase
25	tgf	transforming growth factor
	tgfreceptor	transforming growth factor receptor
	thioesterase	thioesterase
	thiolase	thiolase
	tm7	seven transmembrane domain G-protein coupled receptor
30	tnf	necrosis factor receptor
	traffic	tumor necrosis factor
	tnfreceptor	tumor trafficking associated protein
	TRN	EMBL DATABASE translated entries update (20-JUL-1998)
35	transcriptfactor	transcription factor
	transferase	transferase
	transport	transport protein
	tubulin	tubulin
40	ubiquitin	ubiquitin
	unclassified	Protein not categorized into one of the aforementioned protein families
	water channel	water channel protein

Column 5 of Table 1, entitled, "Cells or Tissues in Which Gene is Expressed", denotes tissues, represented by five digit numbers, in which RNA homologous to the ORF nucleic acid sequences is present. Tissues or cells corresponding to the numbers are provided in Table 2.

ORFX nucleic acids, and their encoded polypeptides, according to the invention are
5 useful in a variety of applications and contexts. For example, various ORFX nucleic acids and polypeptides according to the invention are useful, *inter alia*, as novel members of the protein families indicated in Table 1, and/or according to the presence of domains and sequence relatedness to previously described proteins as summarized in Table 1.

ORFX nucleic acids and polypeptides according to the invention can also be used to
10 identify cell types listed in Table 1 for an indicated ORFX according to the invention. Additional utilities for ORFX nucleic acids and polypeptides according to the invention are disclosed herein.

ORFX Nucleic Acids

15 The novel nucleic acids of the invention include those that encode an ORFX or ORFX-like protein, or biologically active portions thereof. The nucleic acids include nucleic acids encoding polypeptides that include the amino acid sequence of one or more of SEQ ID NO:2*n*, wherein *n* = 1 to 3161. The encoded polypeptides can thus include, *e.g.*, the amino acid sequences of SEQ ID NO: 2, 4, 6, 8, 10, . . . , 6310, 6312, 6314, 6316, 6318, 6320, and/or 6322.

20 In some embodiments, a nucleic acid encoding a polypeptide having the amino acid sequence of one or more of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) includes the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof. Additionally, the invention includes mutant or variant nucleic acids of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a fragment thereof, any of whose bases may be changed from the
25 disclosed sequence while still encoding a protein that maintains its ORFX-like activities and physiological functions. The invention further includes the complement of the nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), including fragments, derivatives,

analog and homolog thereof. The invention additionally includes nucleic acids or nucleic acid fragments, or complements thereto, whose structures include chemical modifications.

Also included are nucleic acid fragments sufficient for use as hybridization probes to identify ORFX-encoding nucleic acids (*e.g.*, ORFX mRNA) and fragments for use as
5 polymerase chain reaction (PCR) primers for the amplification or mutation of ORFX nucleic acid molecules. As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA), RNA molecules (*e.g.*, mRNA), analogs of the DNA or RNA generated using nucleotide analogs, and derivatives, fragments and homologs thereof. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is
10 double-stranded DNA.

"Probes" refer to nucleic acid sequences of variable length, preferably between at least about 10 nucleotides (nt), 100 nt, or as many as about, *e.g.*, 6,000 nt, depending on use. Probes are used in the detection of identical, similar, or complementary nucleic acid sequences. Longer length probes are usually obtained from a natural or recombinant source, are highly specific and
15 much slower to hybridize than oligomers. Probes may be single- or double-stranded and designed to have specificity in PCR, membrane-based hybridization technologies, or ELISA-like technologies.

An "isolated" nucleic acid molecule is one that is separated from other nucleic acid molecules that are present in the natural source of the nucleic acid. Examples of isolated nucleic acid molecules include, but are not limited to, recombinant DNA molecules contained in a
20 vector, recombinant DNA molecules maintained in a heterologous host cell, partially or substantially purified nucleic acid molecules, and synthetic DNA or RNA molecules. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism
25 from which the nucleic acid is derived. For example, in various embodiments, the isolated ORFX nucleic acid molecule can contain less than about 50 kb, 25 kb, 5 kb, 4 kb, 3 kb, 2 kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived. Moreover, an "isolated" nucleic acid molecule, such as a cDNA molecule, can be substantially free of other cellular
30 material or culture medium when produced by recombinant techniques, or of chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement of any of this nucleotide sequence, can be isolated using standard molecular biology techniques and the sequence information provided herein. Using all or a portion of the nucleic acid sequence of any
5 of SEQ ID NO:2*n*-1 (wherein *n*=1 to 3161) as a hybridization probe, ORFX nucleic acid sequences can be isolated using standard hybridization and cloning techniques (*e.g.*, as described in Sambrook *et al.*, eds., MOLECULAR CLONING: A LABORATORY MANUAL 2nd Ed., Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989; and Ausubel, *et al.*, eds., CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993.)

10 A nucleic acid of the invention can be amplified using cDNA, mRNA or alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to ORFX nucleotide sequences can be prepared by standard synthetic techniques, *e.g.*, using an
15 automated DNA synthesizer.

As used herein, the term "oligonucleotide" refers to a series of linked nucleotide residues, which oligonucleotide has a sufficient number of nucleotide bases to be used in a PCR reaction. A short oligonucleotide sequence may be based on, or designed from, a genomic or cDNA sequence and is used to amplify, confirm, or reveal the presence of an identical, similar or
20 complementary DNA or RNA in a particular cell or tissue. Oligonucleotides comprise portions of a nucleic acid sequence having about 10 nt, 50 nt, or 100 nt in length, preferably about 15 nt to 30 nt in length. In one embodiment, an oligonucleotide comprising a nucleic acid molecule less than 100 nt in length would further comprise at least 6 contiguous nucleotides of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a complement thereof. Oligonucleotides may be
25 chemically synthesized and may be used as probes.

In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule that is a complement of the nucleotide sequence
30 shown in any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion of this nucleotide sequence. A nucleic acid molecule that is complementary to the nucleotide sequence shown in

is one that is sufficiently complementary to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) that it can hydrogen bond with little or no mismatches to the nucleotide sequence shown in of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161),, thereby forming a stable duplex.

5 As used herein, the term “complementary” refers to Watson-Crick or Hoogsteen base pairing between nucleotides units of a nucleic acid molecule, and the term “binding” means the physical or chemical interaction between two polypeptides or compounds or associated polypeptides or compounds or combinations thereof. Binding includes ionic, non-ionic, Von der Waals, hydrophobic interactions, etc. A physical interaction can be either direct or indirect.

10 Indirect interactions may be through or due to the effects of another polypeptide or compound. Direct binding refers to interactions that do not take place through, or due to, the effect of another polypeptide or compound, but instead are without other substantial chemical intermediates.

 Moreover, the nucleic acid molecule of the invention can comprise only a portion of the
15 nucleic acid sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), *e.g.*, a fragment that can be used as a probe or primer, or a fragment encoding a biologically active portion of ORFX. Fragments provided herein are defined as sequences of at least 6 (contiguous) nucleic acids or at least 4 (contiguous) amino acids, a length sufficient to allow for specific hybridization in the case of nucleic acids or for specific recognition of an epitope in the case of amino acids, respectively,
20 and are at most some portion less than a full length sequence. Fragments may be derived from any contiguous portion of a nucleic acid or amino acid sequence of choice. Derivatives are nucleic acid sequences or amino acid sequences formed from the native compounds either directly or by modification or partial substitution. Analogs are nucleic acid sequences or amino acid sequences that have a structure similar to, but not identical to, the native compound but
25 differs from it in respect to certain components or side chains. Analogs may be synthetic or from a different evolutionary origin and may have a similar or opposite metabolic activity compared to wild type.

 Derivatives and analogs may be full length or other than full length, if the derivative or analog contains a modified nucleic acid or amino acid, as described below. Derivatives or
30 analogs of the nucleic acids or proteins of the invention include, but are not limited to, molecules comprising regions that are substantially homologous to the nucleic acids or proteins of the

invention, in various embodiments, by at least about 70%, 80%, 85%, 90%, 95%, 98%, or even 99% identity (with a preferred identity of 80-99%) over a nucleic acid or amino acid sequence of identical size or when compared to an aligned sequence in which the alignment is done by a computer homology program known in the art, or whose encoding nucleic acid is capable of hybridizing to the complement of a sequence encoding the aforementioned proteins under stringent, moderately stringent, or low stringent conditions. See *e.g.* Ausubel, *et al.*, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, New York, NY, 1993, and below. An exemplary program is the Gap program (Wisconsin Sequence Analysis Package, Version 8 for UNIX, Genetics Computer Group, University Research Park, Madison, WI) using the default settings, which uses the algorithm of Smith and Waterman (Adv. Appl. Math., 1981, 2: 482-489, which is incorporated herein by reference in its entirety).

A "homologous nucleic acid sequence" or "homologous amino acid sequence," or variations thereof, refer to sequences characterized by a homology at the nucleotide level or amino acid level as discussed above. Homologous nucleotide sequences encode those sequences coding for isoforms of ORFX polypeptide. Isoforms can be expressed in different tissues of the same organism as a result of, for example, alternative splicing of RNA. Alternatively, isoforms can be encoded by different genes. In the present invention, homologous nucleotide sequences include nucleotide sequences encoding for a ORFX polypeptide of species other than humans, including, but not limited to, mammals, and thus can include, *e.g.*, mouse, rat, rabbit, dog, cat, cow, horse, and other organisms. Homologous nucleotide sequences also include, but are not limited to, naturally occurring allelic variations and mutations of the nucleotide sequences set forth herein. A homologous nucleotide sequence does not, however, include the nucleotide sequence encoding human ORFX protein. Homologous nucleic acid sequences include those nucleic acid sequences that encode conservative amino acid substitutions (see below) in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) as well as a polypeptide having ORFX activity. Biological activities of the ORFX proteins are described below. A homologous amino acid sequence does not encode the amino acid sequence of a human ORFX polypeptide.

The nucleotide sequence determined from the cloning of the human ORFX gene allows for the generation of probes and primers designed for use in identifying the cell types disclosed and/or cloning ORFX homologues in other cell types, *e.g.*, from other tissues, as well as ORFX homologues from other mammals. The probe/primer typically comprises a substantially purified

oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, 25, 50, 100, 150, 200, 250, 300, 350 or 400 or more consecutive sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161); or an anti-sense strand nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161);
 5 or of a naturally occurring mutant of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

Probes based on the human ORFX nucleotide sequence can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In various embodiments, the probe further comprises a label group attached thereto, *e.g.*, the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be
 10 used as a part of a diagnostic test kit for identifying cells or tissue which misexpress a ORFX protein, such as by measuring a level of a ORFX-encoding nucleic acid in a sample of cells from a subject *e.g.*, detecting ORFX mRNA levels or determining whether a genomic ORFX gene has been mutated or deleted.

"A polypeptide having a biologically active portion of ORFX" refers to polypeptides
 15 exhibiting activity similar, but not necessarily identical to, an activity of a polypeptide of the present invention, including mature forms, as measured in a particular biological assay, with or without dose dependency. A nucleic acid fragment encoding a "biologically active portion of ORFX" can be prepared by isolating a portion of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), that encodes a polypeptide having a ORFX biological activity (biological activities of the ORFX
 20 proteins are summarized in Table 1), expressing the encoded portion of ORFX protein (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of ORFX. For example, a nucleic acid fragment encoding a biologically active portion of ORFX can optionally include a domain as shown in Table 1, column 4:

25 **ORFX variants**

The invention further encompasses nucleic acid molecules that differ from the disclosed ORFX nucleotide sequences due to degeneracy of the genetic code. These nucleic acids thus encode the same ORFX protein as that encoded by the nucleotide sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). In another embodiment, an isolated nucleic acid molecule of
 30 the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

In addition to the human ORFX nucleotide sequence shown in any of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161), it will be appreciated by those skilled in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of ORFX may exist within a population (*e.g.*, the human population). Such genetic polymorphism in the ORFX gene may exist among individuals within a population due to natural allelic variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding a ORFX protein, preferably a mammalian ORFX protein. Such natural allelic variations can typically result in 1-5% variance in the nucleotide sequence of the ORFX gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in ORFX that are the result of natural allelic variation and that do not alter the functional activity of ORFX are intended to be within the scope of the invention.

Moreover, nucleic acid molecules encoding ORFX proteins from other species, and thus that have a nucleotide sequence that differs from the human sequence of any of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161), are intended to be within the scope of the invention. Nucleic acid molecules corresponding to natural allelic variants and homologues of the ORFX cDNAs of the invention can be isolated based on their homology to the human ORFX nucleic acids disclosed herein using the human cDNAs, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions.

In another embodiment, an isolated nucleic acid molecule of the invention is at least 6 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161). In another embodiment, the nucleic acid is at least 10, 25, 50, 100, 250, 500 or 750 nucleotides in length. In another embodiment, an isolated nucleic acid molecule of the invention hybridizes to the coding region. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other.

Homologs (*i.e.*, nucleic acids encoding ORFX proteins derived from species other than human) or other related sequences (*e.g.*, paralogs) can be obtained by low, moderate or high stringency hybridization with all or a portion of the particular human sequence as a probe using methods well known in the art for nucleic acid hybridization and cloning.

As used herein, the phrase "stringent hybridization conditions" refers to conditions under which a probe, primer or oligonucleotide will hybridize to its target sequence, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures than shorter sequences. Generally, stringent conditions are selected to be about 5°C lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength and pH. The T_m is the temperature (under defined ionic strength, pH and nucleic acid concentration) at which 50% of the probes complementary to the target sequence hybridize to the target sequence at equilibrium. Since the target sequences are generally present at excess, at T_m , 50% of the probes are occupied at equilibrium. Typically, stringent conditions will be those in which the salt concentration is less than about 1.0 M sodium ion, typically about 0.01 to 1.0 M sodium ion (or other salts) at pH 7.0 to 8.3 and the temperature is at least about 30°C for short probes, primers or oligonucleotides (e.g., 10 nt to 50 nt) and at least about 60°C for longer probes, primers and oligonucleotides. Stringent conditions may also be achieved with the addition of destabilizing agents, such as formamide.

Stringent conditions are known to those skilled in the art and can be found in CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. Preferably, the conditions are such that sequences at least about 65%, 70%, 75%, 85%, 90%, 95%, 98%, or 99% homologous to each other typically remain hybridized to each other. A non-limiting example of stringent hybridization conditions is hybridization in a high salt buffer comprising 6X SSC, 50 mM Tris-HCl (pH 7.5), 1 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.02% BSA, and 500 mg/ml denatured salmon sperm DNA at 65°C. This hybridization is followed by one or more washes in 0.2X SSC, 0.01% BSA at 50°C. An isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to the sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161) corresponds to a naturally occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (e.g., encodes a natural protein).

In a second embodiment, a nucleic acid sequence that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein $n = 1$ to 3161), or fragments, analogs or derivatives thereof, under conditions of moderate stringency is provided. A non-limiting example of moderate stringency hybridization conditions are

hybridization in 6X SSC, 5X Denhardt's solution, 0.5% SDS and 100 mg/ml denatured salmon sperm DNA at 55°C, followed by one or more washes in 1X SSC, 0.1% SDS at 37°C. Other conditions of moderate stringency that may be used are well known in the art. See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and
5 Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY.

In a third embodiment, a nucleic acid that is hybridizable to the nucleic acid molecule comprising the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof, under conditions of low stringency, is provided. A
10 non-limiting example of low stringency hybridization conditions are hybridization in 35% formamide, 5X SSC, 50 mM Tris-HCl (pH 7.5), 5 mM EDTA, 0.02% PVP, 0.02% Ficoll, 0.2% BSA, 100 mg/ml denatured salmon sperm DNA, 10% (wt/vol) dextran sulfate at 40°C, followed by one or more washes in 2X SSC, 25 mM Tris-HCl (pH 7.4), 5 mM EDTA, and 0.1% SDS at 50°C. Other conditions of low stringency that may be used are well known in the art (*e.g.*, as
15 employed for cross-species hybridizations). See, *e.g.*, Ausubel *et al.* (eds.), 1993, CURRENT PROTOCOLS IN MOLECULAR BIOLOGY, John Wiley & Sons, NY, and Kriegler, 1990, GENE TRANSFER AND EXPRESSION, A LABORATORY MANUAL, Stockton Press, NY; Shilo and Weinberg, 1981, *Proc Natl Acad Sci USA* 78: 6789-6792.

Conservative mutations

20 In addition to naturally-occurring allelic variants of the ORFX sequence that may exist in the population, the skilled artisan will further appreciate that changes can be introduced by mutation into the nucleotide sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), thereby leading to changes in the amino acid sequence of the encoded ORFX protein, without altering the functional ability of the ORFX protein. For example, nucleotide substitutions
25 leading to amino acid substitutions at "non-essential" amino acid residues can be made in the sequence of any of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161). A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of ORFX without altering the biological activity, whereas an "essential" amino acid residue is required for biological activity. For example, amino acid residues that are conserved among the ORFX proteins of the present
30 invention, are predicted to be particularly unamenable to alteration.

Amino acid residues that are conserved among members of an ORFX family members are predicted to be less amenable to alteration. For example, an ORFX protein according to the present invention can contain at least one domain (*e.g.*, as shown in Table 1) that is a typically conserved region in an ORFX family member. As such, these conserved domains are not likely to be amenable to mutation. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved among members of the ORFX family) may not be as essential for activity and thus are more likely to be amenable to alteration.

Another aspect of the invention pertains to nucleic acid molecules encoding ORFX proteins that contain changes in amino acid residues that are not essential for activity. Such ORFX proteins differ in amino acid sequence from any of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet retain biological activity. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 75% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). Preferably, the protein encoded by the nucleic acid is at least about 80% homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), more preferably at least about 90%, 95%, 98%, and most preferably at least about 99% homologous to SEQ ID NO:2.

An isolated nucleic acid molecule encoding a ORFX protein homologous to the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) can be created by introducing one or more nucleotide substitutions, additions or deletions into the corresponding nucleotide sequence, *i.e.* SEQ ID NO:2*n*-1 for the corresponding *n*, such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein.

Mutations can be introduced into SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline,

phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in ORFX is replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of a ORFX coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for ORFX biological activity to identify mutants that retain activity. Following mutagenesis of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), the encoded protein can be expressed by any recombinant technology known in the art and the activity of the protein can be determined.

In one embodiment, a mutant ORFX protein can be assayed for (1) the ability to form protein:protein interactions with other ORFX proteins, other cell-surface proteins, or biologically active portions thereof, (2) complex formation between a mutant ORFX protein and a ORFX receptor; (3) the ability of a mutant ORFX protein to bind to an intracellular target protein or biologically active portion thereof; (*e.g.*, avidin proteins); (4) the ability to bind BRA protein; or (5) the ability to specifically bind an anti-ORFX protein antibody.

Antisense

Another aspect of the invention pertains to isolated antisense nucleic acid molecules that are hybridizable to or complementary to the nucleic acid molecule comprising the nucleotide sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or fragments, analogs or derivatives thereof. An "antisense" nucleic acid comprises a nucleotide sequence that is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the coding strand of a double-stranded cDNA molecule or complementary to an mRNA sequence. In specific aspects, antisense nucleic acid molecules are provided that comprise a sequence complementary to at least about 10, 25, 50, 100, 250 or 500 nucleotides or an entire ORFX coding strand, or to only a portion thereof. Nucleic acid molecules encoding fragments, homologs, derivatives and analogs of a ORFX protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) or antisense nucleic acids complementary to a ORFX nucleic acid sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) are additionally provided.

In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid

residues (*e.g.*, the protein coding region of a human ORFX that corresponds to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161)). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding ORFX. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding ORFX disclosed herein (*e.g.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick or Hoogsteen base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of ORFX mRNA, but more preferably is an oligonucleotide that is antisense to only a portion of the coding or noncoding region of ORFX mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of ORFX mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis or enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used.

Examples of modified nucleotides that can be used to generate the antisense nucleic acid include: 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxymethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine, 2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil,

3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a subject or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding a ORFX protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule that binds to DNA duplexes, through specific interactions in the major groove of the double helix. An example of a route of administration of antisense nucleic acid molecules of the invention includes direct injection at a tissue site. Alternatively, antisense nucleic acid molecules can be modified to target selected cells and then administered systemically. For example, for systemic administration, antisense molecules can be modified such that they specifically bind to receptors or antigens expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecules to peptides or antibodies that bind to cell surface receptors or antigens. The antisense nucleic acid molecules can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong pol II or pol III promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α -anomeric nucleic acid molecule. An α -anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β -units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids Res* 15: 6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res* 15: 6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett* 215: 327-330).

Ribozymes and PNA moieties

Such modifications include, by way of nonlimiting example, modified bases, and nucleic acids whose sugar phosphate backbones are modified or derivatized. These modifications are

carried out at least in part to enhance the chemical stability of the modified nucleic acid, such that they may be used, for example, as antisense binding nucleic acids in therapeutic applications in a subject.

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme.

- 5 Ribozymes are catalytic RNA molecules with ribonuclease activity that are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave ORFX mRNA transcripts to thereby inhibit translation of ORFX mRNA. A ribozyme having specificity for a ORFX-encoding
- 10 nucleic acid can be designed based upon the nucleotide sequence of a ORFX DNA disclosed herein (*i.e.*, SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161)). For example, a derivative of a Tetrahymena L-19 IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in a ORFX-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Pat. No. 4,987,071; and Cech *et al.* U.S. Pat. No. 5,116,742.
- 15 Alternatively, ORFX mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel *et al.*, (1993) *Science* 261:1411-1418.

- Alternatively, ORFX gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of the ORFX (*e.g.*, the ORFX promoter and/or
- 20 enhancers) to form triple helical structures that prevent transcription of the ORFX gene in target cells. See generally, Helene. (1991) *Anticancer Drug Des.* 6: 569-84; Helene. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher (1992) *Bioassays* 14: 807-15.

- In various embodiments, the nucleic acids of ORFX can be modified at the base moiety, sugar moiety or phosphate backbone to improve, *e.g.*, the stability, hybridization, or solubility of
- 25 the molecule. For example, the deoxyribose phosphate backbone of the nucleic acids can be modified to generate peptide nucleic acids (see Hyrup *et al.* (1996) *Bioorg Med Chem* 4: 5-23). As used herein, the terms "peptide nucleic acids" or "PNAs" refer to nucleic acid mimics, *e.g.*, DNA mimics, in which the deoxyribose phosphate backbone is replaced by a pseudopeptide backbone and only the four natural nucleobases are retained. The neutral backbone of PNAs has
- 30 been shown to allow for specific hybridization to DNA and RNA under conditions of low ionic strength. The synthesis of PNA oligomers can be performed using standard solid phase peptide

synthesis protocols as described in Hyrup *et al.* (1996) above; Perry-O'Keefe *et al.* (1996) *PNAS* 93: 14670-675.

PNAs of ORFX can be used in therapeutic and diagnostic applications. For example, PNAs can be used as antisense or antigene agents for sequence-specific modulation of gene expression by, *e.g.*, inducing transcription or translation arrest or inhibiting replication. PNAs of ORFX can also be used, *e.g.*, in the analysis of single base pair mutations in a gene by, *e.g.*, PNA directed PCR clamping; as artificial restriction enzymes when used in combination with other enzymes, *e.g.*, S1 nucleases (Hyrup B. (1996) above); or as probes or primers for DNA sequence and hybridization (Hyrup *et al.* (1996), above; Perry-O'Keefe (1996), above).

In another embodiment, PNAs of ORFX can be modified, *e.g.*, to enhance their stability or cellular uptake, by attaching lipophilic or other helper groups to PNA, by the formation of PNA-DNA chimeras, or by the use of liposomes or other techniques of drug delivery known in the art. For example, PNA-DNA chimeras of ORFX can be generated that may combine the advantageous properties of PNA and DNA. Such chimeras allow DNA recognition enzymes, *e.g.*, RNase H and DNA polymerases, to interact with the DNA portion while the PNA portion would provide high binding affinity and specificity. PNA-DNA chimeras can be linked using linkers of appropriate lengths selected in terms of base stacking, number of bonds between the nucleobases, and orientation (Hyrup (1996) above). The synthesis of PNA-DNA chimeras can be performed as described in Hyrup (1996) above and Finn *et al.* (1996) *Nucl Acids Res* 24: 3357-63. For example, a DNA chain can be synthesized on a solid support using standard phosphoramidite coupling chemistry, and modified nucleoside analogs, *e.g.*, 5'-(4-methoxytrityl)amino-5'-deoxy-thymidine phosphoramidite, can be used between the PNA and the 5' end of DNA (Mag *et al.* (1989) *Nucl Acid Res* 17: 5973-88). PNA monomers are then coupled in a stepwise manner to produce a chimeric molecule with a 5' PNA segment and a 3' DNA segment (Finn *et al.* (1996) above). Alternatively, chimeric molecules can be synthesized with a 5' DNA segment and a 3' PNA segment. See, Petersen *et al.* (1975) *Bioorg Med Chem Lett* 5: 1119-11124.

In other embodiments, the oligonucleotide may include other appended groups such as peptides (*e.g.*, for targeting host cell receptors *in vivo*), or agents facilitating transport across the cell membrane (see, *e.g.*, Letsinger *et al.*, 1989, *Proc. Natl. Acad. Sci. U.S.A.* 86:6553-6556; Lemaitre *et al.*, 1987, *Proc. Natl. Acad. Sci.* 84:648-652; PCT Publication No. W088/09810) or

the blood-brain barrier (see, *e.g.*, PCT Publication No. W089/10134). In addition, oligonucleotides can be modified with hybridization triggered cleavage agents (See, *e.g.*, Krol *et al.*, 1988, *BioTechniques* 6:958-976) or intercalating agents. (See, *e.g.*, Zon, 1988, *Pharm. Res.* 5: 539-549). To this end, the oligonucleotide may be conjugated to another molecule, *e.g.*, a peptide, a hybridization triggered cross-linking agent, a transport agent, a hybridization-triggered cleavage agent, etc.

ORFX polypeptides

The novel protein of the invention includes the ORFX-like protein whose sequence is provided in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). The invention also includes a mutant or variant protein any of whose residues may be changed from the corresponding residue shown in FIG. 1 while still encoding a protein that maintains its ORFX-like activities and physiological functions, or a functional fragment thereof. For example, the invention includes the polypeptides encoded by the variant ORFX nucleic acids described above. In the mutant or variant protein, up to 20% or more of the residues may be so changed.

In general, an ORFX-like variant that preserves ORFX-like function includes any variant in which residues at a particular position in the sequence have been substituted by other amino acids, and further include the possibility of inserting an additional residue or residues between two residues of the parent protein as well as the possibility of deleting one or more residues from the parent sequence. Any amino acid substitution, insertion, or deletion is encompassed by the invention. In favorable circumstances, the substitution is a conservative substitution as defined above. Furthermore, without limiting the scope of the invention, positions of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) may be substituted such that a mutant or variant protein may include one or more substitutions

The invention also includes isolated ORFX proteins, and biologically active portions thereof, or derivatives, fragments, analogs or homologs thereof. Also provided are polypeptide fragments suitable for use as immunogens to raise anti-ORFX antibodies. In one embodiment, native ORFX proteins can be isolated from cells or tissue sources by an appropriate purification scheme using standard protein purification techniques. In another embodiment, ORFX proteins are produced by recombinant DNA techniques. Alternative to recombinant expression, a ORFX

protein or polypeptide can be synthesized chemically using standard peptide synthesis techniques.

An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material or other contaminating proteins from the cell or tissue source from which the ORFX protein is derived, or substantially free from chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of ORFX protein in which the protein is separated from cellular components of the cells from which it is isolated or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of ORFX protein having less than about 30% (by dry weight) of non-ORFX protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-ORFX protein, still more preferably less than about 10% of non-ORFX protein, and most preferably less than about 5% non-ORFX protein. When the ORFX protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation.

The language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein in which the protein is separated from chemical precursors or other chemicals that are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of ORFX protein having less than about 30% (by dry weight) of chemical precursors or non-ORFX chemicals, more preferably less than about 20% chemical precursors or non-ORFX chemicals, still more preferably less than about 10% chemical precursors or non-ORFX chemicals, and most preferably less than about 5% chemical precursors or non-ORFX chemicals.

Biologically active portions of a ORFX protein include peptides comprising amino acid sequences sufficiently homologous to or derived from the amino acid sequence of the ORFX protein, *e.g.*, the amino acid sequence shown in SEQ ID NO:2 that include fewer amino acids than the full length ORFX proteins, and exhibit at least one activity of a ORFX protein. Typically, biologically active portions comprise a domain or motif with at least one activity of the ORFX protein. A biologically active portion of a ORFX protein can be a polypeptide which is, for example, 10, 25, 50, 100 or more amino acids in length.

A biologically active portion of a ORFX protein of the present invention may contain at least one of the above-identified domains conserved between the FGF family of proteins. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the functional activities of a native ORFX protein.

In an embodiment, the ORFX protein has an amino acid sequence shown in any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161). In other embodiments, the ORFX protein is substantially homologous to any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the protein of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161), yet differs in amino acid sequence due to natural allelic variation or mutagenesis, as described in detail below. Accordingly, in another embodiment, the ORFX protein is a protein that comprises an amino acid sequence at least about 45% homologous, and more preferably about 55, 65, 70, 75, 80, 85, 90, 95, 98 or even 99% homologous to the amino acid sequence of any of SEQ ID NO:2*n* (wherein *n* = 1 to 3161) and retains the functional activity of the ORFX proteins of the corresponding polypeptide having the sequence of SEQ ID NO:2*n* (wherein *n* = 1 to 3161).

Determining homology between two or more sequences

To determine the percent homology of two amino acid sequences or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in either of the sequences being compared for optimal alignment between the sequences). The amino acid residues or nucleotides at corresponding amino acid positions or nucleotide positions are then compared. When a position in the first sequence is occupied by the same amino acid residue or nucleotide as the corresponding position in the second sequence, then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity").

The nucleic acid sequence homology may be determined as the degree of identity between two sequences. The homology may be determined using computer programs known in the art, such as GAP software provided in the GCG program package. See, *Needleman and Wunsch* 1970 *J Mol Biol* 48: 443-453. Using GCG GAP software with the following settings for nucleic acid sequence comparison: GAP creation penalty of 5.0 and GAP extension penalty of 0.3, the coding region of the analogous nucleic acid sequences referred to above exhibits a

degree of identity preferably of at least 70%, 75%, 80%, 85%, 90%, 95%, 98%, or 99%, with the CDS (encoding) part of the DNA sequence shown in SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161).

The term "sequence identity" refers to the degree to which two polynucleotide or polypeptide sequences are identical on a residue-by-residue basis over a particular region of comparison. The term "percentage of sequence identity" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical nucleic acid base (*e.g.*, A, T, C, G, U, or I, in the case of nucleic acids) occurs in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of sequence identity. The term "substantial identity" as used herein denotes a characteristic of a polynucleotide sequence, wherein the polynucleotide comprises a sequence that has at least 80 percent sequence identity, preferably at least 85 percent identity and often 90 to 95 percent sequence identity, more usually at least 99 percent sequence identity as compared to a reference sequence over a comparison region. The term "percentage of positive residues" is calculated by comparing two optimally aligned sequences over that region of comparison, determining the number of positions at which the identical and conservative amino acid substitutions, as defined above, occur in both sequences to yield the number of matched positions, dividing the number of matched positions by the total number of positions in the region of comparison (*i.e.*, the window size), and multiplying the result by 100 to yield the percentage of positive residues.

Chimeric and fusion proteins

The invention also provides ORFX chimeric or fusion proteins. As used herein, a ORFX "chimeric protein" or "fusion protein" includes a ORFX polypeptide operatively linked to a non-ORFX polypeptide. A "ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to ORFX, whereas a "non-ORFX polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein that is not substantially homologous to the ORFX protein, *e.g.*, a protein that is different from the ORFX protein and that is derived from the same or a different organism. Within a ORFX fusion protein the ORFX polypeptide can correspond to all or a portion of a ORFX protein. In one embodiment, a ORFX fusion protein comprises at least one biologically active portion of a ORFX protein. In another embodiment, a ORFX fusion protein comprises at least two biologically active portions of a

ORFX protein. Within the fusion protein, the term "operatively linked" is intended to indicate that the ORFX polypeptide and the non-ORFX polypeptide are fused in-frame to each other. The non-ORFX polypeptide can be fused to the N-terminus or C-terminus of the ORFX polypeptide.

5 For example, in one embodiment a ORFX fusion protein comprises a ORFX polypeptide operably linked to the extracellular domain of a second protein. Such fusion proteins can be further utilized in screening assays for compounds that modulate ORFX activity (such assays are described in detail below).

10 In another embodiment, the fusion protein is a GST-ORFX fusion protein in which the ORFX sequences are fused to the C-terminus of the GST (i.e., glutathione S-transferase) sequences. Such fusion proteins can facilitate the purification of recombinant ORFX.

15 In yet another embodiment, the fusion protein is a ORFX protein containing a heterologous signal sequence at its N-terminus. For example, the native ORFX signal sequence can be removed and replaced with a signal sequence from another protein. In certain host cells (e.g., mammalian host cells), expression and/or secretion of ORFX can be increased through use of a heterologous signal sequence.

20 In another embodiment, the fusion protein is a ORFX-immunoglobulin fusion protein in which the ORFX sequences comprising one or more domains are fused to sequences derived from a member of the immunoglobulin protein family. The ORFX-immunoglobulin fusion proteins of the invention can be incorporated into pharmaceutical compositions and administered to a subject to inhibit an interaction between a ORFX ligand and a ORFX protein on the surface of a cell, to thereby suppress ORFX-mediated signal transduction *in vivo*. In one nonlimiting example, a contemplated ORFX ligand of the invention is an ORFX receptor. The ORFX-immunoglobulin fusion proteins can be used to modulate the bioavailability of a ORFX cognate ligand. Inhibition of the ORFX ligand/ORFX interaction may be useful therapeutically for both the treatment of proliferative and differentiative disorders, as well as modulating (e.g., promoting or inhibiting) cell survival. Moreover, the ORFX-immunoglobulin fusion proteins of the invention can be used as immunogens to produce anti-ORFX antibodies in a subject, to purify ORFX ligands, and in screening assays to identify molecules that inhibit the interaction of
30 ORFX with a ORFX ligand.

A ORFX chimeric or fusion protein of the invention can be produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, *e.g.*, by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor primers that give rise to complementary overhangs between two consecutive gene fragments that can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, Ausubel et al. (eds.) *CURRENT PROTOCOLS IN MOLECULAR BIOLOGY*, John Wiley & Sons, 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). A ORFX-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the ORFX protein.

ORFX agonists and antagonists

The present invention also pertains to variants of the ORFX proteins that function as either ORFX agonists (mimetics) or as ORFX antagonists. Variants of the ORFX protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the ORFX protein. An agonist of the ORFX protein can retain substantially the same, or a subset of, the biological activities of the naturally occurring form of the ORFX protein. An antagonist of the ORFX protein can inhibit one or more of the activities of the naturally occurring form of the ORFX protein by, for example, competitively binding to a downstream or upstream member of a cellular signaling cascade which includes the ORFX protein. Thus, specific biological effects can be elicited by treatment with a variant of limited function. In one embodiment, treatment of a subject with a variant having a subset of the biological activities of the naturally occurring form of the protein has fewer side effects in a subject relative to treatment with the naturally occurring form of the ORFX proteins.

Variants of the ORFX protein that function as either ORFX agonists (mimetics) or as ORFX antagonists can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the ORFX protein for ORFX protein agonist or antagonist activity. In one

embodiment, a variegated library of ORFX variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of ORFX variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential ORFX sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (e.g., for phage display) containing the set of ORFX sequences therein. There are a variety of methods which can be used to produce libraries of potential ORFX variants from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential ORFX sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, e.g., Narang (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu Rev Biochem* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucl Acid Res* 11:477).

Polypeptide libraries

In addition, libraries of fragments of the ORFX protein coding sequence can be used to generate a variegated population of ORFX fragments for screening and subsequent selection of variants of a ORFX protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of a ORFX coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA that can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal and internal fragments of various sizes of the ORFX protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of ORFX proteins. The most widely used techniques, which are amenable to high throughput analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors,

transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique that enhances the frequency of functional mutants in the libraries, can
5 be used in combination with the screening assays to identify ORFX variants (Arkin and Yourvan (1992) PNAS 89:7811-7815; Delgrave *et al.* (1993) Protein Engineering 6:327-331).

Anti-ORFX Antibodies

The invention further encompasses antibodies and antibody fragments, such as F_{ab} or $(F_{ab})_2$, that bind immunospecifically to any of the proteins of the invention.

10 An isolated ORFX protein, or a portion or fragment thereof, can be used as an immunogen to generate antibodies that bind ORFX using standard techniques for polyclonal and monoclonal antibody preparation. Full-length ORFX protein can be used. Alternatively, the invention provides antigenic peptide fragments of ORFX for use as immunogens. The antigenic peptide of ORFX comprises at least 4 amino acid residues of the amino acid sequence shown in
15 any of SEQ ID NO:2n (wherein n = 1 to 3161). The antigenic peptide encompasses an epitope of ORFX such that an antibody raised against the peptide forms a specific immune complex with ORFX. The antigenic peptide may comprise at least 6 aa residues, at least 8 aa residues, at least 10 aa residues, at least 15 aa residues, at least 20 aa residues, or at least 30 aa residues. In one embodiment of the invention, the antigenic peptide comprises a polypeptide comprising at least 6
20 contiguous amino acids of any of SEQ ID NO:2n (wherein n = 1 to 3161).

In an embodiment of the invention, epitopes encompassed by the antigenic peptide are regions of ORFX that are located on the surface of the protein, *e.g.*, hydrophilic regions. As a means for targeting antibody production, hydropathy plots showing regions of hydrophilicity and hydrophobicity may be generated by any method well known in the art, including, for example,
25 the Kyte Doolittle or the Hopp Woods methods, either with or without Fourier transformation. See, *e.g.*, Hopp and Woods, 1981, Proc. Nat. Acad. Sci. USA 78: 3824-3828; Kyte and Doolittle 1982, J. Mol. Biol. 157: 105-142, each incorporated herein by reference in their entirety.

As disclosed herein, an ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161), or derivatives, fragments, analogs or homologs thereof, may be utilized as
30 immunogens in the generation of antibodies that immunospecifically-bind these protein components. The term "antibody" as used herein refers to immunoglobulin molecules and

immunologically active portions of immunoglobulin molecules, i.e., molecules that contain an antigen binding site that specifically binds (immunoreacts with) an antigen, such as ORFX. Such antibodies include, but are not limited to, polyclonal, monoclonal, chimeric, single chain, F_{ab} and $F_{(ab)}_2$ fragments, and an F_{ab} expression library. In a specific embodiment, antibodies to human ORFX proteins are disclosed. Various procedures known within the art may be used for the production of polyclonal or monoclonal antibodies to a ORFX protein sequence of any of SEQ ID NO:2n (wherein n = 1 to 3161) or derivative, fragment, analog or homolog thereof. Some of these proteins are discussed below.

For the production of polyclonal antibodies, various suitable host animals (e.g., rabbit, goat, mouse or other mammal) may be immunized by injection with the native protein, or a synthetic variant thereof, or a derivative of the foregoing. An appropriate immunogenic preparation can contain, for example, recombinantly expressed ORFX protein or a chemically synthesized ORFX polypeptide. The preparation can further include an adjuvant. Various adjuvants used to increase the immunological response include, but are not limited to, Freund's (complete and incomplete), mineral gels (e.g., aluminum hydroxide), surface active substances (e.g., lysolecithin, pluronic polyols, polyanions, peptides, oil emulsions, dinitrophenol, etc.), human adjuvants such as *Bacille Calmette-Guerin* and *Corynebacterium parvum*, or similar immunostimulatory agents. If desired, the antibody molecules directed against ORFX can be isolated from the mammal (e.g., from the blood) and further purified by well known techniques, such as protein A chromatography to obtain the IgG fraction.

The term "monoclonal antibody" or "monoclonal antibody composition", as used herein, refers to a population of antibody molecules that contain only one species of an antigen binding site capable of immunoreacting with a particular epitope of ORFX. A monoclonal antibody composition thus typically displays a single binding affinity for a particular ORFX protein with which it immunoreacts. For preparation of monoclonal antibodies directed towards a particular ORFX protein, or derivatives, fragments, analogs or homologs thereof, any technique that provides for the production of antibody molecules by continuous cell line culture may be utilized. Such techniques include, but are not limited to, the hybridoma technique (see Kohler & Milstein, 1975 *Nature* 256: 495-497); the trioma technique; the human B-cell hybridoma technique (see Kozbor, *et al.*, 1983 *Immunol Today* 4: 72) and the EBV hybridoma technique to produce human monoclonal antibodies (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND

CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Human monoclonal antibodies may be utilized in the practice of the present invention and may be produced by using human hybridomas (see Cote, *et al.*, 1983. *Proc Natl Acad Sci USA* 80: 2026-2030) or by transforming human B-cells with Epstein Barr Virus *in vitro* (see Cole, *et al.*, 1985 In: MONOCLONAL ANTIBODIES AND
5 CANCER THERAPY, Alan R. Liss, Inc., pp. 77-96). Each of the above citations are incorporated herein by reference in their entirety

According to the invention, techniques can be adapted for the production of single-chain antibodies specific to a ORFX protein (see *e.g.*, U.S. Patent No. 4,946,778). In addition, methods can be adapted for the construction of F_{ab} expression libraries (see *e.g.*, Huse, *et al.*,
10 1989 *Science* 246: 1275-1281) to allow rapid and effective identification of monoclonal F_{ab} fragments with the desired specificity for a ORFX protein or derivatives, fragments, analogs or homologs thereof. Non-human antibodies can be "humanized" by techniques well known in the art. See *e.g.*, U.S. Patent No. 5,225,539. Each of the above citations are incorporated herein by reference. Antibody fragments that contain the idiotypes to a ORFX protein may be produced by
15 techniques known in the art including, but not limited to: (i) an F_{(ab)₂} fragment produced by pepsin digestion of an antibody molecule; (ii) an F_{ab} fragment generated by reducing the disulfide bridges of an F_{(ab)₂} fragment; (iii) an F_{ab} fragment generated by the treatment of the antibody molecule with papain and a reducing agent and (iv) F_v fragments.

Additionally, recombinant anti-ORFX antibodies, such as chimeric and humanized
20 monoclonal antibodies, comprising both human and non-human portions, which can be made using standard recombinant DNA techniques, are within the scope of the invention. Such chimeric and humanized monoclonal antibodies can be produced by recombinant DNA techniques known in the art, for example using methods described in PCT International Application No. PCT/US86/02269; European Patent Application No. 184,187; European Patent
25 Application No. 171,496; European Patent Application No. 173,494; PCT International Publication No. WO 86/01533; U.S. Pat. No. 4,816,567; European Patent Application No. 125,023; Better *et al.* (1988) *Science* 240:1041-1043; Liu *et al.* (1987) *PNAS* 84:3439-3443; Liu *et al.* (1987) *J Immunol.* 139:3521-3526; Sun *et al.* (1987) *PNAS* 84:214-218; Nishimura *et al.* (1987) *Cancer Res* 47:999-1005; Wood *et al.* (1985) *Nature* 314:446-449; Shaw *et al.* (1988), *J.*
30 *Natl Cancer Inst* 80:1553-1559; Morrison (1985) *Science* 229:1202-1207; Oi *et al.* (1986) *BioTechniques* 4:214; U.S. Pat. No. 5,225,539; Jones *et al.* (1986) *Nature* 321:552-525;

Verhoeyan *et al.* (1988) *Science* 239:1534; and Beidler *et al.* (1988) *J Immunol* 141:4053-4060. Each of the above citations are incorporated herein by reference.

In one embodiment, methods for the screening of antibodies that possess the desired specificity include, but are not limited to, enzyme-linked immunosorbent assay (ELISA) and other immunologically-mediated techniques known within the art. In a specific embodiment, selection of antibodies that are specific to a particular domain of a ORFX protein is facilitated by generation of hybridomas that bind to the fragment of a ORFX protein possessing such a domain. Antibodies that are specific for one or more domains within a ORFX protein, *e.g.*, the domain spanning the first fifty amino-terminal residues specific to ORFX when compared to FGF-9, or derivatives, fragments, analogs or homologs thereof, are also provided herein.

Anti-ORFX antibodies may be used in methods known within the art relating to the localization and/or quantitation of a ORFX protein (*e.g.*, for use in measuring levels of the ORFX protein within appropriate physiological samples, for use in diagnostic methods, for use in imaging the protein, and the like). In a given embodiment, antibodies for ORFX proteins, or derivatives, fragments, analogs or homologs thereof, that contain the antibody derived binding domain, are utilized as pharmacologically-active compounds [hereinafter "Therapeutics"].

An anti-ORFX antibody (*e.g.*, monoclonal antibody) can be used to isolate ORFX by standard techniques, such as affinity chromatography or immunoprecipitation. An anti-ORFX antibody can facilitate the purification of natural ORFX from cells and of recombinantly produced ORFX expressed in host cells. Moreover, an anti-ORFX antibody can be used to detect ORFX protein (*e.g.*, in a cellular lysate or cell supernatant) in order to evaluate the abundance and pattern of expression of the ORFX protein. Anti-ORFX antibodies can be used diagnostically to monitor protein levels in tissue as part of a clinical testing procedure, *e.g.*, to, for example, determine the efficacy of a given treatment regimen. Detection can be facilitated by coupling (*i.e.*, physically linking) the antibody to a detectable substance. Examples of detectable substances include various enzymes, prosthetic groups, fluorescent materials, luminescent materials, bioluminescent materials, and radioactive materials. Examples of suitable enzymes include horseradish peroxidase, alkaline phosphatase, β -galactosidase, or acetylcholinesterase; examples of suitable prosthetic group complexes include streptavidin/biotin and avidin/biotin; examples of suitable fluorescent materials include umbelliferone, fluorescein, fluorescein isothiocyanate, rhodamine, dichlorotriazinylamine fluorescein, dansyl chloride or

phycoerythrin; an example of a luminescent material includes luminol; examples of bioluminescent materials include luciferase, luciferin, and aequorin, and examples of suitable radioactive material include ^{125}I , ^{131}I , ^{35}S or ^3H .

ORFX Recombinant Vectors and Host Cells

5 Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding ORFX protein, or derivatives, fragments, analogs or homologs thereof. As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can
10 be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are
15 replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the
20 invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the
25 recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, that is operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner that allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation
30 system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements

(*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Regulatory sequences include those that direct constitutive expression of a nucleotide sequence in many types of host cell and those that direct expression of the nucleotide sequence only in certain host cells (*e.g.*, tissue-specific regulatory sequences). It will be appreciated by those skilled in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, ORFX proteins, mutant forms of ORFX, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of ORFX in prokaryotic or eukaryotic cells. For example, ORFX can be expressed in bacterial cells such as *E. coli*, insect cells (using baculovirus expression vectors) yeast cells or mammalian cells. Suitable host cells are discussed further in Goeddel, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out in *E. coli* with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein. Such fusion vectors typically serve three purposes: (1) to increase expression of recombinant protein; (2) to increase the solubility of the recombinant protein; and (3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase. Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith and Johnson (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, Mass.) and pRIT5 (Pharmacia, Piscataway, N.J.) that fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amrann *et al.*, (1988) *Gene* 69:301-315) and pET 11d (Studier *et al.*, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 60-89).

5 One strategy to maximize recombinant protein expression in *E. coli* is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein. See, Gottesman, GENE EXPRESSION TECHNOLOGY: METHODS IN ENZYMOLOGY 185, Academic Press, San Diego, Calif. (1990) 119-128. Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons
10 for each amino acid are those preferentially utilized in *E. coli* (Wada *et al.*, (1992) *Nucleic Acids Res.* 20:2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the ORFX expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*,
15 (1987) *EMBO J* 6:229-234), pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), pYES2 (Invitrogen Corporation, San Diego, Calif.), and picZ (Invitrogen Corp, San Diego, Calif.).

Alternatively, ORFX can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*,
20 SF9 cells) include the pAc series (Smith *et al.* (1983) *Mol Cell Biol* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J*
25 6: 187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells. See, *e.g.*, Chapters 16 and 17 of Sambrook *et al.*, MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory,
30 Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv Immunol* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Pat. No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, *e.g.*, the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α -fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner that allows for expression (by transcription of the DNA molecule) of an RNA molecule that is antisense to ORFX mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen that direct the continuous expression of the antisense RNA molecule in a variety of cell types, for instance viral promoters and/or enhancers, or regulatory sequences can be chosen that direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub *et al.*, "Antisense RNA as a molecular tool for genetic analysis," Reviews—Trends in Genetics, Vol. 1(1) 1986.

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant

host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, ORFX protein can be expressed in bacterial cells such as *E. coli*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those skilled in the art.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (MOLECULAR CLONING: A LABORATORY MANUAL. 2nd ed., Cold Spring Harbor Laboratory, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y., 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Various selectable markers include those that confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding ORFX or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) ORFX protein. Accordingly, the invention further provides methods for producing ORFX protein using the host cells of the invention. In one embodiment,

the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding ORFX has been introduced) in a suitable medium such that ORFX protein is produced. In another embodiment, the method further comprises isolating ORFX from the medium or the host cell.

5 **Transgenic animals**

The host cells of the invention can also be used to produce nonhuman transgenic animals. For example, in one embodiment, a host cell of the invention is a fertilized oocyte or an embryonic stem cell into which ORFX-coding sequences have been introduced. Such host cells can then be used to create non-human transgenic animals in which exogenous ORFX sequences
10 have been introduced into their genome or homologous recombinant animals in which endogenous ORFX sequences have been altered. Such animals are useful for studying the function and/or activity of ORFX and for identifying and/or evaluating modulators of ORFX activity. As used herein, a "transgenic animal" is a non-human animal, preferably a mammal, more preferably a rodent such as a rat or mouse, in which one or more of the cells of the animal
15 includes a transgene. Other examples of transgenic animals include non-human primates, sheep, dogs, cows, goats, chickens, amphibians, etc. A transgene is exogenous DNA that is integrated into the genome of a cell from which a transgenic animal develops and that remains in the genome of the mature animal, thereby directing the expression of an encoded gene product in one or more cell types or tissues of the transgenic animal. As used herein, a "homologous
20 recombinant animal" is a non-human animal, preferably a mammal, more preferably a mouse, in which an endogenous ORFX gene has been altered by homologous recombination between the endogenous gene and an exogenous DNA molecule introduced into a cell of the animal, *e.g.*, an embryonic cell of the animal, prior to development of the animal.

A transgenic animal of the invention can be created by introducing ORFX-encoding
25 nucleic acid into the male pronuclei of a fertilized oocyte, *e.g.*, by microinjection, retroviral infection, and allowing the oocyte to develop in a pseudopregnant female foster animal. The human ORFX DNA sequence of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) can be introduced as a transgene into the genome of a non-human animal. Alternatively, a nonhuman homologue of the human ORFX gene, such as a mouse ORFX gene, can be isolated based on hybridization to
30 the human ORFX cDNA (described further above) and used as a transgene. Intronic sequences and polyadenylation signals can also be included in the transgene to increase the efficiency of

expression of the transgene. A tissue-specific regulatory sequence(s) can be operably linked to the ORFX transgene to direct expression of ORFX protein to particular cells. Methods for generating transgenic animals via embryo manipulation and microinjection, particularly animals such as mice, have become conventional in the art and are described, for example, in U.S. Pat. Nos. 4,736,866; 4,870,009; and 4,873,191; and Hogan 1986, In: MANIPULATING THE MOUSE EMBRYO, Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N.Y. Similar methods are used for production of other transgenic animals. A transgenic founder animal can be identified based upon the presence of the ORFX transgene in its genome and/or expression of ORFX mRNA in tissues or cells of the animals. A transgenic founder animal can then be used to breed additional animals carrying the transgene. Moreover, transgenic animals carrying a transgene encoding ORFX can further be bred to other transgenic animals carrying other transgenes.

To create a homologous recombinant animal, a vector is prepared which contains at least a portion of a ORFX gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the ORFX gene. The ORFX gene can be a human gene (*e.g.*, SEQ ID NO:2n-1 (wherein $n = 1$ to 3161)), but more preferably, is a non-human homologue of a human ORFX gene. For example, a mouse homologue of human ORFX gene of SEQ ID NO:2n-1 (wherein $n = 1$ to 3161) can be used to construct a homologous recombination vector suitable for altering an endogenous ORFX gene in the mouse genome. In one embodiment, the vector is designed such that, upon homologous recombination, the endogenous ORFX gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector).

Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous ORFX gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous ORFX protein). In the homologous recombination vector, the altered portion of the ORFX gene is flanked at its 5' and 3' ends by additional nucleic acid of the ORFX gene to allow for homologous recombination to occur between the exogenous ORFX gene carried by the vector and an endogenous ORFX gene in an embryonic stem cell. The additional flanking ORFX nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector. See *e.g.*, Thomas *et al.* (1987) *Cell* 51:503 for a description of

homologous recombination vectors. The vector is introduced into an embryonic stem cell line (e.g., by electroporation) and cells in which the introduced ORFX gene has homologously recombined with the endogenous ORFX gene are selected (see e.g., Li *et al.* (1992) *Cell* 69:915).

The selected cells are then injected into a blastocyst of an animal (e.g., a mouse) to form aggregation chimeras. See e.g., Bradley 1987, In: TERATOCARCINOMAS AND EMBRYONIC STEM CELLS: A PRACTICAL APPROACH, Robertson, ed. IRL, Oxford, pp. 113-152. A chimeric embryo can then be implanted into a suitable pseudopregnant female foster animal and the embryo brought to term. Progeny harboring the homologously recombined DNA in their germ cells can be used to breed animals in which all cells of the animal contain the homologously recombined DNA by germline transmission of the transgene. Methods for constructing homologous recombination vectors and homologous recombinant animals are described further in Bradley (1991) *Curr Opin Biotechnol* 2:823-829; PCT International Publication Nos.: WO 90/11354; WO 91/01140; WO 92/0968; and WO 93/04169.

In another embodiment, transgenic non-humans animals can be produced that contain selected systems that allow for regulated expression of the transgene. One example of such a system is the cre/loxP recombinase system of bacteriophage P1. For a description of the cre/loxP recombinase system, see, e.g., Lakso *et al.* (1992) *PNAS* 89:6232-6236. Another example of a recombinase system is the FLP recombinase system of *Saccharomyces cerevisiae* (O'Gorman *et al.* (1991) *Science* 251:1351-1355. If a cre/loxP recombinase system is used to regulate expression of the transgene, animals containing transgenes encoding both the Cre recombinase and a selected protein are required. Such animals can be provided through the construction of "double" transgenic animals, e.g., by mating two transgenic animals, one containing a transgene encoding a selected protein and the other containing a transgene encoding a recombinase.

Clones of the non-human transgenic animals described herein can also be produced according to the methods described in Wilmut *et al.* (1997) *Nature* 385:810-813. In brief, a cell, e.g., a somatic cell, from the transgenic animal can be isolated and induced to exit the growth cycle and enter G₀ phase. The quiescent cell can then be fused, e.g., through the use of electrical pulses, to an enucleated oocyte from an animal of the same species from which the quiescent cell is isolated. The reconstructed oocyte is then cultured such that it develops to morula or blastocyte and then transferred to pseudopregnant female foster animal. The offspring borne of

this female foster animal will be a clone of the animal from which the cell, *e.g.*, the somatic cell, is isolated.

Pharmaceutical Compositions

The ORFX nucleic acid molecules, ORFX proteins, and anti-ORFX antibodies (also referred to herein as "active compounds") of the invention, and derivatives, fragments, analogs and homologs thereof, can be incorporated into pharmaceutical compositions suitable for administration. Such compositions typically comprise the nucleic acid molecule, protein, or antibody and a pharmaceutically acceptable carrier. As used herein, "pharmaceutically acceptable carrier" is intended to include any and all solvents, dispersion media, coatings, antibacterial and antifungal agents, isotonic and absorption delaying agents, and the like, compatible with pharmaceutical administration. Suitable carriers are described in the most recent edition of Remington's Pharmaceutical Sciences, a standard reference text in the field, which is incorporated herein by reference. Preferred examples of such carriers or diluents include, but are not limited to, water, saline, finger's solutions, dextrose solution, and 5% human serum albumin. Liposomes and non-aqueous vehicles such as fixed oils may also be used. The use of such media and agents for pharmaceutically active substances is well known in the art. Except insofar as any conventional media or agent is incompatible with the active compound, use thereof in the compositions is contemplated. Supplementary active compounds can also be incorporated into the compositions.

A pharmaceutical composition of the invention is formulated to be compatible with its intended route of administration. Examples of routes of administration include parenteral, *e.g.*, intravenous, intradermal, subcutaneous, oral (*e.g.*, inhalation), transdermal (topical), transmucosal, and rectal administration. Solutions or suspensions used for parenteral, intradermal, or subcutaneous application can include the following components: a sterile diluent such as water for injection, saline solution, fixed oils, polyethylene glycols, glycerine, propylene glycol or other synthetic solvents; antibacterial agents such as benzyl alcohol or methyl parabens; antioxidants such as ascorbic acid or sodium bisulfite; chelating agents such as ethylenediaminetetraacetic acid; buffers such as acetates, citrates or phosphates, and agents for the adjustment of tonicity such as sodium chloride or dextrose. The pH can be adjusted with acids or bases, such as hydrochloric acid or sodium hydroxide. The parenteral preparation can be enclosed in ampoules, disposable syringes or multiple dose vials made of glass or plastic.

Pharmaceutical compositions suitable for injectable use include sterile aqueous solutions (where water soluble) or dispersions and sterile powders for the extemporaneous preparation of sterile injectable solutions or dispersion. For intravenous administration, suitable carriers include physiological saline, bacteriostatic water, Cremophor EL™ (BASF, Parsippany, N.J.) or phosphate buffered saline (PBS). In all cases, the composition must be sterile and should be fluid to the extent that easy syringeability exists. It must be stable under the conditions of manufacture and storage and must be preserved against the contaminating action of microorganisms such as bacteria and fungi. The carrier can be a solvent or dispersion medium containing, for example, water, ethanol, polyol (for example, glycerol, propylene glycol, and liquid polyethylene glycol, and the like), and suitable mixtures thereof. The proper fluidity can be maintained, for example, by the use of a coating such as lecithin, by the maintenance of the required particle size in the case of dispersion and by the use of surfactants. Prevention of the action of microorganisms can be achieved by various antibacterial and antifungal agents, for example, parabens, chlorobutanol, phenol, ascorbic acid, thimerosal, and the like. In many cases, it will be preferable to include isotonic agents, for example, sugars, polyalcohols such as manitol, sorbitol, sodium chloride in the composition. Prolonged absorption of the injectable compositions can be brought about by including in the composition an agent which delays absorption, for example, aluminum monostearate and gelatin.

Sterile injectable solutions can be prepared by incorporating the active compound (*e.g.*, a ORFX protein or anti-ORFX antibody) in the required amount in an appropriate solvent with one or a combination of ingredients enumerated above, as required, followed by filtered sterilization. Generally, dispersions are prepared by incorporating the active compound into a sterile vehicle that contains a basic dispersion medium and the required other ingredients from those enumerated above. In the case of sterile powders for the preparation of sterile injectable solutions, methods of preparation are vacuum drying and freeze-drying that yields a powder of the active ingredient plus any additional desired ingredient from a previously sterile-filtered solution thereof.

Oral compositions generally include an inert diluent or an edible carrier. They can be enclosed in gelatin capsules or compressed into tablets. For the purpose of oral therapeutic administration, the active compound can be incorporated with excipients and used in the form of tablets, troches, or capsules. Oral compositions can also be prepared using a fluid carrier for use

as a mouthwash, wherein the compound in the fluid carrier is applied orally and swished and expectorated or swallowed. Pharmaceutically compatible binding agents, and/or adjuvant materials can be included as part of the composition. The tablets, pills, capsules, troches and the like can contain any of the following ingredients, or compounds of a similar nature: a binder
5 such as microcrystalline cellulose, gum tragacanth or gelatin; an excipient such as starch or lactose, a disintegrating agent such as alginic acid, Primogel, or corn starch; a lubricant such as magnesium stearate or Sterotes; a glidant such as colloidal silicon dioxide; a sweetening agent such as sucrose or saccharin; or a flavoring agent such as peppermint, methyl salicylate, or orange flavoring.

10 For administration by inhalation, the compounds are delivered in the form of an aerosol spray from pressured container or dispenser which contains a suitable propellant, *e.g.*, a gas such as carbon dioxide, or a nebulizer.

Systemic administration can also be by transmucosal or transdermal means. For transmucosal or transdermal administration, penetrants appropriate to the barrier to be permeated
15 are used in the formulation. Such penetrants are generally known in the art, and include, for example, for transmucosal administration, detergents, bile salts, and fusidic acid derivatives. Transmucosal administration can be accomplished through the use of nasal sprays or suppositories. For transdermal administration, the active compounds are formulated into ointments, salves, gels, or creams as generally known in the art.

20 The compounds can also be prepared in the form of suppositories (*e.g.*, with conventional suppository bases such as cocoa butter and other glycerides) or retention enemas for rectal delivery.

In one embodiment, the active compounds are prepared with carriers that will protect the compound against rapid elimination from the body, such as a controlled release formulation, including implants and microencapsulated delivery systems. Biodegradable, biocompatible
25 polymers can be used, such as ethylene vinyl acetate, polyanhydrides, polyglycolic acid, collagen, polyorthoesters, and polylactic acid. Methods for preparation of such formulations will be apparent to those skilled in the art. The materials can also be obtained commercially from Alza Corporation and Nova Pharmaceuticals, Inc. Liposomal suspensions (including liposomes targeted to infected cells with monoclonal antibodies to viral antigens) can also be used as
30 pharmaceutically acceptable carriers. These can be prepared according to methods known to those skilled in the art, for example, as described in U.S. Pat. No. 4,522,811.

It is especially advantageous to formulate oral or parenteral compositions in dosage unit form for ease of administration and uniformity of dosage. Dosage unit form as used herein refers to physically discrete units suited as unitary dosages for the subject to be treated; each unit containing a predetermined quantity of active compound calculated to produce the desired therapeutic effect in association with the required pharmaceutical carrier. The specification for the dosage unit forms of the invention are dictated by and directly dependent on the unique characteristics of the active compound and the particular therapeutic effect to be achieved.

The nucleic acid molecules of the invention can be inserted into vectors and used as gene therapy vectors. Gene therapy vectors can be delivered to a subject by any of a number of routes, *e.g.*, as described in U.S. Patent Nos. 5,703,055. Delivery can thus also include, *e.g.*, intravenous injection, local administration (see U.S. Pat. No. 5,328,470) or stereotactic injection (see *e.g.*, Chen *et al.* (1994) *PNAS* 91:3054-3057). The pharmaceutical preparation of the gene therapy vector can include the gene therapy vector in an acceptable diluent, or can comprise a slow release matrix in which the gene delivery vehicle is imbedded. Alternatively, where the complete gene delivery vector can be produced intact from recombinant cells, *e.g.*, retroviral vectors, the pharmaceutical preparation can include one or more cells that produce the gene delivery system.

The pharmaceutical compositions can be included in a container, pack, or dispenser together with instructions for administration.

Additional Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, and antibodies described herein can be used in one or more of the following methods: (a) screening assays; (b) detection assays (*e.g.*, chromosomal mapping, cell and tissue typing, forensic biology), (c) predictive medicine (*e.g.*, diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics); and (d) methods of treatment (*e.g.*, therapeutic and prophylactic).

The isolated nucleic acid molecules of the invention can be used to express ORFX protein (*e.g.*, via a recombinant expression vector in a host cell in gene therapy applications), to detect ORFX mRNA (*e.g.*, in a biological sample) or a genetic lesion in a ORFX gene, and to modulate ORFX activity, as described further below. In addition, the ORFX proteins can be used to screen drugs or compounds that modulate the ORFX activity or expression as well as to treat disorders characterized by insufficient or excessive production of ORFX protein, for

example proliferative or differentiative disorders, or production of ORFX protein forms that have decreased or aberrant activity compared to ORFX wild type protein. In addition, the anti-ORFX antibodies of the invention can be used to detect and isolate ORFX proteins and modulate ORFX activity.

5 This invention further pertains to novel agents identified by the above described screening assays and uses thereof for treatments as described herein.

Screening Assays

 The invention provides a method (also referred to herein as a "screening assay") for identifying modulators, *i.e.*, candidate or test compounds or agents (*e.g.*, peptides,
10 peptidomimetics, small molecules or other drugs) that bind to ORFX proteins or have a stimulatory or inhibitory effect on, for example, ORFX expression or ORFX activity.

 In one embodiment, the invention provides assays for screening candidate or test compounds which bind to or modulate the activity of a ORFX protein or polypeptide or biologically active portion thereof. The test compounds of the present invention can be obtained
15 using any of the numerous approaches in combinatorial library methods known in the art, including: biological libraries; spatially addressable parallel solid phase or solution phase libraries; synthetic library methods requiring deconvolution; the "one-bead one-compound" library method; and synthetic library methods using affinity chromatography selection. The biological library approach is limited to peptide libraries, while the other four approaches are
20 applicable to peptide, non-peptide oligomer or small molecule libraries of compounds (Lam (1997) *Anticancer Drug Des* 12:145).

 Examples of methods for the synthesis of molecular libraries can be found in the art, for example in: DeWitt *et al.* (1993) *Proc Natl Acad Sci U.S.A.* 90:6909; Erb *et al.* (1994) *Proc Natl Acad Sci U.S.A.* 91:11422; Zuckermann *et al.* (1994) *J Med Chem* 37:2678; Cho *et al.* (1993)
25 *Science* 261:1303; Carrell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2059; Carell *et al.* (1994) *Angew Chem Int Ed Engl* 33:2061; and Gallop *et al.* (1994) *J Med Chem* 37:1233.

 Libraries of compounds may be presented in solution (*e.g.*, Houghten (1992) *Biotechniques* 13:412-421), or on beads (Lam (1991) *Nature* 354:82-84), on chips (Fodor (1993) *Nature* 364:555-556), bacteria (Ladner U.S. Pat. No. 5,223,409), spores (Ladner USP '409),
30 plasmids (Cull *et al.* (1992) *Proc Natl Acad Sci USA* 89:1865-1869) or on phage (Scott and

Smith (1990) *Science* 249:386-390; Devlin (1990) *Science* 249:404-406; Cwirla *et al.* (1990) *Proc Natl Acad Sci U.S.A.* 87:6378-6382; Felici (1991) *J Mol Biol* 222:301-310; Ladner above.).

In one embodiment, an assay is a cell-based assay in which a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface is contacted with a test compound and the ability of the test compound to bind to a ORFX protein determined. The cell, for example, can of mammalian origin or a yeast cell. Determining the ability of the test compound to bind to the ORFX protein can be accomplished, for example, by coupling the test compound with a radioisotope or enzymatic label such that binding of the test compound to the ORFX protein or biologically active portion thereof can be determined by detecting the labeled compound in a complex. For example, test compounds can be labeled with ^{125}I , ^{35}S , ^{14}C , or ^3H , either directly or indirectly, and the radioisotope detected by direct counting of radioemission or by scintillation counting. Alternatively, test compounds can be enzymatically labeled with, for example, horseradish peroxidase, alkaline phosphatase, or luciferase, and the enzymatic label detected by determination of conversion of an appropriate substrate to product. In one embodiment, the assay comprises contacting a cell which expresses a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or a biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-based assay comprising contacting a cell expressing a membrane-bound form of ORFX protein, or a biologically active portion thereof, on the cell surface with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX or a biologically active portion thereof can be accomplished, for example, by determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule. As used herein, a "target molecule" is a molecule with which a ORFX protein binds or interacts in nature, for example, a molecule on the surface of a cell which expresses a ORFX interacting protein, a molecule on the surface of a second cell, a molecule in the extracellular milieu, a molecule

associated with the internal surface of a cell membrane or a cytoplasmic molecule. A ORFX target molecule can be a non-ORFX molecule or a ORFX protein or polypeptide of the present invention. In one embodiment, a ORFX target molecule is a component of a signal transduction pathway that facilitates transduction of an extracellular signal (*e.g.*, a signal generated by binding
5 of a compound to a membrane-bound ORFX molecule) through the cell membrane and into the cell. The target, for example, can be a second intercellular protein that has catalytic activity or a protein that facilitates the association of downstream signaling molecules with ORFX.

Determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by one of the methods described above for determining direct
10 binding. In one embodiment, determining the ability of the ORFX protein to bind to or interact with a ORFX target molecule can be accomplished by determining the activity of the target molecule. For example, the activity of the target molecule can be determined by detecting induction of a cellular second messenger of the target (*i.e.* intracellular Ca^{2+} , diacylglycerol, IP_3 , etc.), detecting catalytic/enzymatic activity of the target an appropriate substrate, detecting the
15 induction of a reporter gene (comprising a ORFX-responsive regulatory element operatively linked to a nucleic acid encoding a detectable marker, *e.g.*, luciferase), or detecting a cellular response, for example, cell survival, cellular differentiation, or cell proliferation.

In yet another embodiment, an assay of the present invention is a cell-free assay comprising contacting a ORFX protein or biologically active portion thereof with a test
20 compound and determining the ability of the test compound to bind to the ORFX protein or biologically active portion thereof. Binding of the test compound to the ORFX protein can be determined either directly or indirectly as described above. In one embodiment, the assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test
25 compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the test compound to preferentially bind to ORFX or biologically active portion thereof as compared to the known compound.

In another embodiment, an assay is a cell-free assay comprising contacting ORFX protein
30 or biologically active portion thereof with a test compound and determining the ability of the test compound to modulate (*e.g.*, stimulate or inhibit) the activity of the ORFX protein or

biologically active portion thereof. Determining the ability of the test compound to modulate the activity of ORFX can be accomplished, for example, by determining the ability of the ORFX protein to bind to a ORFX target molecule by one of the methods described above for determining direct binding. In an alternative embodiment, determining the ability of the test compound to modulate the activity of ORFX can be accomplished by determining the ability of the ORFX protein further modulate a ORFX target molecule. For example, the catalytic/enzymatic activity of the target molecule on an appropriate substrate can be determined as previously described.

In yet another embodiment, the cell-free assay comprises contacting the ORFX protein or biologically active portion thereof with a known compound which binds ORFX to form an assay mixture, contacting the assay mixture with a test compound, and determining the ability of the test compound to interact with a ORFX protein, wherein determining the ability of the test compound to interact with a ORFX protein comprises determining the ability of the ORFX protein to preferentially bind to or modulate the activity of a ORFX target molecule.

The cell-free assays of the present invention are amenable to use of both the soluble form or the membrane-bound form of ORFX. In the case of cell-free assays comprising the membrane-bound form of ORFX, it may be desirable to utilize a solubilizing agent such that the membrane-bound form of ORFX is maintained in solution. Examples of such solubilizing agents include non-ionic detergents such as n-octylglucoside, n-dodecylglucoside, n-dodecylmaltoside, octanoyl-N-methylglucamide, decanoyl-N-methylglucamide, Triton[®] X-100, Triton[®] X-114, Thesit[®], Isotridecypoly(ethylene glycol ether)_n, N-dodecyl--N,N-dimethyl-3-ammonio-1-propane sulfonate, 3-(3-cholamidopropyl)dimethylamminiol-1-propane sulfonate (CHAPS), or 3-(3-cholamidopropyl)dimethylamminiol-2-hydroxy-1-propane sulfonate (CHAPSO).

In more than one embodiment of the above assay methods of the present invention, it may be desirable to immobilize either ORFX or its target molecule to facilitate separation of complexed from uncomplexed forms of one or both of the proteins, as well as to accommodate automation of the assay. Binding of a test compound to ORFX, or interaction of ORFX with a target molecule in the presence and absence of a candidate compound, can be accomplished in any vessel suitable for containing the reactants. Examples of such vessels include microtiter plates, test tubes, and micro-centrifuge tubes. In one embodiment, a fusion protein can be provided that adds a domain that allows one or both of the proteins to be bound to a matrix. For

example, GST-ORFX fusion proteins or GST-target fusion proteins can be adsorbed onto glutathione sepharose beads (Sigma Chemical, St. Louis, MO) or glutathione derivatized microtiter plates, that are then combined with the test compound or the test compound and either the non-adsorbed target protein or ORFX protein, and the mixture is incubated under conditions conducive to complex formation (*e.g.*, at physiological conditions for salt and pH). Following incubation, the beads or microtiter plate wells are washed to remove any unbound components, the matrix immobilized in the case of beads, complex determined either directly or indirectly, for example, as described above. Alternatively, the complexes can be dissociated from the matrix, and the level of ORFX binding or activity determined using standard techniques.

Other techniques for immobilizing proteins on matrices can also be used in the screening assays of the invention. For example, either ORFX or its target molecule can be immobilized utilizing conjugation of biotin and streptavidin. Biotinylated ORFX or target molecules can be prepared from biotin-NHS (N-hydroxy-succinimide) using techniques well known in the art (*e.g.*, biotinylation kit, Pierce Chemicals, Rockford, Ill.), and immobilized in the wells of streptavidin-coated 96 well plates (Pierce Chemical). Alternatively, antibodies reactive with ORFX or target molecules, but which do not interfere with binding of the ORFX protein to its target molecule, can be derivatized to the wells of the plate, and unbound target or ORFX trapped in the wells by antibody conjugation. Methods for detecting such complexes, in addition to those described above for the GST-immobilized complexes, include immunodetection of complexes using antibodies reactive with the ORFX or target molecule, as well as enzyme-linked assays that rely on detecting an enzymatic activity associated with the ORFX or target molecule.

In another embodiment, modulators of ORFX expression are identified in a method wherein a cell is contacted with a candidate compound and the expression of ORFX mRNA or protein in the cell is determined. The level of expression of ORFX mRNA or protein in the presence of the candidate compound is compared to the level of expression of ORFX mRNA or protein in the absence of the candidate compound. The candidate compound can then be identified as a modulator of ORFX expression based on this comparison. For example, when expression of ORFX mRNA or protein is greater (statistically significantly greater) in the presence of the candidate compound than in its absence, the candidate compound is identified as a stimulator of ORFX mRNA or protein expression. Alternatively, when expression of ORFX mRNA or protein is less (statistically significantly less) in the presence of the candidate

compound than in its absence, the candidate compound is identified as an inhibitor of ORFX mRNA or protein expression. The level of ORFX mRNA or protein expression in the cells can be determined by methods described herein for detecting ORFX mRNA or protein.

5 In yet another aspect of the invention, the ORFX proteins can be used as "bait proteins" in a two-hybrid assay or three hybrid assay (see, *e.g.*, U.S. Pat. No. 5,283,317; Zervos *et al.* (1993) Cell 72:223-232; Madura *et al.* (1993) J Biol Chem 268:12046-12054; Bartel *et al.* (1993) Biotechniques 14:920-924; Iwabuchi *et al.* (1993) Oncogene 8:1693-1696; and Brent WO94/10300), to identify other proteins that bind to or interact with ORFX ("ORFX-binding proteins" or "ORFX-bp") and modulate ORFX activity. Such ORFX-binding proteins are also
10 likely to be involved in the propagation of signals by the ORFX proteins as, for example, upstream or downstream elements of the ORFX pathway.

The two-hybrid system is based on the modular nature of most transcription factors, which consist of separable DNA-binding and activation domains. Briefly, the assay utilizes two different DNA constructs. In one construct, the gene that codes for ORFX is fused to a gene
15 encoding the DNA binding domain of a known transcription factor (*e.g.*, GAL-4). In the other construct, a DNA sequence, from a library of DNA sequences, that encodes an unidentified protein ("prey" or "sample") is fused to a gene that codes for the activation domain of the known transcription factor. If the "bait" and the "prey" proteins are able to interact, *in vivo*, forming a ORFX-dependent complex, the DNA-binding and activation domains of the transcription factor
20 are brought into close proximity. This proximity allows transcription of a reporter gene (*e.g.*, LacZ) that is operably linked to a transcriptional regulatory site responsive to the transcription factor. Expression of the reporter gene can be detected and cell colonies containing the functional transcription factor can be isolated and used to obtain the cloned gene that encodes the protein which interacts with ORFX.

25 This invention further pertains to novel agents identified by the above-described screening assays and uses thereof for treatments as described herein.

Detection Assays

Portions or fragments of the cDNA sequences identified herein (and the corresponding complete gene sequences) can be used in numerous ways as polynucleotide reagents. For
30 example, these sequences can be used to: (i) map their respective genes on a chromosome; and, thus, locate gene regions associated with genetic disease; (ii) identify an individual from a

minute biological sample (tissue typing); and (iii) aid in forensic identification of a biological sample.

The ORFX sequences of the present invention can also be used to identify individuals from minute biological samples. In this technique, an individual's genomic DNA is digested with one or more restriction enzymes, and probed on a Southern blot to yield unique bands for identification. The sequences of the present invention are useful as additional DNA markers for RFLP ("restriction fragment length polymorphisms," described in U.S. Pat. No. 5,272,057).

Furthermore, the sequences of the present invention can be used to provide an alternative technique that determines the actual base-by-base DNA sequence of selected portions of an individual's genome. Thus, the ORFX sequences described herein can be used to prepare two PCR primers from the 5' and 3' ends of the sequences. These primers can then be used to amplify an individual's DNA and subsequently sequence it.

Panels of corresponding DNA sequences from individuals, prepared in this manner, can provide unique individual identifications, as each individual will have a unique set of such DNA sequences due to allelic differences. The sequences of the present invention can be used to obtain such identification sequences from individuals and from tissue. The ORFX sequences of the invention uniquely represent portions of the human genome. Allelic variation occurs to some degree in the coding regions of these sequences, and to a greater degree in the noncoding regions. It is estimated that allelic variation between individual humans occurs with a frequency of about once per each 500 bases. Much of the allelic variation is due to single nucleotide polymorphisms (SNPs), which include restriction fragment length polymorphisms (RFLPs).

Each of the sequences described herein can, to some degree, be used as a standard against which DNA from an individual can be compared for identification purposes. Because greater numbers of polymorphisms occur in the noncoding regions, fewer sequences are necessary to differentiate individuals. The noncoding sequences of SEQ ID NO:2 n -1 (wherein $n = 1$ to 3161), as described above, can comfortably provide positive individual identification with a panel of perhaps 10 to 1,000 primers that each yield a noncoding amplified sequence of 100 bases. If predicted coding sequences are used, a more appropriate number of primers for positive individual identification would be 500-2,000.

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

Use of Partial ORFX Sequences in Forensic Biology

DNA-based identification techniques can also be used in forensic biology. Forensic biology is a scientific field employing genetic typing of biological evidence found at a crime scene as a means for positively identifying, for example, a perpetrator of a crime. To make such an identification, PCR technology can be used to amplify DNA sequences taken from very small biological samples such as tissues, *e.g.*, hair or skin, or body fluids, *e.g.*, blood, saliva, or semen

found at a crime scene. The amplified sequence can then be compared to a standard, thereby allowing identification of the origin of the biological sample.

The sequences of the present invention can be used to provide polynucleotide reagents, *e.g.*, PCR primers, targeted to specific loci in the human genome, that can enhance the reliability of DNA-based forensic identifications by, for example, providing another "identification marker" (*i.e.* another DNA sequence that is unique to a particular individual). As mentioned above, actual base sequence information can be used for identification as an accurate alternative to patterns formed by restriction enzyme generated fragments. Sequences targeted to noncoding regions of SEQ ID NOs: __ are particularly appropriate for this use as greater numbers of polymorphisms occur in the noncoding regions, making it easier to differentiate individuals using this technique. Examples of polynucleotide reagents include the ORFX sequences or portions thereof, *e.g.*, fragments derived from the noncoding regions of one or more of SEQ ID NO:2*n*-1 (where *n* = 1 to 3161), having a length of at least 20 bases, preferably at least 30 bases.

The ORFX sequences described herein can further be used to provide polynucleotide reagents, *e.g.*, labeled or label-able probes that can be used, for example, in an *in situ* hybridization technique, to identify a specific tissue, *e.g.*, brain tissue, etc. This can be very useful in cases where a forensic pathologist is presented with a tissue of unknown origin. Panels of such ORFX probes can be used to identify tissue by species and/or by organ type.

In a similar fashion, these reagents, *e.g.*, ORFX primers or probes can be used to screen tissue culture for contamination (*i.e.* screen for the presence of a mixture of different types of cells in a culture).

Predictive Medicine

The present invention also pertains to the field of predictive medicine in which diagnostic assays, prognostic assays, pharmacogenomics, and monitoring clinical trials are used for prognostic (predictive) purposes to thereby treat an individual prophylactically. Accordingly, one aspect of the present invention relates to diagnostic assays for determining ORFX protein and/or nucleic acid expression as well as ORFX activity, in the context of a biological sample (*e.g.*, blood, serum, cells, tissue) to thereby determine whether an individual is afflicted with a disease or disorder, or is at risk of developing a disorder, associated with aberrant ORFX expression or activity. The invention also provides for prognostic (or predictive) assays for determining whether an individual is at risk of developing a disorder associated with ORFX protein, nucleic

acid expression or activity. For example, mutations in a ORFX gene can be assayed in a biological sample. Such assays can be used for prognostic or predictive purpose to thereby prophylactically treat an individual prior to the onset of a disorder characterized by or associated with ORFX protein, nucleic acid expression or activity.

5 Another aspect of the invention provides methods for determining ORFX protein, nucleic acid expression or ORFX activity in an individual to thereby select appropriate therapeutic or prophylactic agents for that individual (referred to herein as "pharmacogenomics").

Pharmacogenomics allows for the selection of agents (*e.g.*, drugs) for therapeutic or prophylactic treatment of an individual based on the genotype of the individual (*e.g.*, the genotype of the

10 individual examined to determine the ability of the individual to respond to a particular agent.)

Yet another aspect of the invention pertains to monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX in clinical trials.

These and other agents are described in further detail in the following sections.

Diagnostic Assays

15 Other conditions in which proliferation of cells plays a role include tumors, restenosis, psoriasis, Dupuytren's contracture, diabetic complications, Kaposi's sarcoma and rheumatoid arthritis.

An ORFX polypeptide may be used to identify an interacting polypeptide a sample or tissue. The method comprises contacting the sample or tissue with ORFX, allowing formation of
20 a complex between the ORFX polypeptide and the interacting polypeptide, and detecting the complex, if present.

The proteins of the invention may be used to stimulate production of antibodies specifically binding the proteins. Such antibodies may be used in immunodiagnostic procedures to detect the occurrence of the protein in a sample. The proteins of the invention may be used to
25 stimulate cell growth and cell proliferation in conditions in which such growth would be favorable. An example would be to counteract toxic side effects of chemotherapeutic agents on, for example, hematopoiesis and platelet formation, linings of the gastrointestinal tract, and hair follicles. They may also be used to stimulate new cell growth in neurological disorders including, for example, Alzheimer's disease. Alternatively, antagonistic treatments may be
30 administered in which an antibody specifically binding the ORFX-like proteins of the invention

would abrogate the specific growth-inducing effects of the proteins. Such antibodies may be useful, for example, in the treatment of proliferative disorders including various tumors and benign hyperplasias.

Polynucleotides or oligonucleotides corresponding to any one portion of the ORFX
5 nucleic acids of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161) may be used to detect DNA containing a corresponding ORF gene, or detect the expression of a corresponding ORFX gene, or ORFX-like gene. For example, an ORFX nucleic acid expressed in a particular cell or tissue, as noted in Table 2, can be used to identify the presence of that particular cell type.

An exemplary method for detecting the presence or absence of ORFX in a biological
10 sample involves obtaining a biological sample from a test subject and contacting the biological sample with a compound or an agent capable of detecting ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) that encodes ORFX protein such that the presence of ORFX is detected in the biological sample. An agent for detecting ORFX mRNA or genomic DNA is a labeled nucleic acid probe capable of hybridizing to ORFX mRNA or genomic DNA. The nucleic acid
15 probe can be, for example, a full-length ORFX nucleic acid, such as the nucleic acid of SEQ ID NO:2*n*-1 (wherein *n* = 1 to 3161), or a portion thereof, such as an oligonucleotide of at least 15, 30, 50, 100, 250 or 500 nucleotides in length and sufficient to specifically hybridize under stringent conditions to ORFX mRNA or genomic DNA, as described above. Other suitable probes for use in the diagnostic assays of the invention are described herein.

20 An agent for detecting ORFX protein is an antibody capable of binding to ORFX protein, preferably an antibody with a detectable label. Antibodies can be polyclonal, or more preferably, monoclonal. An intact antibody, or a fragment thereof (*e.g.*, Fab or F(ab')₂) can be used. The term "labeled", with regard to the probe or antibody, is intended to encompass direct labeling of the probe or antibody by coupling (*i.e.*, physically linking) a detectable substance to the probe or
25 antibody, as well as indirect labeling of the probe or antibody by reactivity with another reagent that is directly labeled. Examples of indirect labeling include detection of a primary antibody using a fluorescently labeled secondary antibody and end-labeling of a DNA probe with biotin such that it can be detected with fluorescently labeled streptavidin. The term "biological sample" is intended to include tissues, cells and biological fluids isolated from a subject, as well as
30 tissues, cells and fluids present within a subject. That is, the detection method of the invention can be used to detect ORFX mRNA, protein, or genomic DNA in a biological sample *in vitro* as

well as *in vivo*. For example, *in vitro* techniques for detection of ORFX mRNA include Northern hybridizations and *in situ* hybridizations. *In vitro* techniques for detection of ORFX protein include enzyme linked immunosorbent assays (ELISAs), Western blots, immunoprecipitations and immunofluorescence. *In vitro* techniques for detection of ORFX genomic DNA include
5 Southern hybridizations. Furthermore, *in vivo* techniques for detection of ORFX protein include introducing into a subject a labeled anti-ORFX antibody. For example, the antibody can be labeled with a radioactive marker whose presence and location in a subject can be detected by standard imaging techniques.

In one embodiment, the biological sample contains protein molecules from the test
10 subject. Alternatively, the biological sample can contain mRNA molecules from the test subject or genomic DNA molecules from the test subject. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject.

In another embodiment, the methods further involve obtaining a control biological sample from a control subject, contacting the control sample with a compound or agent capable
15 of detecting ORFX protein, mRNA, or genomic DNA, such that the presence of ORFX protein, mRNA or genomic DNA is detected in the biological sample, and comparing the presence of ORFX protein, mRNA or genomic DNA in the control sample with the presence of ORFX protein, mRNA or genomic DNA in the test sample.

The invention also encompasses kits for detecting the presence of ORFX in a biological
20 sample. For example, the kit can comprise: a labeled compound or agent capable of detecting ORFX protein or mRNA in a biological sample; means for determining the amount of ORFX in the sample; and means for comparing the amount of ORFX in the sample with a standard. The compound or agent can be packaged in a suitable container. The kit can further comprise instructions for using the kit to detect ORFX protein or nucleic acid.

25 Prognostic Assays

The diagnostic methods described herein can furthermore be utilized to identify subjects having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. For example, the assays described herein, such as the preceding diagnostic assays or the following assays, can be utilized to identify a subject having or at risk of developing a
30 disorder associated with ORFX protein, nucleic acid expression or activity in, *e.g.*, proliferative or differentiative disorders such as hyperplasias, tumors, restenosis, psoriasis, Dupuytren's

contracture, diabetic complications, or rheumatoid arthritis, etc.; and glia-associated disorders such as cerebral lesions, diabetic neuropathies, cerebral edema, senile dementia, Alzheimer's disease, etc. Alternatively, the prognostic assays can be utilized to identify a subject having or at risk for developing a disease or disorder. Thus, the present invention provides a method for
5 identifying a disease or disorder associated with aberrant ORFX expression or activity in which a test sample is obtained from a subject and ORFX protein or nucleic acid (*e.g.*, mRNA, genomic DNA) is detected, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject having or at risk of developing a disease or disorder associated with aberrant ORFX expression or activity. As used herein, a "test sample" refers to a biological sample obtained
10 from a subject of interest. For example, a test sample can be a biological fluid (*e.g.*, serum), cell sample, or tissue.

Furthermore, the prognostic assays described herein can be used to determine whether a subject can be administered an agent (*e.g.*, an agonist, antagonist, peptidomimetic, protein, peptide, nucleic acid, small molecule, or other drug candidate) to treat a disease or disorder
15 associated with aberrant ORFX expression or activity. For example, such methods can be used to determine whether a subject can be effectively treated with an agent for a disorder, such as a proliferative disorder, differentiative disorder, glia-associated disorders, etc. Thus, the present invention provides methods for determining whether a subject can be effectively treated with an agent for a disorder associated with aberrant ORFX expression or activity in which a test sample
20 is obtained and ORFX protein or nucleic acid is detected (*e.g.*, wherein the presence of ORFX protein or nucleic acid is diagnostic for a subject that can be administered the agent to treat a disorder associated with aberrant ORFX expression or activity.)

The methods of the invention can also be used to detect genetic lesions in a ORFX gene, thereby determining if a subject with the lesioned gene is at risk for, or suffers from, a
25 proliferative disorder, differentiative disorder, glia-associated disorder, etc. In various embodiments, the methods include detecting, in a sample of cells from the subject, the presence or absence of a genetic lesion characterized by at least one of an alteration affecting the integrity of a gene encoding a ORFX-protein, or the mis-expression of the ORFX gene. For example, such genetic lesions can be detected by ascertaining the existence of at least one of (1) a deletion
30 of one or more nucleotides from a ORFX gene; (2) an addition of one or more nucleotides to a ORFX gene; (3) a substitution of one or more nucleotides of a ORFX gene, (4) a chromosomal

rearrangement of a ORFX gene; (5) an alteration in the level of a messenger RNA transcript of a ORFX gene, (6) aberrant modification of a ORFX gene, such as of the methylation pattern of the genomic DNA, (7) the presence of a non-wild type splicing pattern of a messenger RNA transcript of a ORFX gene, (8) a non-wild type level of a ORFX-protein, (9) allelic loss of a ORFX gene, and (10) inappropriate post-translational modification of a ORFX-protein. As described herein, there are a large number of assay techniques known in the art which can be used for detecting lesions in a ORFX gene. A preferred biological sample is a peripheral blood leukocyte sample isolated by conventional means from a subject. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

In certain embodiments, detection of the lesion involves the use of a probe/primer in a polymerase chain reaction (PCR) (see, *e.g.*, U.S. Pat. Nos. 4,683,195 and 4,683,202), such as anchor PCR or RACE PCR, or, alternatively, in a ligation chain reaction (LCR) (see, *e.g.*, Landegran *et al.* (1988) *Science* 241:1077-1080; and Nakazawa *et al.* (1994) *PNAS* 91:360-364), the latter of which can be particularly useful for detecting point mutations in the ORFX-gene (see Abravaya *et al.* (1995) *Nucl Acids Res* 23:675-682). This method can include the steps of collecting a sample of cells from a patient, isolating nucleic acid (*e.g.*, genomic, mRNA or both) from the cells of the sample, contacting the nucleic acid sample with one or more primers that specifically hybridize to a ORFX gene under conditions such that hybridization and amplification of the ORFX gene (if present) occurs, and detecting the presence or absence of an amplification product, or detecting the size of the amplification product and comparing the length to a control sample. It is anticipated that PCR and/or LCR may be desirable to use as a preliminary amplification step in conjunction with any of the techniques used for detecting mutations described herein.

Alternative amplification methods include: self sustained sequence replication (Guatelli *et al.*, 1990, *Proc Natl Acad Sci USA* 87:1874-1878), transcriptional amplification system (Kwoh, *et al.*, 1989, *Proc Natl Acad Sci USA* 86:1173-1177), Q-Beta Replicase (Lizardi *et al.*, 1988, *BioTechnology* 6:1197), or any other nucleic acid amplification method, followed by the detection of the amplified molecules using techniques well known to those of skill in the art. These detection schemes are especially useful for the detection of nucleic acid molecules if such molecules are present in very low numbers.

In an alternative embodiment, mutations in a ORFX gene from a sample cell can be identified by alterations in restriction enzyme cleavage patterns. For example, sample and control DNA is isolated, amplified (optionally), digested with one or more restriction endonucleases, and fragment length sizes are determined by gel electrophoresis and compared.

5 Differences in fragment length sizes between sample and control DNA indicates mutations in the sample DNA. Moreover, the use of sequence specific ribozymes (see, for example, U.S. Pat. No. 5,493,531) can be used to score for the presence of specific mutations by development or loss of a ribozyme cleavage site.

In other embodiments, genetic mutations in ORFX can be identified by hybridizing a
10 sample and control nucleic acids, *e.g.*, DNA or RNA, to high density arrays containing hundreds or thousands of oligonucleotides probes (Cronin *et al.* (1996) *Human Mutation* 7: 244-255; Kozal *et al.* (1996) *Nature Medicine* 2: 753-759). For example, genetic mutations in ORFX can be identified in two dimensional arrays containing light-generated DNA probes as described in Cronin *et al.* above. Briefly, a first hybridization array of probes can be used to scan through
15 long stretches of DNA in a sample and control to identify base changes between the sequences by making linear arrays of sequential overlapping probes. This step allows the identification of point mutations. This step is followed by a second hybridization array that allows the characterization of specific mutations by using smaller, specialized probe arrays complementary to all variants or mutations detected. Each mutation array is composed of parallel probe sets, one
20 complementary to the wild-type gene and the other complementary to the mutant gene.

In yet another embodiment, any of a variety of sequencing reactions known in the art can be used to directly sequence the ORFX gene and detect mutations by comparing the sequence of the sample ORFX with the corresponding wild-type (control) sequence. Examples of sequencing reactions include those based on techniques developed by Maxim and Gilbert (1977) *PNAS*
25 74:560 or Sanger (1977) *PNAS* 74:5463. It is also contemplated that any of a variety of automated sequencing procedures can be utilized when performing the diagnostic assays (Naeve *et al.*, (1995) *Biotechniques* 19:448), including sequencing by mass spectrometry (see, *e.g.*, PCT International Publ. No. WO 94/16101; Cohen *et al.* (1996) *Adv Chromatogr* 36:127-162; and Griffin *et al.* (1993) *Appl Biochem Biotechnol* 38:147-159).

30 Other methods for detecting mutations in the ORFX gene include methods in which protection from cleavage agents is used to detect mismatched bases in RNA/RNA or RNA/DNA

heteroduplexes (Myers *et al.* (1985) *Science* 230:1242). In general, the art technique of "mismatch cleavage" starts by providing heteroduplexes of formed by hybridizing (labeled) RNA or DNA containing the wild-type ORFX sequence with potentially mutant RNA or DNA obtained from a tissue sample. The double-stranded duplexes are treated with an agent that cleaves single-stranded regions of the duplex such as which will exist due to basepair mismatches between the control and sample strands. For instance, RNA/DNA duplexes can be treated with RNase and DNA/DNA hybrids treated with S1 nuclease to enzymatically digesting the mismatched regions. In other embodiments, either DNA/DNA or RNA/DNA duplexes can be treated with hydroxylamine or osmium tetroxide and with piperidine in order to digest mismatched regions. After digestion of the mismatched regions, the resulting material is then separated by size on denaturing polyacrylamide gels to determine the site of mutation. See, for example, Cotton *et al* (1988) *Proc Natl Acad Sci USA* 85:4397; Saleeba *et al* (1992) *Methods Enzymol* 217:286-295. In an embodiment, the control DNA or RNA can be labeled for detection.

In still another embodiment, the mismatch cleavage reaction employs one or more proteins that recognize mismatched base pairs in double-stranded DNA (so called "DNA mismatch repair" enzymes) in defined systems for detecting and mapping point mutations in ORFX cDNAs obtained from samples of cells. For example, the mutY enzyme of *E. coli* cleaves A at G/A mismatches and the thymidine DNA glycosylase from HeLa cells cleaves T at G/T mismatches (Hsu *et al.* (1994) *Carcinogenesis* 15:1657-1662). According to an exemplary embodiment, a probe based on a ORFX sequence, *e.g.*, a wild-type ORFX sequence, is hybridized to a cDNA or other DNA product from a test cell(s). The duplex is treated with a DNA mismatch repair enzyme, and the cleavage products, if any, can be detected from electrophoresis protocols or the like. See, for example, U.S. Pat. No. 5,459,039.

In other embodiments, alterations in electrophoretic mobility will be used to identify mutations in ORFX genes. For example, single strand conformation polymorphism (SSCP) may be used to detect differences in electrophoretic mobility between mutant and wild type nucleic acids (Orita *et al.* (1989) *Proc Natl Acad Sci USA*: 86:2766, see also Cotton (1993) *Mutat Res* 285:125-144; Hayashi (1992) *Genet Anal Tech Appl* 9:73-79). Single-stranded DNA fragments of sample and control ORFX nucleic acids will be denatured and allowed to renature. The secondary structure of single-stranded nucleic acids varies according to sequence, the resulting

alteration in electrophoretic mobility enables the detection of even a single base change. The DNA fragments may be labeled or detected with labeled probes. The sensitivity of the assay may be enhanced by using RNA, rather than DNA, in which the secondary structure is more sensitive to a change in sequence. In one embodiment, the subject method utilizes heteroduplex analysis to separate double stranded heteroduplex molecules on the basis of changes in electrophoretic mobility. See, e.g., Keen *et al.* (1991) *Trends Genet* 7:5.

In yet another embodiment the movement of mutant or wild-type fragments in polyacrylamide gels containing a gradient of denaturant is assayed using denaturing gradient gel electrophoresis (DGGE). See, e.g., Myers *et al.* (1985) *Nature* 313:495. When DGGE is used as the method of analysis, DNA will be modified to insure that it does not completely denature, for example by adding a GC clamp of approximately 40 bp of high-melting GC-rich DNA by PCR. In a further embodiment, a temperature gradient is used in place of a denaturing gradient to identify differences in the mobility of control and sample DNA. See, e.g., Rosenbaum and Reissner (1987) *Biophys Chem* 265:12753.

Examples of other techniques for detecting point mutations include, but are not limited to, selective oligonucleotide hybridization, selective amplification, or selective primer extension. For example, oligonucleotide primers may be prepared in which the known mutation is placed centrally and then hybridized to target DNA under conditions that permit hybridization only if a perfect match is found. See, e.g., Saiki *et al.* (1986) *Nature* 324:163; Saiki *et al.* (1989) *Proc Natl Acad. Sci USA* 86:6230. Such allele specific oligonucleotides are hybridized to PCR amplified target DNA or a number of different mutations when the oligonucleotides are attached to the hybridizing membrane and hybridized with labeled target DNA.

Alternatively, allele specific amplification technology that depends on selective PCR amplification may be used in conjunction with the instant invention. Oligonucleotides used as primers for specific amplification may carry the mutation of interest in the center of the molecule (so that amplification depends on differential hybridization) (Gibbs *et al.* (1989) *Nucleic Acids Res* 17:2437-2448) or at the extreme 3' end of one primer where, under appropriate conditions, mismatch can prevent, or reduce polymerase extension (Prossner (1993) *Tibtech* 11:238). In addition it may be desirable to introduce a novel restriction site in the region of the mutation to create cleavage-based detection. See, e.g., Gasparini *et al.* (1992) *Mol Cell Probes* 6:1. It is anticipated that in certain embodiments amplification may also be performed using Taq ligase

for amplification. See, *e.g.*, Barany (1991) *Proc Natl Acad Sci USA* 88:189. In such cases, ligation will occur only if there is a perfect match at the 3' end of the 5' sequence, making it possible to detect the presence of a known mutation at a specific site by looking for the presence or absence of amplification.

5 The methods described herein may be performed, for example, by utilizing pre-packaged diagnostic kits comprising at least one probe nucleic acid or antibody reagent described herein, which may be conveniently used, *e.g.*, in clinical settings to diagnose patients exhibiting symptoms or family history of a disease or illness involving a ORFX gene.

10 Furthermore, any cell type or tissue, preferably peripheral blood leukocytes, in which ORFX is expressed may be utilized in the prognostic assays described herein. However, any biological sample containing nucleated cells may be used, including, for example, buccal mucosal cells.

Pharmacogenomics

15 Agents, or modulators that have a stimulatory or inhibitory effect on ORFX activity (*e.g.*, ORFX gene expression), as identified by a screening assay described herein can be administered to individuals to treat (prophylactically or therapeutically) disorders (*e.g.*, neurological, cancer-related or gestational disorders) associated with aberrant ORFX activity. In conjunction with such treatment, the pharmacogenomics (*i.e.*, the study of the relationship between an individual's genotype and that individual's response to a foreign compound or drug) of the individual may be
20 considered. Differences in metabolism of therapeutics can lead to severe toxicity or therapeutic failure by altering the relation between dose and blood concentration of the pharmacologically active drug. Thus, the pharmacogenomics of the individual permits the selection of effective agents (*e.g.*, drugs) for prophylactic or therapeutic treatments based on a consideration of the individual's genotype. Such pharmacogenomics can further be used to determine appropriate
25 dosages and therapeutic regimens. Accordingly, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual.

30 Pharmacogenomics deals with clinically significant hereditary variations in the response to drugs due to altered drug disposition and abnormal action in affected persons. See *e.g.*, Eichelbaum, 1996, *Clin Exp Pharmacol Physiol*, 23:983-985 and Linder, 1997, *Clin Chem*, 43:254-266. In general, two types of pharmacogenetic conditions can be differentiated. Genetic

conditions transmitted as a single factor altering the way drugs act on the body (altered drug action) or genetic conditions transmitted as single factors altering the way the body acts on drugs (altered drug metabolism). These pharmacogenetic conditions can occur either as rare defects or as polymorphisms. For example, glucose-6-phosphate dehydrogenase (G6PD) deficiency is a
5 common inherited enzymopathy in which the main clinical complication is haemolysis after ingestion of oxidant drugs (anti-malarials, sulfonamides, analgesics, nitrofurans) and consumption of fava beans.

As an illustrative embodiment, the activity of drug metabolizing enzymes is a major determinant of both the intensity and duration of drug action. The discovery of genetic
10 polymorphisms of drug metabolizing enzymes (*e.g.*, N-acetyltransferase 2 (NAT 2) and cytochrome P450 enzymes CYP2D6 and CYP2C19) has provided an explanation as to why some patients do not obtain the expected drug effects or show exaggerated drug response and serious toxicity after taking the standard and safe dose of a drug. These polymorphisms are expressed in two phenotypes in the population, the extensive metabolizer (EM) and poor
15 metabolizer (PM). The prevalence of PM is different among different populations. For example, the gene coding for CYP2D6 is highly polymorphic and several mutations have been identified in PM, which all lead to the absence of functional CYP2D6. Poor metabolizers of CYP2D6 and CYP2C19 quite frequently experience exaggerated drug response and side effects when they receive standard doses. If a metabolite is the active therapeutic moiety, PM show no therapeutic
20 response, as demonstrated for the analgesic effect of codeine mediated by its CYP2D6-formed metabolite morphine. The other extreme are the so called ultra-rapid metabolizers who do not respond to standard doses. Recently, the molecular basis of ultra-rapid metabolism has been identified to be due to CYP2D6 gene amplification.

Thus, the activity of ORFX protein, expression of ORFX nucleic acid, or mutation
25 content of ORFX genes in an individual can be determined to thereby select appropriate agent(s) for therapeutic or prophylactic treatment of the individual. In addition, pharmacogenetic studies can be used to apply genotyping of polymorphic alleles encoding drug-metabolizing enzymes to the identification of an individual's drug responsiveness phenotype. This knowledge, when applied to dosing or drug selection, can avoid adverse reactions or therapeutic failure and thus
30 enhance therapeutic or prophylactic efficiency when treating a subject with a ORFX modulator, such as a modulator identified by one of the exemplary screening assays described herein.

Monitoring Clinical Efficacy

Monitoring the influence of agents (*e.g.*, drugs, compounds) on the expression or activity of ORFX (*e.g.*, the ability to modulate aberrant cell proliferation and/or differentiation) can be applied in basic drug screening and in clinical trials. For example, the effectiveness of an agent determined by a screening assay as described herein to increase ORFX gene expression, protein levels, or upregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting decreased ORFX gene expression, protein levels, or downregulated ORFX activity.

Alternatively, the effectiveness of an agent determined by a screening assay to decrease ORFX gene expression, protein levels, or downregulate ORFX activity, can be monitored in clinical trials of subjects exhibiting increased ORFX gene expression, protein levels, or upregulated ORFX activity. In such clinical trials, the expression or activity of ORFX and, preferably, other genes that have been implicated in, for example, a proliferative or neurological disorder, can be used as a "read out" or marker of the responsiveness of a particular cell.

For example, genes, including ORFX, that are modulated in cells by treatment with an agent (*e.g.*, compound, drug or small molecule) that modulates ORFX activity (*e.g.*, identified in a screening assay as described herein) can be identified. Thus, to study the effect of agents on cellular proliferation disorders, for example, in a clinical trial, cells can be isolated and RNA prepared and analyzed for the levels of expression of ORFX and other genes implicated in the disorder. The levels of gene expression (*i.e.*, a gene expression pattern) can be quantified by Northern blot analysis or RT-PCR, as described herein, or alternatively by measuring the amount of protein produced, by one of the methods as described herein, or by measuring the levels of activity of ORFX or other genes. In this way, the gene expression pattern can serve as a marker, indicative of the physiological response of the cells to the agent. Accordingly, this response state may be determined before, and at various points during, treatment of the individual with the agent.

In one embodiment, the invention provides a method for monitoring the effectiveness of treatment of a subject with an agent (*e.g.*, an agonist, antagonist, protein, peptide, nucleic acid, peptidomimetic, small molecule, or other drug candidate identified by the screening assays described herein) comprising the steps of (i) obtaining a pre-administration sample from a subject prior to administration of the agent; (ii) detecting the level of expression of a ORFX protein, mRNA, or genomic DNA in the preadministration sample; (iii) obtaining one or more

post-administration samples from the subject; (iv) detecting the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the post-administration samples; (v) comparing the level of expression or activity of the ORFX protein, mRNA, or genomic DNA in the pre-administration sample with the ORFX protein, mRNA, or genomic DNA in the post administration sample or samples; and (vi) altering the administration of the agent to the subject accordingly. For example, increased administration of the agent may be desirable to increase the expression or activity of ORFX to higher levels than detected, *i.e.*, to increase the effectiveness of the agent. Alternatively, decreased administration of the agent may be desirable to decrease expression or activity of ORFX to lower levels than detected, *i.e.*, to decrease the effectiveness of the agent.

Methods of Treatment

The present invention provides for both prophylactic and therapeutic methods of treating a subject at risk of (or susceptible to) a disorder or having a disorder associated with aberrant ORFX expression or activity.

Diseases and disorders that are characterized by increased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that antagonize (*i.e.*, reduce or inhibit) activity. Therapeutics that antagonize activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized include, but are not limited to, (i) a ORFX polypeptide, or analogs, derivatives, fragments or homologs thereof; (ii) antibodies to a ORFX peptide; (iii) nucleic acids encoding a ORFX peptide; (iv) administration of antisense nucleic acid and nucleic acids that are "dysfunctional" (*i.e.*, due to a heterologous insertion within the coding sequences of coding sequences to a ORFX peptide) that are utilized to "knockout" endogenous function of a ORFX peptide by homologous recombination (see, *e.g.*, Capecchi, 1989, *Science* 244: 1288-1292); or (v) modulators (*i.e.*, inhibitors, agonists and antagonists, including additional peptide mimetic of the invention or antibodies specific to a peptide of the invention) that alter the interaction between a ORFX peptide and its binding partner.

Diseases and disorders that are characterized by decreased (relative to a subject not suffering from the disease or disorder) levels or biological activity may be treated with Therapeutics that increase (*i.e.*, are agonists to) activity. Therapeutics that upregulate activity may be administered in a therapeutic or prophylactic manner. Therapeutics that may be utilized

include, but are not limited to, a ORFX peptide, or analogs, derivatives, fragments or homologs thereof; or an agonist that increases bioavailability.

Increased or decreased levels can be readily detected by quantifying peptide and/or RNA, by obtaining a patient tissue sample (*e.g.*, from biopsy tissue) and assaying it *in vitro* for RNA or peptide levels, structure and/or activity of the expressed peptides (or mRNAs of a ORFX peptide). Methods that are well-known within the art include, but are not limited to, immunoassays (*e.g.*, by Western blot analysis, immunoprecipitation followed by sodium dodecyl sulfate (SDS) polyacrylamide gel electrophoresis, immunocytochemistry, etc.) and/or hybridization assays to detect expression of mRNAs (*e.g.*, Northern assays, dot blots, *in situ* hybridization, etc.).

In one aspect, the invention provides a method for preventing, in a subject, a disease or condition associated with an aberrant ORFX expression or activity, by administering to the subject an agent that modulates ORFX expression or at least one ORFX activity. Subjects at risk for a disease that is caused or contributed to by aberrant ORFX expression or activity can be identified by, for example, any or a combination of diagnostic or prognostic assays as described herein. Administration of a prophylactic agent can occur prior to the manifestation of symptoms characteristic of the ORFX aberrancy, such that a disease or disorder is prevented or, alternatively, delayed in its progression. Depending on the type of ORFX aberrancy, for example, a ORFX agonist or ORFX antagonist agent can be used for treating the subject. The appropriate agent can be determined based on screening assays described herein.

Another aspect of the invention pertains to methods of modulating ORFX expression or activity for therapeutic purposes. The modulatory method of the invention involves contacting a cell with an agent that modulates one or more of the activities of ORFX protein activity associated with the cell. An agent that modulates ORFX protein activity can be an agent as described herein, such as a nucleic acid or a protein, a naturally-occurring cognate ligand of a ORFX protein, a peptide, a ORFX peptidomimetic, or other small molecule. In one embodiment, the agent stimulates one or more ORFX protein activity. Examples of such stimulatory agents include active ORFX protein and a nucleic acid molecule encoding ORFX that has been introduced into the cell. In another embodiment, the agent inhibits one or more ORFX protein activity. Examples of such inhibitory agents include antisense ORFX nucleic acid molecules and anti-ORFX antibodies. These modulatory methods can be performed *in vitro*

(*e.g.*, by culturing the cell with the agent) or, alternatively, *in vivo* (*e.g.*, by administering the agent to a subject). As such, the present invention provides methods of treating an individual afflicted with a disease or disorder characterized by aberrant expression or activity of a ORFX protein or nucleic acid molecule. In one embodiment, the method involves administering an agent (*e.g.*, an agent identified by a screening assay described herein), or combination of agents that modulates (*e.g.*, upregulates or downregulates) ORFX expression or activity. In another embodiment, the method involves administering a ORFX protein or nucleic acid molecule as therapy to compensate for reduced or aberrant ORFX expression or activity.

Determination of the Biological Effect of a Therapeutic

In various embodiments of the present invention, suitable *in vitro* or *in vivo* assays are utilized to determine the effect of a specific Therapeutic and whether its administration is indicated for treatment of the affected tissue.

In various specific embodiments, *in vitro* assays may be performed with representative cells of the type(s) involved in the patient's disorder, to determine if a given Therapeutic exerts the desired effect upon the cell type(s). Compounds for use in therapy may be tested in suitable animal model systems including, but not limited to rats, mice, chicken, cows, monkeys, rabbits, and the like, prior to testing in human subjects. Similarly, for *in vivo* testing, any of the animal model system known in the art may be used prior to administration to human subjects.

Malignancies

Some ORFX polypeptides are expressed in cancerous cells (*see, e.g.*, Tables 1 and 2). Accordingly, the corresponding ORF protein is involved in the regulation of cell proliferation. Accordingly, Therapeutics of the present invention may be useful in the therapeutic or prophylactic treatment of diseases or disorders that are associated with cell hyperproliferation and/or loss of control of cell proliferation (*e.g.*, cancers, malignancies and tumors). For a review of such hyperproliferation disorders, *see e.g.*, Fishman, *et al.*, 1985. MEDICINE, 2nd ed., J.B. Lippincott Co., Philadelphia, PA.

Therapeutics of the present invention may be assayed by any method known within the art for efficacy in treating or preventing malignancies and related disorders. Such assays include,

but are not limited to, *in vitro* assays utilizing transformed cells or cells derived from the patient's tumor, as well as *in vivo* assays using animal models of cancer or malignancies. Potentially effective Therapeutics are those that, for example, inhibit the proliferation of tumor-derived or transformed cells in culture or cause a regression of tumors in animal models,
5 in comparison to the controls.

In the practice of the present invention, once a malignancy or cancer has been shown to be amenable to treatment by modulating (*i.e.*, inhibiting, antagonizing or agonizing) activity, that cancer or malignancy may subsequently be treated or prevented by the administration of a Therapeutic that serves to modulate protein function.

10 Premalignant conditions

The Therapeutics of the present invention that are effective in the therapeutic or prophylactic treatment of cancer or malignancies may also be administered for the treatment of pre-malignant conditions and/or to prevent the progression of a pre-malignancy to a neoplastic or malignant state. Such prophylactic or therapeutic use is indicated in conditions known or
15 suspected of preceding progression to neoplasia or cancer, in particular, where non-neoplastic cell growth consisting of hyperplasia, metaplasia or, most particularly, dysplasia has occurred. For a review of such abnormal cell growth see *e.g.*, Robbins & Angell, 1976. BASIC PATHOLOGY, 2nd ed., W.B. Saunders Co., Philadelphia, PA.

Hyperplasia is a form of controlled cell proliferation involving an increase in cell number
20 in a tissue or organ, without significant alteration in its structure or function. For example, it has been demonstrated that endometrial hyperplasia often precedes endometrial cancer. Metaplasia is a form of controlled cell growth in which one type of mature or fully differentiated cell substitutes for another type of mature cell. Metaplasia may occur in epithelial or connective tissue cells. Dysplasia is generally considered a precursor of cancer, and is found mainly in the
25 epithelia. Dysplasia is the most disorderly form of non-neoplastic cell growth, and involves a loss in individual cell uniformity and in the architectural orientation of cells. Dysplasia characteristically occurs where there exists chronic irritation or inflammation, and is often found in the cervix, respiratory passages, oral cavity, and gall bladder.

Alternatively, or in addition to the presence of abnormal cell growth characterized as hyperplasia, metaplasia, or dysplasia, the presence of one or more characteristics of a transformed or malignant phenotype displayed either *in vivo* or *in vitro* within a cell sample derived from a patient, is indicative of the desirability of prophylactic/therapeutic administration of a Therapeutic that possesses the ability to modulate activity of An aforementioned protein. Characteristics of a transformed phenotype include, but are not limited to: (i) morphological changes; (ii) looser substratum attachment; (iii) loss of cell-to-cell contact inhibition; (iv) loss of anchorage dependence; (v) protease release; (vi) increased sugar transport; (vii) decreased serum requirement; (viii) expression of fetal antigens, (ix) disappearance of the 250 kDal cell-surface protein, and the like. See *e.g.*, Richards, *et al.*, 1986. MOLECULAR PATHOLOGY, W.B. Saunders Co., Philadelphia, PA.

In a specific embodiment of the present invention, a patient that exhibits one or more of the following predisposing factors for malignancy is treated by administration of an effective amount of a Therapeutic: (i) a chromosomal translocation associated with a malignancy (*e.g.*, the Philadelphia chromosome (*bcr/abl*) for chronic myelogenous leukemia and t(14;18) for follicular lymphoma, etc.); (ii) familial polyposis or Gardner's syndrome (possible forerunners of colon cancer); (iii) monoclonal gammopathy of undetermined significance (a possible precursor of multiple myeloma) and (iv) a first degree kinship with persons having a cancer or pre-cancerous disease showing a Mendelian (genetic) inheritance pattern (*e.g.*, familial polyposis of the colon, Gardner's syndrome, hereditary exostosis, polyendocrine adenomatosis, Peutz-Jeghers syndrome, neurofibromatosis of Von Recklinghausen, medullary thyroid carcinoma with amyloid production and pheochromocytoma, retinoblastoma, carotid body tumor, cutaneous melanocarcinoma, intraocular melanocarcinoma, xeroderma pigmentosum, ataxia telangiectasia, Chediak-Higashi syndrome, albinism, Fanconi's aplastic anemia and Bloom's syndrome).

In another embodiment, a Therapeutic of the present invention is administered to a human patient to prevent the progression to breast, colon, lung, pancreatic, or uterine cancer, or melanoma or sarcoma.

Hyperproliferative and dysproliferative disorders

In one embodiment of the present invention, a Therapeutic is administered in the therapeutic or prophylactic treatment of hyperproliferative or benign dysproliferative disorders. The efficacy in treating or preventing hyperproliferative diseases or disorders of a Therapeutic of the present invention may be assayed by any method known within the art. Such assays include *in vitro* cell proliferation assays, *in vitro* or *in vivo* assays using animal models of hyperproliferative diseases or disorders, or the like. Potentially effective Therapeutics may, for example, promote cell proliferation in culture or cause growth or cell proliferation in animal models in comparison to controls.

Specific embodiments of the present invention are directed to the treatment or prevention of cirrhosis of the liver (a condition in which scarring has overtaken normal liver regeneration processes); treatment of keloid (hypertrophic scar) formation causing disfiguring of the skin in which the scarring process interferes with normal renewal; psoriasis (a common skin condition characterized by excessive proliferation of the skin and delay in proper cell fate determination); benign tumors; fibrocystic conditions and tissue hypertrophy (*e.g.*, benign prostatic hypertrophy).

Neurodegenerative disorders

Some ORFX proteins are found in cell types have been implicated in the deregulation of cellular maturation and apoptosis, which are both characteristic of neurodegenerative disease. Accordingly, Therapeutics of the invention, particularly but not limited to those that modulate (or supply) activity of an aforementioned protein, may be effective in treating or preventing neurodegenerative disease. Therapeutics of the present invention that modulate the activity of an aforementioned protein involved in neurodegenerative disorders can be assayed by any method known in the art for efficacy in treating or preventing such neurodegenerative diseases and disorders. Such assays include *in vitro* assays for regulated cell maturation or inhibition of apoptosis or *in vivo* assays using animal models of neurodegenerative diseases or disorders, or any of the assays described below. Potentially effective Therapeutics, for example but not by way of limitation, promote regulated cell maturation and prevent cell apoptosis in culture, or reduce neurodegeneration in animal models in comparison to controls.

Disorders related to organ transplantation

Accordingly, once diseases and disorders related to organ transplantation are shown to be amenable to treatment by modulation of activity, such diseases or disorders can be treated or prevented by administration of a Therapeutic that modulates activity.

20 Cardiovascular Disease

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atherosclerosis-associated diseases or disorders. Therapeutics of the invention (particularly Therapeutics that modulate the levels or activity) can be assayed by any method known in the art, including those described below, for efficacy in treating or preventing such diseases and disorders.

5 A vast array of animal and cell culture models exist for processes involved in atherosclerosis. A limited and non-exclusive list of animal models includes knockout mice for premature atherosclerosis (Kurabayashi and Yazaki, 1996, *Int. Angiol.* 15: 187-194), transgenic mouse models of atherosclerosis (Kappel *et al.*, 1994, *FASEB J.* 8: 583-592), antisense oligonucleotide treatment of animal models (Callow, 1995, *Curr. Opin. Cardiol.* 10: 569-576),
10 transgenic rabbit models for atherosclerosis (Taylor, 1997, *Ann. N.Y. Acad. Sci.* 811: 146-152), hypercholesterolemic animal models (Rosenfeld, 1996, *Diabetes Res. Clin. Pract.* 30 Suppl.: 1-11), hyperlipidemic mice (Paigen *et al.*, 1994, *Curr. Opin. Lipidol.* 5: 258-264), and inhibition of lipoxygenase in animals (Sigal *et al.*, 1994, *Ann. N.Y. Acad. Sci.* 714: 211-224). In addition, *in vitro* cell models include but are not limited to monocytes exposed to low density lipoprotein
15 (Frostegard *et al.*, 1996, *Atherosclerosis* 121: 93-103), cloned vascular smooth muscle cells (Suttles *et al.*, 1995, *Exp. Cell Res.* 218: 331-338), endothelial cell-derived chemoattractant exposed T cells (Katz *et al.*, 1994, *J. Leukoc. Biol.* 55: 567-573), cultured human aortic endothelial cells (Farber *et al.*, 1992, *Am. J. Physiol.* 262: H1088-1085), and foam cell cultures (Libby *et al.*, 1996, *Curr Opin Lipidol* 7: 330-335). Potentially effective Therapeutics, for
20 example but not by way of limitation, reduce foam cell formation in cell culture models, or reduce atherosclerotic plaque formation in hypercholesterolemic mouse models of atherosclerosis in comparison to controls.

 Accordingly, once an atherosclerosis-associated disease or disorder has been shown to be amenable to treatment by modulation of activity or formation, that disease or disorder can be
25 treated or prevented by administration of a Therapeutic that modulates activity.

Cytokine and Cell Proliferation/Differentiation Activity

A GENX protein of the present invention may exhibit cytokine, cell proliferation (either inducing or inhibiting) or cell differentiation (either inducing or inhibiting) activity or may induce production of other cytokines in certain cell populations. Many protein factors discovered

to date, including all known cytokines, have exhibited activity in one or more factor dependent cell proliferation assays, and hence the assays serve as a convenient confirmation of cytokine activity. The activity of a protein of the present invention is evidenced by any one of a number of routine factor dependent cell proliferation assays for cell lines including, without limitation, 32D,
5 DA2, DA1G, T10, B9, B9/11, BaF3, MC9/G, M+ (preB M+), 2E8, RB5, DA1, 123, T1165, HT2, CTLL2, TF-1, Mo7e and CMK.

The activity of a protein of the invention may, among other means, be measured by the following methods: Assays for T-cell or thymocyte proliferation include without limitation those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan *et al.*, Greene Publishing
10 Associates and Wiley-Interscience (Chapter 3 and Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bertagnoli *et al.*, *J Immunol* 145:1706-1712, 1990; Bertagnoli *et al.*, *Cell Immunol* 133:327-341, 1991; Bertagnoli, *et al.*, *J Immunol* 149:3778-3783, 1992; Bowman *et al.*, *J Immunol* 152:1756-1761, 1994.

Assays for cytokine production and/or proliferation of spleen cells, lymph node cells or
15 thymocytes include, without limitation, those described by Kruisbeek and Shevach, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1, pp. 3.12.1-14, John Wiley and Sons, Toronto 1994; and by Schreiber, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan eds. Vol 1 pp. 6.8.1-8, John Wiley and Sons, Toronto 1994.

Assays for proliferation and differentiation of hematopoietic and lymphopoietic cells
20 include, without limitation, those described by Bottomly *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.3.1-6.3.12, John Wiley and Sons, Toronto 1991; deVries *et al.*, *J Exp Med* 173:1205-1211, 1991; Moreau *et al.*, *Nature* 336:690-692, 1988; Greenberger *et al.*, *Proc Natl Acad Sci U.S.A.* 80:2931-2938, 1983; Nordan, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.6.1-5, John Wiley and Sons,
25 Toronto 1991; Smith *et al.*, *Proc Natl Acad Sci U.S.A.* 83:1857-1861, 1986; Measurement of human Interleukin 11-Bennett, *et al.* In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.15.1 John Wiley and Sons, Toronto 1991; Ciarletta, *et al.*, In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Vol 1 pp. 6.13.1, John Wiley and Sons, Toronto 1991.

30 Assays for T-cell clone responses to antigens (which will identify, among others, proteins that affect APC-T cell interactions as well as direct T-cell effects by measuring proliferation and

cytokine production) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds., Greene Publishing Associates and Wiley-Interscience (Chapter 3Chapter 6, Chapter 7); Weinberger *et al.*, *Proc Natl Acad Sci USA* 77:6091-6095, 1980; Weinberger *et al.*, *Eur J Immun* 11:405-411, 1981; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988.

Immune Stimulating or Suppressing Activity

A GENX protein of the present invention may also exhibit immune stimulating or immune suppressing activity, including without limitation the activities for which assays are described herein. A protein may be useful in the treatment of various immune deficiencies and disorders (including severe combined immunodeficiency (SCID)), *e.g.*, in regulating (up or down) growth and proliferation of T and/or B lymphocytes, as well as effecting the cytolytic activity of NK cells and other cell populations. These immune deficiencies may be genetic or be caused by vital (*e.g.*, HIV) as well as bacterial or fungal infections, or may result from autoimmune disorders. More specifically, infectious diseases causes by vital, bacterial, fungal or other infection may be treatable using a protein of the present invention, including infections by HIV, hepatitis viruses, herpesviruses, mycobacteria, Leishmania species., malaria species. and various fungal infections such as candidiasis. Of course, in this regard, a protein of the present invention may also be useful where a boost to the immune system generally may be desirable, *i.e.*, in the treatment of cancer.

Autoimmune disorders which may be treated using a protein of the present invention include, for example, connective tissue disease, multiple sclerosis, systemic lupus erythematosus, rheumatoid arthritis, autoimmune pulmonary inflammation, Guillain-Barre syndrome, autoimmune thyroiditis, insulin dependent diabetes mellitus, myasthenia gravis, graft-versus-host disease and autoimmune inflammatory eye disease. Such a protein of the present invention may also to be useful in the treatment of allergic reactions and conditions, such as asthma (particularly allergic asthma) or other respiratory problems. Other conditions, in which immune suppression is desired (including, for example, organ transplantation), may also be treatable using a protein of the present invention.

Using the proteins of the invention it may also be possible to immune responses, in a number of ways. Down regulation may be in the form of inhibiting or blocking an immune response already in progress or may involve preventing the induction of an immune response.

The functions of activated T cells may be inhibited by suppressing T cell responses or by inducing specific tolerance in T cells, or both. Immunosuppression of T cell responses is generally an active, non-antigen-specific, process which requires continuous exposure of the T cells to the suppressive agent. Tolerance, which involves inducing non-responsiveness or energy in T cells, is distinguishable from immunosuppression in that it is generally antigen-specific and persists after exposure to the tolerizing agent has ceased. Operationally, tolerance can be demonstrated by the lack of a T cell response upon re-exposure to specific antigen in the absence of the tolerizing agent.

Down regulating or preventing one or more antigen functions (including without limitation B lymphocyte antigen functions (such as, for example, B7), *e.g.*, preventing high level lymphokine synthesis by activated T cells, will be useful in situations of tissue, skin and organ transplantation and in graft-versus-host disease (GVHD). For example, blockage of T cell function should result in reduced tissue destruction in tissue transplantation. Typically, in tissue transplants, rejection of the transplant is initiated through its recognition as foreign by T cells, followed by an immune reaction that destroys the transplant. The administration of a molecule which inhibits or blocks interaction of a B7 lymphocyte antigen with its natural ligand(s) on immune cells (such as a soluble, monomeric form of a peptide having B7-2 activity alone or in conjunction with a monomeric form of a peptide having an activity of another B lymphocyte antigen (*e.g.*, B7-1, B7-3) or blocking antibody), prior to transplantation can lead to the binding of the molecule to the natural ligand(s) on the immune cells without transmitting the corresponding costimulatory signal. Blocking B lymphocyte antigen function in this matter prevents cytokine synthesis by immune cells, such as T cells, and thus acts as an immunosuppressant. Moreover, the lack of costimulation may also be sufficient to energize the T cells, thereby inducing tolerance in a subject. Induction of long-term tolerance by B lymphocyte antigen-blocking reagents may avoid the necessity of repeated administration of these blocking reagents. To achieve sufficient immunosuppression or tolerance in a subject, it may also be necessary to block the function of B lymphocyte antigens.

The efficacy of particular blocking reagents in preventing organ transplant rejection or GVHD can be assessed using animal models that are predictive of efficacy in humans. Examples of appropriate systems which can be used include allogeneic cardiac grafts in rats and xenogeneic pancreatic islet cell grafts in mice, both of which have been used to examine the

immunosuppressive effects of CTLA4Ig fusion proteins *in vivo* as described in Lenschow *et al.*, Science 257:789-792 (1992) and Turka *et al.*, Proc Natl Acad Sci USA, 89:11102-11105 (1992). In addition, murine models of GVHD (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 846-847) can be used to determine the effect of blocking B lymphocyte antigen function *in vivo* on the development of that disease.

Blocking antigen function may also be therapeutically useful for treating autoimmune diseases. Many autoimmune disorders are the result of inappropriate activation of T cells that are reactive against self tissue and which promote the production of cytokines and auto-antibodies involved in the pathology of the diseases. Preventing the activation of autoreactive T cells may reduce or eliminate disease symptoms. Administration of reagents which block costimulation of T cells by disrupting receptor:ligand interactions of B lymphocyte antigens can be used to inhibit T cell activation and prevent production of auto-antibodies or T cell-derived cytokines which may be involved in the disease process. Additionally, blocking reagents may induce antigen-specific tolerance of autoreactive T cells which could lead to long-term relief from the disease. The efficacy of blocking reagents in preventing or alleviating autoimmune disorders can be determined using a number of well-characterized animal models of human autoimmune diseases. Examples include murine experimental autoimmune encephalitis, systemic lupus erythematosus in MRL/lpr/lpr mice or NZB hybrid mice, murine autoimmune collagen arthritis, diabetes mellitus in NOD mice and BB rats, and murine experimental myasthenia gravis (see Paul ed., FUNDAMENTAL IMMUNOLOGY, Raven Press, New York, 1989, pp. 840-856).

Upregulation of an antigen function (preferably a B lymphocyte antigen function), as a means of up regulating immune responses, may also be useful in therapy. Upregulation of immune responses may be in the form of enhancing an existing immune response or eliciting an initial immune response. For example, enhancing an immune response through stimulating B lymphocyte antigen function may be useful in cases of viral infection. In addition, systemic vital diseases such as influenza, the common cold, and encephalitis might be alleviated by the administration of stimulatory forms of B lymphocyte antigens systemically.

Alternatively, anti-viral immune responses may be enhanced in an infected patient by removing T cells from the patient, costimulating the T cells *in vitro* with viral antigen-pulsed APCs either expressing a peptide of the present invention or together with a stimulatory form of a soluble peptide of the present invention and reintroducing the *in vitro* activated T cells into the

patient. Another method of enhancing anti-vital immune responses would be to isolate infected cells from a patient, transfect them with a nucleic acid encoding a protein of the present invention as described herein such that the cells express all or a portion of the protein on their surface, and reintroduce the transfected cells into the patient. The infected cells would now be capable of delivering a costimulatory signal to, and thereby activate, T cells *in vivo*.

In another application, up regulation or enhancement of antigen function (preferably B lymphocyte antigen function) may be useful in the induction of tumor immunity. Tumor cells (e.g., sarcoma, melanoma, lymphoma, leukemia, neuroblastoma, carcinoma) transfected with a nucleic acid encoding at least one peptide of the present invention can be administered to a subject to overcome tumor-specific tolerance in the subject. If desired, the tumor cell can be transfected to express a combination of peptides. For example, tumor cells obtained from a patient can be transfected *ex vivo* with an expression vector directing the expression of a peptide having B7-2-like activity alone, or in conjunction with a peptide having B7-1-like activity and/or B7-3-like activity. The transfected tumor cells are returned to the patient to result in expression of the peptides on the surface of the transfected cell. Alternatively, gene therapy techniques can be used to target a tumor cell for transfection *in vivo*.

The presence of the peptide of the present invention having the activity of a B lymphocyte antigen(s) on the surface of the tumor cell provides the necessary costimulation signal to T cells to induce a T cell mediated immune response against the transfected tumor cells. In addition, tumor cells which lack MHC class I or MHC class II molecules, or which fail to reexpress sufficient amounts of MHC class I or MHC class II molecules, can be transfected with nucleic acid encoding all or a portion of (e.g., a cytoplasmic-domain truncated portion) of an MHC class I α chain protein and β_2 microglobulin protein or an MHC class II α chain protein and an MHC class II β chain protein to thereby express MHC class I or MHC class II proteins on the cell surface. Expression of the appropriate class I or class II MHC in conjunction with a peptide having the activity of a B lymphocyte antigen (e.g., B7-1, B7-2, B7-3) induces a T cell mediated immune response against the transfected tumor cell. Optionally, a gene encoding an antisense construct which blocks expression of an MHC class II associated protein, such as the invariant chain, can also be cotransfected with a DNA encoding a peptide having the activity of a B lymphocyte antigen to promote presentation of tumor associated antigens and induce tumor

specific immunity. Thus, the induction of a T cell mediated immune response in a human subject may be sufficient to overcome tumor-specific tolerance in the subject.

The activity of a protein of the invention may, among other means, be measured by the following methods: Suitable assays for thymocyte or splenocyte cytotoxicity include, without
5 limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981; Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Herrmann *et al.*, *Proc Natl Acad Sci USA* 78:2488-2492, 1981;
10 Herrmann *et al.*, *J Immunol* 128:1968-1974, 1982; Handa *et al.*, *J Immunol* 135:1564-1572, 1985; Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Bowman *et al.*, *J Virology* 61:1992-1998; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *Cell Immunol* 133:327-341, 1991; Brown *et al.*, *J Immunol* 153:3079-3092, 1994.

Assays for T-cell-dependent immunoglobulin responses and isotype switching (which
15 will identify, among others, proteins that modulate T-cell dependent antibody responses and that affect Th1/Th2 profiles) include, without limitation, those described in: Maliszewski, *J Immunol* 144:3028-3033, 1990; and Mond and Brunswick In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, (eds.) Vol 1 pp. 3.8.1-3.8.16, John Wiley and Sons, Toronto 1994.

Mixed lymphocyte reaction (MLR) assays (which will identify, among others, proteins
20 that generate predominantly Th1 and CTL responses) include, without limitation, those described In: CURRENT PROTOCOLS IN IMMUNOLOGY. Coligan *et al.*, eds. Greene Publishing Associates and Wiley-Interscience (Chapter 3, Chapter 7); Takai *et al.*, *J Immunol* 137:3494-3500, 1986; Takai *et al.*, *J Immunol* 140:508-512, 1988; Bertagnolli *et al.*, *J Immunol* 149:3778-3783, 1992.

Dendritic cell-dependent assays (which will identify, among others, proteins expressed by
25 dendritic cells that activate naive T-cells) include, without limitation, those described in: Guery *et al.*, *J Immunol* 134:536-544, 1995; Inaba *et al.*, *J Exp Med* 173:549-559, 1991; Macatonia *et al.*, *J Immunol* 154:5071-5079, 1995; Porgador *et al.*, *J Exp Med* 182:255-260, 1995; Nair *et al.*, *J Virol* 67:4062-4069, 1993; Huang *et al.*, *Science* 264:961-965, 1994; Macatonia *et al.*, *J Exp Med* 169:1255-1264, 1989; Bhardwaj *et al.*, *J Clin Investig* 94:797-807, 1994; and Inaba *et al.*, *J Exp Med* 172:631-640, 1990.
30

Assays for lymphocyte survival/apoptosis (which will identify, among others, proteins that prevent apoptosis after superantigen induction and proteins that regulate lymphocyte homeostasis) include, without limitation, those described in: Darzynkiewicz *et al.*, *Cytometry* 13:795-808, 1992; Gorczyca *et al.*, *Leukemia* 7:659-670, 1993; Gorczyca *et al.*, *Cancer Res* 53:1945-1951, 1993; Itoh *et al.*, *Cell* 66:233-243, 1991; Zacharchuk, *J Immunol* 145:4037-4045, 1990; Zamai *et al.*, *Cytometry* 14:891-897, 1993; Gorczyca *et al.*, *Internat J Oncol* 1:639-648, 1992.

Assays for proteins that influence early steps of T-cell commitment and development include, without limitation, those described in: Antica *et al.*, *Blood* 84:111-117, 1994; Fine *et al.*, *Cell Immunol* 155: 111-122, 1994; Galy *et al.*, *Blood* 85:2770-2778, 1995; Toki *et al.*, *Proc Nat Acad Sci USA* 88:7548-7551, 1991.

Hematopoiesis Regulating Activity

A GENX protein of the present invention may be useful in regulation of hematopoiesis and, consequently, in the treatment of myeloid or lymphoid cell deficiencies. Even marginal biological activity in support of colony forming cells or of factor-dependent cell lines indicates involvement in regulating hematopoiesis, *e.g.* in supporting the growth and proliferation of erythroid progenitor cells alone or in combination with other cytokines, thereby indicating utility, for example, in treating various anemias or for use in conjunction with irradiation/chemotherapy to stimulate the production of erythroid precursors and/or erythroid cells; in supporting the growth and proliferation of myeloid cells such as granulocytes and monocytes/macrophages (*i.e.*, traditional CSF activity) useful, for example, in conjunction with chemotherapy to prevent or treat consequent myelo-suppression; in supporting the growth and proliferation of megakaryocytes and consequently of platelets thereby allowing prevention or treatment of various platelet disorders such as thrombocytopenia, and generally for use in place of or complimentary to platelet transfusions; and/or in supporting the growth and proliferation of hematopoietic stem cells which are capable of maturing to any and all of the above-mentioned hematopoietic cells and therefore find therapeutic utility in various stem cell disorders (such as those usually treated with transplantation, including, without limitation, aplastic anemia and paroxysmal nocturnal hemoglobinuria), as well as in repopulating the stem cell compartment post irradiation/chemotherapy, either in-vivo or ex-vivo (*i.e.*, in conjunction with bone marrow

transplantation or with peripheral progenitor cell transplantation (homologous or heterologous)) as normal cells or genetically manipulated for gene therapy.

The activity of a protein of the invention may, among other means, be measured by the following methods:

5 Suitable assays for proliferation and differentiation of various hematopoietic lines are cited above.

Assays for embryonic stem cell differentiation (which will identify, among others, proteins that influence embryonic differentiation hematopoiesis) include, without limitation, those described in: Johansson *et al.* *Cellular Biology* 15:141-151, 1995; Keller *et al.*, *Mol. Cell.*
10 *Biol.* 13:473-486, 1993; McClanahan *et al.*, *Blood* 81:2903-2915, 1993.

Assays for stem cell survival and differentiation (which will identify, among others, proteins that regulate lympho-hematopoiesis) include, without limitation, those described in: Methylcellulose colony forming assays, Freshney, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 265-268, Wiley-Liss, Inc., New York, N.Y. 1994; Hirayama *et al.*,
15 *Proc Natl Acad Sci USA* 89:5907-5911, 1992; McNiece and Briddeli, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* (eds.) Vol pp. 23-39, Wiley-Liss, Inc., New York, N.Y. 1994; Neben *et al.*, *Exp Hematol* 22:353-359, 1994; Ploemacher, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.* eds. Vol pp. 1-21, Wiley-Liss, Inc., New York, N.Y. 1994; Spoonceret *et al.*, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp.
20 163-179, Wiley-Liss, Inc., New York, N.Y. 1994; Sutherland, In: CULTURE OF HEMATOPOIETIC CELLS. Freshney, *et al.*, (eds.) Vol pp. 139-162, Wiley-Liss, Inc., New York, N.Y. 1994.

Tissue Growth Activity

A GENX protein of the present invention also may have utility in compositions used for bone, cartilage, tendon, ligament and/or nerve tissue growth or regeneration, as well as for
25 wound healing and tissue repair and replacement, and in the treatment of burns, incisions and ulcers.

A protein of the present invention, which induces cartilage and/or bone growth in circumstances where bone is not normally formed, has application in the healing of bone fractures and cartilage damage or defects in humans and other animals. Such a preparation
30 employing a protein of the invention may have prophylactic use in closed as well as open fracture reduction and also in the improved fixation of artificial joints. De novo bone formation

induced by an osteogenic agent contributes to the repair of congenital, trauma induced, or oncologic resection induced craniofacial defects, and also is useful in cosmetic plastic surgery.

5 A protein of this invention may also be used in the treatment of periodontal disease, and in other tooth repair processes. Such agents may provide an environment to attract bone-forming cells, stimulate growth of bone-forming cells or induce differentiation of progenitors of bone-forming cells. A protein of the invention may also be useful in the treatment of osteoporosis or osteoarthritis, such as through stimulation of bone and/or cartilage repair or by blocking inflammation or processes of tissue destruction (collagenase activity, osteoclast activity, etc.) mediated by inflammatory processes.

10 Another category of tissue regeneration activity that may be attributable to the protein of the present invention is tendon/ligament formation. A protein of the present invention, which induces tendon/ligament-like tissue or other tissue formation in circumstances where such tissue is not normally formed, has application in the healing of tendon or ligament tears, deformities and other tendon or ligament defects in humans and other animals. Such a preparation employing
15 a tendon/ligament-like tissue inducing protein may have prophylactic use in preventing damage to tendon or ligament tissue, as well as use in the improved fixation of tendon or ligament to bone or other tissues, and in repairing defects to tendon or ligament tissue. De novo tendon/ligament-like tissue formation induced by a composition of the present invention contributes to the repair of congenital, trauma induced, or other tendon or ligament defects of
20 other origin, and is also useful in cosmetic plastic surgery for attachment or repair of tendons or ligaments. The compositions of the present invention may provide an environment to attract tendon- or ligament-forming cells, stimulate growth of tendon- or ligament-forming cells, induce differentiation of progenitors of tendon- or ligament-forming cells, or induce growth of tendon/ligament cells or progenitors *ex vivo* for return *in vivo* to effect tissue repair. The
25 compositions of the invention may also be useful in the treatment of tendonitis, carpal tunnel syndrome and other tendon or ligament defects. The compositions may also include an appropriate matrix and/or sequestering agent as a carrier as is well known in the art.

30 The protein of the present invention may also be useful for proliferation of neural cells and for regeneration of nerve and brain tissue, *i.e.* for the treatment of central and peripheral nervous system diseases and neuropathies, as well as mechanical and traumatic disorders, which involve degeneration, death or trauma to neural cells or nerve tissue. More specifically, a protein

may be used in the treatment of diseases of the peripheral nervous system, such as peripheral nerve injuries, peripheral neuropathy and localized neuropathies, and central nervous system diseases, such as Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic lateral sclerosis, and Shy-Drager syndrome. Further conditions which may be treated in accordance with the present invention include mechanical and traumatic disorders, such as spinal cord disorders, head trauma and cerebrovascular diseases such as stroke. Peripheral neuropathies resulting from chemotherapy or other medical therapies may also be treatable using a protein of the invention.

Proteins of the invention may also be useful to promote better or faster closure of non-healing wounds, including without limitation pressure ulcers, ulcers associated with vascular insufficiency, surgical and traumatic wounds, and the like.

It is expected that a protein of the present invention may also exhibit activity for generation or regeneration of other tissues, such as organs (including, for example, pancreas, liver, intestine, kidney, skin, endothelium), muscle (smooth, skeletal or cardiac) and vascular (including vascular endothelium) tissue, or for promoting the growth of cells comprising such tissues. Part of the desired effects may be by inhibition or modulation of fibrotic scarring to allow normal tissue to regenerate. A protein of the invention may also exhibit angiogenic activity.

A protein of the present invention may also be useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues, and conditions resulting from systemic cytokine damage.

A protein of the present invention may also be useful for promoting or inhibiting differentiation of tissues described above from precursor tissues or cells; or for inhibiting the growth of tissues described above.

The activity of a protein of the invention may, among other means, be measured by the following methods:

Assays for tissue generation activity include, without limitation, those described in: International Patent Publication No. WO95/16035 (bone, cartilage, tendon); International Patent Publication No. WO95/05846 (nerve, neuronal); International Patent Publication No. WO91/07491 (skin, endothelium).

Assays for wound healing activity include, without limitation, those described in: Winter, EPIDERMAL WOUND HEALING, pp. 71-112 (Maibach and Rovee, eds.), Year Book Medical

Publishers, Inc., Chicago, as modified by Eaglstein and Menz, *J. Invest. Dermatol* 71:382-84 (1978).

Activin/Inhibin Activity

5 A GENX protein of the present invention may also exhibit activin- or inhibin-related activities. Inhibins are characterized by their ability to inhibit the release of follicle stimulating hormone (FSH), while activins are characterized by their ability to stimulate the release of follicle stimulating hormone (FSH). Thus, a protein of the present invention, alone or in heterodimers with a member of the inhibin family, may be useful as a contraceptive based on the ability of inhibins to decrease fertility in female mammals and decrease spermatogenesis in 10 male mammals. Administration of sufficient amounts of other inhibins can induce infertility in these mammals. Alternatively, the protein of the invention, as a homodimer or as a heterodimer with other protein subunits of the inhibin-b group, may be useful as a fertility inducing therapeutic, based upon the ability of activin molecules in stimulating FSH release from cells of the anterior pituitary. See, for example, U.S. Pat. No. 4,798,885. A protein of the invention may 15 also be useful for advancement of the onset of fertility in sexually immature mammals, so as to increase the lifetime reproductive performance of domestic animals such as cows, sheep and pigs.

The activity of a protein of the invention may, among other means, be measured by the following methods:

20 Assays for activin/inhibin activity include, without limitation, those described in: Vale *et al.*, *Endocrinology* 91:562-572, 1972; Ling *et al.*, *Nature* 321:779-782, 1986; Vale *et al.*, *Nature* 321:776-779, 1986; Mason *et al.*, *Nature* 318:659-663, 1985; Forage *et al.*, *Proc Natl Acad Sci USA* 83:3091-3095, 1986.

Chemotactic/Chemokinetic Activity

25 A protein of the present invention may have chemotactic or chemokinetic activity (*e.g.*, act as a chemokine) for mammalian cells, including, for example, monocytes, fibroblasts, neutrophils, T-cells, mast cells, eosinophils, epithelial and/or endothelial cells. Chemotactic and chemokinetic proteins can be used to mobilize or attract a desired cell population to a desired site of action. Chemotactic or chemokinetic proteins provide particular advantages in treatment of 30 wounds and other trauma to tissues, as well as in treatment of localized infections. For example,

attraction of lymphocytes, monocytes or neutrophils to tumors or sites of infection may result in improved immune responses against the tumor or infecting agent.

A protein or peptide has chemotactic activity for a particular cell population if it can stimulate, directly or indirectly, the directed orientation or movement of such cell population.

- 5 Preferably, the protein or peptide has the ability to directly stimulate directed movement of cells. Whether a particular protein has chemotactic activity for a population of cells can be readily determined by employing such protein or peptide in any known assay for cell chemotaxis.

The activity of a protein of the invention may, among other means, be measured by following methods:

- 10 Assays for chemotactic activity (which will identify proteins that induce or prevent chemotaxis) consist of assays that measure the ability of a protein to induce the migration of cells across a membrane as well as the ability of a protein to induce the adhesion of one cell population to another cell population. Suitable assays for movement and adhesion include, without limitation, those described in: CURRENT PROTOCOLS IN IMMUNOLOGY, Coligan *et al.*,
15 eds. (Chapter 6.12, MEASUREMENT OF ALPHA AND BETA CHEMOKINES 6.12.1-6.12.28); Taub *et al. J Clin Invest* 95:1370-1376, 1995; Lind *et al. APMIS* 103:140-146, 1995; Muller *et al., Eur J Immunol* 25: 1744-1748; Gruber *et al. J Immunol* 152:5860-5867, 1994; Johnston *et al., J Immunol* 153: 1762-1768, 1994.

Hemostatic and Thrombolytic Activity

- 20 A protein of the invention may also exhibit hemostatic or thrombolytic activity. As a result, such a protein is expected to be useful in treatment of various coagulation disorders (including hereditary disorders, such as hemophilias) or to enhance coagulation and other hemostatic events in treating wounds resulting from trauma, surgery or other causes. A protein of the invention may also be useful for dissolving or inhibiting formation of thromboses and for
25 treatment and prevention of conditions resulting therefrom (such as, for example, infarction of cardiac and central nervous system vessels (*e.g.*, stroke).

The activity of a protein of the invention may, among other means, be measured by the following methods:

- 30 Assay for hemostatic and thrombolytic activity include, without limitation, those described in: Linet *et al., J. Clin. Pharmacol.* 26:131-140, 1986; Burdick *et al., Thrombosis Res.*

45:413-419, 1987; Humphrey *et al.*, *Fibrinolysis* 5:71-79 (1991); Schaub, *Prostaglandins* 35:467-474, 1988.

Receptor/Ligand Activity

A protein of the present invention may also demonstrate activity as receptors, receptor
5 ligands or inhibitors or agonists of receptor/ligand interactions. Examples of such receptors and
ligands include, without limitation, cytokine receptors and their ligands, receptor kinases and
their ligands, receptor phosphatases and their ligands, receptors involved in cell—cell
interactions and their ligands (including without limitation, cellular adhesion molecules (such as
selectins, integrins and their ligands) and receptor/ligand pairs involved in antigen presentation,
10 antigen recognition and development of cellular and humoral immune responses). Receptors and
ligands are also useful for screening of potential peptide or small molecule inhibitors of the
relevant receptor/ligand interaction. A protein of the present invention (including, without
limitation, fragments of receptors and ligands) may themselves be useful as inhibitors of
receptor/ligand interactions.

15 The activity of a protein of the invention may, among other means, be measured by the
following methods:

Suitable assays for receptor-ligand activity include without limitation those described in:
CURRENT PROTOCOLS IN IMMUNOLOGY, Ed by Coligan, *et al.*, Greene Publishing Associates and
Wiley-Interscience (Chapter 7.28, Measurement of Cellular Adhesion under static conditions
20 7.28.1-7.28.22), Takai *et al.*, *Proc Natl Acad Sci USA* 84:6864-6868, 1987; Bierer *et al.*, *J. Exp.*
Med. 168:1145-1156, 1988; Rosenstein *et al.*, *J. Exp. Med.* 169:149-160 1989; Stoltenborg *et al.*,
J Immunol Methods 175:59-68, 1994; Stitt *et al.*, *Cell* 80:661-670, 1995.

Anti-Inflammatory Activity

Proteins of the present invention may also exhibit anti-inflammatory activity. The
25 anti-inflammatory activity may be achieved by providing a stimulus to cells involved in the
inflammatory response, by inhibiting or promoting cell—cell interactions (such as, for example,
cell adhesion), by inhibiting or promoting chemotaxis of cells involved in the inflammatory
process, inhibiting or promoting cell extravasation, or by stimulating or suppressing production
of other factors which more directly inhibit or promote an inflammatory response. Proteins
30 exhibiting such activities can be used to treat inflammatory conditions including chronic or acute

conditions), including without limitation inflammation associated with infection (such as septic shock, sepsis or systemic inflammatory response syndrome (SIRS)), ischemia-reperfusion injury, endotoxin lethality, arthritis, complement-mediated hyperacute rejection, nephritis, cytokine or chemokine-induced lung injury, inflammatory bowel disease, Crohn's disease or resulting from over production of cytokines such as TNF or IL-1. Proteins of the invention may also be useful to treat anaphylaxis and hypersensitivity to an antigenic substance or material.

Tumor Inhibition Activity

In addition to the activities described above for immunological treatment or prevention of tumors, a protein of the invention may exhibit other anti-tumor activities. A protein may inhibit tumor growth directly or indirectly (such as, for example, via ADCC). A protein may exhibit its tumor inhibitory activity by acting on tumor tissue or tumor precursor tissue, by inhibiting formation of tissues necessary to support tumor growth (such as, for example, by inhibiting angiogenesis), by causing production of other factors, agents or cell types which inhibit tumor growth, or by suppressing, eliminating or inhibiting factors, agents or cell types which promote tumor growth.

Other Activities

A protein of the invention may also exhibit one or more of the following additional activities or effects: inhibiting the growth, infection or function of, or killing, infectious agents, including, without limitation, bacteria, viruses, fungi and other parasites; effecting (suppressing or enhancing) bodily characteristics, including, without limitation, height, weight, hair color, eye color, skin, fat to lean ratio or other tissue pigmentation, or organ or body part size or shape (such as, for example, breast augmentation or diminution, change in bone form or shape); effecting biorhythms or circadian cycles or rhythms; effecting the fertility of male or female subjects; effecting the metabolism, catabolism, anabolism, processing, utilization, storage or elimination of dietary fat, lipid, protein, carbohydrate, vitamins, minerals, cofactors or other nutritional factors or component(s); effecting behavioral characteristics, including, without limitation, appetite, libido, stress, cognition (including cognitive disorders), depression (including depressive disorders) and violent behaviors; providing analgesic effects or other pain reducing effects; promoting differentiation and growth of embryonic stem cells in lineages other than hematopoietic lineages; hormonal or endocrine activity; in the case of enzymes, correcting

deficiencies of the enzyme and treating deficiency-related diseases; treatment of hyperproliferative disorders (such as, for example, psoriasis); immunoglobulin-like activity (such as, for example, the ability to bind antigens or complement); and the ability to act as an antigen in a vaccine composition to raise an immune response against such protein or another material or entity which is cross-reactive with such protein.

Neural disorders in general include Parkinson's disease, Alzheimer's disease, Huntington's disease, multiple sclerosis, amyotrophic lateral sclerosis (ALS), peripheral neuropathy, tumors of the nervous system, exposure to neurotoxins, acute brain injury, peripheral nerve trauma or injury, and other neuropathies, epilepsy, and/or tremors.

10 EQUIVALENTS

From the foregoing detailed description of the specific embodiments of the invention, it should be apparent that particular novel compositions and methods involving nucleic acids, polypeptides, antibodies, detection and treatment have been described. Although these particular embodiments have been disclosed herein in detail, this has been done by way of example for purposes of illustration only, and is not intended to be limiting with respect to the scope of the appended claims that follow. In particular, it is contemplated by the inventors that various substitutions, alterations, and modifications may be made as a matter of routine for a person of ordinary skill in the art to the invention without departing from the spirit and scope of the invention as defined by the claims. Indeed, various modifications of the invention in addition to those described herein will become apparent to those skilled in the art from the foregoing description and accompanying figures. Such modifications are intended to fall within the scope of the appended claims.

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Table 1

ORF#	Internal Identification Number	Protein similarity	Protein domain	Protein Classification	Cells or Tissues in which Gene is Expressed
1	13076366 (1, 2)	Novel Protein sim. GBank gij4691395[emb CAB41562.1] - (AL049727) putative large secreted protein [Streptomyces coelicolor]		UNCLASSIFIED	264636
2	80248091 (3, 4)	Novel Protein sim. GBank gij282508[sp P71559 SUCC_MYCTU - SUCCINYL-COA SYNTHETASE BETA CHAIN (SCS-BETA)]	Contains protein domain (PF00549) - CoA-ligases	UNCLASSIFIED	264907, 264600, 264602, 264762, 264769, 264889, 264638, 264587
3	80415924 (5, 6)			UNCLASSIFIED	264910, 264604, 264634, 264805, 264636, 264891, 264907, 264892, 264829
4	82018837 (7, 8)			UNCLASSIFIED	264908, 264909, 264760, 264628, 264635
5	79970035 (9, 10)			UNCLASSIFIED	22278002, 264583
6	79842462 (11, 12)		Contains protein domain (PF00127) - Copper binding proteins, plastocyanin/azurin family	UNCLASSIFIED	264908
7	85515576 (13, 14)	Novel Protein sim. GBank gij4415926[sp AAD20157] - (AC008282) unknown protein (Arabidopsis thaliana)		UNCLASSIFIED	20281099, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 265008, 264512, 265009, 264910, 264955, 264598, 264758, 264603, 264604, 264760, 264762, 264683, 264766, 264787, 264889, 35695917, 264690, 264692, 264693, 33657109, 264628, 264629, 35698423, 55811576, 35695855, 264630, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264566, 264488
8	56824278 (15, 16)	Novel Protein sim. GBank gij565582[sp Q06456 NIRB_KLEPN - NITRITE REDUCTASE (NAD(P)H) LARGE SUBUNIT		reductase	264907
9	79394457 (17, 18)			UNCLASSIFIED	265007, 265019, 263972
10	79556459 (19, 20)			UNCLASSIFIED	264908
11	20414027 (21, 22)			UNCLASSIFIED	264605
12	94141210 (23, 24)	Novel Protein sim. GBank gij3878145[emb CAA9987.1] - (Z75543) similar to potassium channel protein (Caenorhabditis elegans)		misc_channel	264259, 265007, 83373044
13	20750551 (25, 26)			UNCLASSIFIED	264556, 264557, 264584
14	93105114 (27, 28)	Novel Protein sim. GBank gij2832761[emb CAA12645] - (A225805) inward potassium channel alpha subunit [Egeria densa]	Contains protein domain (PF00023) - Ank repeat	potassium_channel	35696298, 35696052, 264510, 35695917, 264691, 264628, 35698423, 264555, 264558, 264559, 83373044
15	20456307 (29, 30)	Novel Protein sim. GBank gij1710781[sp Q10234 RT05_SCHPO - PROBABLE MITOCHONDRIAL 40S RIBOSOMAL PROTEIN S5	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	264604
16	20760356 (31, 32)				264555

17	20292744 (33, 34)	Novel Protein sim. GBank gll117484[sp]P44391[URE1_HAEN - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)]	Contains protein domain (PF00449) - Urease		284600
18	80246804 (35, 36)	Novel Protein sim. GBank gll2281102 (AC002333) - SF16 isolog [Arabidopsis thaliana]			28331827, 284555, 284557, 284638, 284558
19	80076824 (37, 38)	Novel Protein sim. GBank gll2508112[sp]P43672[UUP - ECOLI - ABC TRANSPORTER ATP-BINDING PROTEIN UUP]	UNCLASSIFIED transport		22278898, 284907, 284910, 284600, 284693
20	20724558 (39, 40)	Novel Protein sim. GBank gll1730203[sp]P50442[GATM_RAT - GLYCINE AMIDINOTRANSFERASE PRECURSOR (L- ARGININE:GLYCINE AMIDINOTRANSFERASE) (TRANSAMIDINASE) (AT)]	UNCLASSIFIED		22278895, 284908, 285008, 285010, 285011, 284602, 284605, 284768, 284888, 21908764, 284891, 18108376, 284636, 18108387, 284486
21	80417554 (41, 42)	Novel Protein sim. GBank gll187329[emb]CAB070771 - (Z82771) fadE25 [Mycobacterium tuberculosis]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase		284885
22	11705858 (43, 44)	Novel Protein sim. GBank gll4803369[emb]CAB42783.11 - (AL049841) putative 30S ribosomal protein S14 [Streptomyces coelicolor]	UNCLASSIFIED ribosomal prot		284488, 284907, 284909, 284600, 284602, 284603, 284605, 284682, 284768, 32833866, 284636, 284486
23	80418178 (45, 46)	Novel Protein sim. GBank gll3122280[sp]O08333[K6PF_STRCO - 6- PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE) (PHOSPHOHEXOKINASE) (ATP-PFK)]	UNCLASSIFIED kinase		284601, 284762, 284766, 284768, 284636
24	20291897 (47, 48)	Novel Protein sim. GBank gll3580504 (AF027770) - unknown [Mycobacterium emegmatis]	UNCLASSIFIED		284908, 285019, 284887, 21908764, 21908766
25	80253774 (49, 50)	Novel Protein sim. GBank gll2128003[pir]G84507 - hypothetical protein MJ1685 - Methanococcus jannaschii	UNCLASSIFIED		284534
26	80255384 (51, 52)	Novel Protein sim. GBank gll6420387[emb]CAB46678.11 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED		284905, 284605, 284762, 284766, 284687, 284689
27	80235795 (53, 54)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED synthase		284687
28	79483581 (55, 56)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		60432289, 284600, 284602, 284760, 18108357, 284789, 285020, 284891 284600, 284687, 284558, 284639
29	82448765 (57, 58)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		284566
30	78189333 (59, 60)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		284603
31	19848158 (61, 62)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		
32	82448485 (63, 64)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		
33	79582628 (65, 66)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		
34	87467657 (67, 68)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		
35	95005170 (69, 70)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		
36	19842042 (71, 72)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		
37	20369215 (73, 74)	Novel Protein sim. GBank gll2313134[gb]AAD07128.11 - (AE000527) delta-1-pyrroline-5-carboxylate dehydrogenase [Helicobacter pylori 26895]	UNCLASSIFIED dehydrogenase		

38	20468334 (75, 76)	Novel Protein sim. GBank gl 360597 omb CAA06231 - (AJ004833) periplasmic nitrate reductase, large subunit [Rhodospirillum rubrum sp.]		reductase	284605	
39	94300715 (77, 78)	Novel Protein sim. GBank gl 1929449 L63543 - endodermis [Xenopus laevis]	Contains protein domain (PF00207) - Alpha-2-macroglobulin family	complement	284905, 284908, 284907, 68712502, 284908, 284909, 284511, 265009, 284910, 55812038, 284758, 285011, 284782, 284882, 284783, 284784, 284786, 285022, 284893, 284628, 284831, 284634, 284635, 284555, 284638, 18108381, 284558, 18108385, 284482	
40	20535825 (79, 80)			UNCLASSIFIED	284592	
41	80023287 (81, 82)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			284591, 3585917	
42	20724568 (83, 84)			UNCLASSIFIED	284602	
43	20487069 (85, 86)	Novel Protein sim. GBank gl 3620584 AF086781 - carbamoylphosphate synthetase large subunit [Zymomonas mobilis]		synthase	284605	
44	13085287 (87, 88)	Novel Protein sim. GBank gl 2494764 sp Q50729 GUAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)	Contains protein domain (PF00958) - GMP synthase C terminal domain	synthase	284769, 284638	
45	39384711 (89, 90)	Novel Protein sim. GBank gl 1861738 U89888 - myosin-I binding protein Acan125 [Acanthamoeba castellanii]		UNCLASSIFIED	284769, 284510, 284508	
46	95003398 (91, 92)			ngf	284566	
47	11898624 (93, 94)			UNCLASSIFIED	284889	
48	79407218 (95, 96)				18108385, 284635, 284828	
49	21659844 (97, 98)			UNCLASSIFIED	284603	
50	80503998 (99, 100)				284508, 284603, 284769, 284689, 284638, 284558, 284488	
51	80255569 (101, 102)	Novel Protein sim. GBank gl 3411177 AF078240 - MccC [Rhizobium leguminosarum bv. viciae]		UNCLASSIFIED	284593, 18108387	
52	78208528 (103, 104)	Novel Protein sim. GBank gl 3814992 sp Q28284 SM41_HEMPU - 41 KD SPICULE MATRIX PROTEIN PRECURSOR (HSM41) (HPSMC)		struct	284634	
53	36996970 (105, 106)	Novel Protein sim. GBank gl 3880411 AC004561 - putative proline-rich protein [Arabidopsis thaliana]		UNCLASSIFIED	284762	
54	78570887 (107, 108)					
55	80202703 (109, 110)	Novel Protein sim. GBank gl 1833572 U52084 - Herpesvirus salmone ORF73 homolog [Kaposi's sarcoma-associated herpes-like virus]		UNCLASSIFIED	284630, 284908, 284768	
56	8758408 (111, 112)	Novel Protein sim. GBank gl 4321580 gb AAD15785 - (AF050114) arginate lyase [Pseudomonas sp. W7]			28331824, 284102, 285018, 18108376	
57	11223386 (113, 114)		Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284604	

58	91227508 (115, 116)	Novel Protein sim. GBank gi 5916074 gb AAD45616.1 AF08194 - (AF08194) protate- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	58182575, 284259, 60432049, 35696052, 68712502, 284908, 285008, 285010, 285011, 284891, 29148784, 35695917, 60170615, 284891, 284692, 284693, 18108374, 35696423, 58182323, 80432113 284600, 284688, 284638
59	80077371 (117, 118)	Novel Protein sim. GBank gi 1172820 sp P45830 RFE_MYCLE - PUTATIVE UNDECAPRENYL-PHOSPHATE ALPHA-N- ACETYLGLUCOSAMINYLTRANSFERASE	Contains protein domain (PF00853) - Glycosyl transferase	transferase	
60	12958341 (119, 120)				
61	80426808 (121, 122)	Novel Protein sim. GBank gi 1710218 (U78280) - unknown [Homo sapiens]		glycoprotein	284689 284766
62	13504986 (123, 124)				284630
63	18474553 (125, 126)			UNCLASSIFIED	285019
64	20724578 (127, 128)	Novel Protein sim. GBank gi 420845 pir JA47041 - transposase homolog (insertion element [SAE1]) - Alcaligenes eutrophus		UNCLASSIFIED	284602
65	78326308 (129, 130)	Novel Protein sim. GBank gi 3122312 sp O08134 KPYK_MYCTU - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	kinase	284563
66	46854384 (131, 132)	Novel Protein sim. GBank gi 3282723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		transport	22278986, 284558
67	78952543 (133, 134)	Novel Protein sim. GBank gi 231985 sp P30234 DHA_MYCTU - ALANINE DEHYDROGENASE (40 KD ANTIGEN)		dehydrogenase	285021
68	79817382 (135, 136)				
69	79841764 (137, 138)				284909
70	79871328 (139, 140)			UNCLASSIFIED	284908
71	85697458 (141, 142)				284906, 284908
72	87734977 (143, 144)	Novel Protein sim. GBank gi 4415928 gb AAD201571 - (AC006282) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	284602, 285021
73	80025241 (145, 146)			UNCLASSIFIED	284488, 284903, 284906, 284907, 284908, 284511, 285008, 284910, 284758, 87168474, 284682, 284766, 284688, 284689, 35695917, 285021, 60170615, 284891, 33857023, 284692, 284693, 284629, 284631, 284639, 22279000
74	20377410 (147, 148)			UNCLASSIFIED	60424179, 284508, 284908, 285007, 284603, 284687, 284689, 284692, 18108387
75	11819032 (149, 150)	Novel Protein sim. GBank gi 2853098 emb CAA189141 - (AL021767) vacuolar protein sorting [Schizosaccharomyces pombe]		UNCLASSIFIED	284605
76	95105303 (151, 152)	Novel Protein sim. GBank gi 4468811 emb CAB38212 - (AL035601) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	284689
77	10144718 (153, 154)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	83373044, 284908, 284557
78	8758258 (155, 156)			UNCLASSIFIED	284683 284604

79	94140180 (157, 158)	Novel Protein sim. GBank gl 5689453 dbj BAA83010.1 - (AB028881) KIAA1058 protein [Homo sapiens]	Contains protein domain (PF00189) - PH domain		35698288, 22278998, 29331822, 29331824, 29331825, 29331827, 284905, 284906, 284907, 66712502, 284908, 284909, 285008, 285009, 284910, 60170831, 55812038, 33108954, 285017, 285018, 284288, 284768, 56181582, 21908785, 21908789, 29148764, 265020, 284690, 284691, 284692, 284693, 80431528, 35898423, 284631, 284632, 284634, 284636, 284639, 83373044, 284564, 284568, 284567
80	82314840 (159, 160)			UNCLASSIFIED	284769, 284801, 265008, 284910, 284604, 284605, 284634, 284635, 284605, 284762, 284637, 284592, 284628, 284807, 284691, 284908, 284567, 284909, 284768
81	20467247 (161, 162)	Novel Protein sim. GBank gl 1723442 sp Q10258 YD2A_SCHPO - HYPOTHETICAL 69.0 KD PROTEIN C8F8.10 IN CHROMOSOME I		reductase	284605
82	16331388 (163, 164)	Novel Protein sim. GBank gl 2895868 (AF045770) - methylmalonate semi-aldehyde dehydrogenase (Oryza sativa)		dehydrogenase	284567
83	94741180 (165, 166)	Novel Protein sim. GBank gl 3402673 (AC004697) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	284488, 284508, 284509, 284905, 284908, 284909, 284511, 284591, 284593, 284594, 284595, 284596, 284758, 284603, 284760, 284681, 18108351, 284762, 284682, 284764, 284684, 284768, 284686, 284688, 284632, 284637, 284557, 284638, 284639, 18108385, 284568
84	80355375 (167, 168)	Novel Protein sim. GBank gl 173384 sp P45380 SAT1_RAT - SULFATE ANION TRANSPORTER 1 (CANALICULAR SULFATE TRANSPORTER) (SULFATE/CARBONATE ANTIPORTER)		transport	284508, 284908, 284907, 284908, 284909, 284910, 284760, 284763, 284764, 284768, 284768, 284769, 35898555, 284636, 284637
85	80498600 (169, 170)	Novel Protein sim. GBank gl 2120998 pir S70882 - glycosyltransferase homolog - Bordetella pertussis		transferase	284605, 284762, 284667, 284769, 18108374, 284636, 284488
86	39559043 (171, 172)	Novel Protein sim. GBank gl 3256023 emb CAA17228.1 - (AL021897) hypothetical protein Rv1112 [Mycobacterium tuberculosis]			284910
87	13658808 (173, 174)			UNCLASSIFIED	284093

88	95344718 (175, 176)	Novel Protein sim. GBank gij559703[dbj BAA07552] - (D38548) ha1025 is new [Homo sapiens]		52844507, 52846365, 18108398, 85274572, 58182575, 56994075, 35686286, 22278997, 22278998, 22278999, 264092, 264093, 264094, 264095, 264259, 29331822, 29331824, 56182181, 66714117, 29331825, 29331826, 80432289, 29331827, 29331828, 35686052, 33656970, 264105, 264508, 264905, 264908, 264907, 264908, 29331830, 66712502, 52844045, 58182435, 285007, 265009, 264910, 60170831, 264592, 60431735, 60433358, 33657402, 264757, 60433438, 55812038, 264758, 21908754, 52846317, 33109954, 52844298, 87168474, 265011, 87168559, 264601, 265017, 265018, 264604, 265019, 264448, 264369, 264288, 264788, 52844229, 21908786, 21908787, 21908788, 21908789, 55811957, 35685917, 285020, 265021, 265022, 60170815, 52644150, 33657023, 65274620, 33657109, 27486261, 27486264, 33657349, 35685763, 264828, 263972, 18108374, 55810764, 35688423, 55811578, 65274791, 35685855, 60431850, 264636, 52844332, 56182323, 60170394, 83373044, 18108385, 18108387, 18108388, 56526486, 87168518, 60432113, 22279000, 22279002, 264482, 264584, 264488, 264600
89	80077389 (177, 178)	Novel Protein sim. GBank gij1710383[sp P46352 RIPX_BACSU - PROBABLE INTEGRASE/RECOMBINASE RIPX		
90	82115998 (179, 180)			
91	78908950 (181, 182)	Novel Protein sim. GBank gij2489891[sp P76403 YEGQ_ECOLI - PUTATIVE PROTEASE IN BAER-OGRK INTERGENIC REGION	UNCLASSIFIED protease	264760 265008
92	79554871 (183, 184)	Novel Protein sim. GBank gij3387754[emb CAA20079] - (AL031155) hypothetical protein SC3A7.18c [Streptomyces coelicolor]	UNCLASSIFIED	264691
93	80498778 (185, 186)	Novel Protein sim. GBank gij2885095 (AF011337) - putative E1-E2 ATPase [Mus musculus]	ATPase_associated	264907, 264908, 264910, 265008, 264605, 264769
94	79848649 (187, 188)	Novel Protein sim. GBank gij1719191[sp P46820 OPUA_BACSU - GLYCINE BETAINES TRANSPORT ATP-BINDING PROTEIN OPUAA	Contains protein domain (PF00571) - CBS domain	264908
95	11080238 (189, 190)			264594

98	94322125 (191, 192)	Novel Protein sim. GBank gj4589560[idj]BAA76802.1] - (AB023175) KIAA0958 protein (Homo sapiens)	UNCLASSIFIED	22278995, 22278999, 264259, 28331822, 29331826, 35866052, 29148499, 284509, 284906, 284907, 284908, 284909, 265007, 265008, 284910, 263008, 284593, 265010, 285017, 284604, 285019, 18108351, 284288, 284786, 284788, 284789, 21906765, 21906767, 21906769, 265020, 264892, 33857182, 35895783, 264828, 264829, 18108379, 284631, 284638, 18108381, 284559, 18108382, 8337304, 22278002, 284508
97	79605200 (193, 194)	Novel Protein sim. GBank gj4583559[emb]CAB40388.1] - (AJ05255) OxyR [Erwinia chrysanthemii]	UNCLASSIFIED	
98	79427000 (195, 196)	Novel Protein sim. GBank gj1001693[idj]BAA10430] - (DB4002) hypothetical protein [Synecococcus sp.]	UNCLASSIFIED	284908
99	20466524 (197, 198)	Novel Protein sim. GBank gj1168479[idj]P43925[EF]G_HAEN - ELONGATION FACTOR G (EF-G)	UNCLASSIFIED	284605
100	79640113 (199, 200)	Novel Protein sim. GBank gj480897[idj]S37465 - gene	UNCLASSIFIED	284693
101	80203298 (201, 202)	msg1 protein - mouse	UNCLASSIFIED	265020, 284102, 263972
102	20467258 (203, 204)	Novel Protein sim. GBank gj2894186[emb]CAA11773.1] - (AJ223998) PCZA381.18 [Amycolatopsis orientalis]	synthase	284605
103	20466368 (205, 206)	Novel Protein sim. GBank gj173104[idj]P54509[QHH_BACSU - HYPOTHETICAL HELICASE IN SINI-GCVT INTERGENIC REGION	Contains protein domain (PF00271) - helicase	284605
104	80247572 (207, 208)	Novel Protein sim. GBank gj854085[emb]CAA56337] - (X83413) U88 [Human herpesvirus 8]	UNCLASSIFIED	284591, 284595, 284602
105	79605208 (209, 210)	Novel Protein sim. GBank gj17685117 (U70770) - furrowed	complement	284508
106	28382058 (211, 212)	[Drosophila melanogaster]	UNCLASSIFIED	284511, 265009
107	80057791 (213, 214)	Novel Protein sim. GBank gj1705505[idj]P54729[BS4_MOUSE - BS4 PROTEIN	ATPase-associated	28331824, 284591, 21906754, 265019
108	80237938 (215, 216)	Novel Protein sim. GBank gj263577[idj]BAA15264] - (Z99120) similar to ABC transporter (ATP-binding protein) [Bacillus subtilis]	transport	18108374, 35865917, 22278996, 284113, 284600, 284602, 284603, 285017, 284910, 284908, 284638, 284786
109	95194148 (217, 218)	Novel Protein sim. GBank gj2330781[idj]CAB11265] - (Z98601) carboxypeptidase a precursor [Schizosaccharomyces pombe]	UNCLASSIFIED	284758, 284603, 284630, 284636, 284637
110	79582823 (219, 220)			284687
111	39565458 (221, 222)			284564
112	79856038 (223, 224)		UNCLASSIFIED	284908
113	17959439 (225, 226)		UNCLASSIFIED	285007
114	80502101 (227, 228)		UNCLASSIFIED	284769

115	80251003 (228, 230)	Novel Protein sim. GBank gl 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	52845156, 52845080, 33856970, 264592, 21906754, 27486264, 18108379, 35698423, 264635, 52844332, 18108382
116	81288888 (231, 232)				264905, 264906, 264907, 264908, 264909, 264910, 264758, 265010, 264763, 264682, 264764, 264766, 264685, 264688, 264768, 264769, 33657023, 264693, 33657108, 264628, 18108374, 264631, 264632, 264634, 264636, 264637, 264638, 264639, 56526488, 264585, 264588
117	78636895 (233, 234)			UNCLASSIFIED	264639, 264693
118	80222170 (235, 236)		Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263974
119	91013071 (237, 238)	Novel Protein sim. GBank gl 732526 (U22327) - alpha2(IV) collagen [Caenorhabditis elegans]		UNCLASSIFIED	22278996, 29331824, 60432289, 265007, 60433438, 264603, 264605, 18108351, 264769, 264689, 265020, 264534, 27466261, 264558, 83373044, 18108385, 264564
120	8756481 (239, 240)	Novel Protein sim. GBank gl 2131219 (pir S50157) - cyclin-dependent kinase chain SRB10 - yeast (Saccharomyces cerevisiae)		kinase	264603
121	80028163 (241, 242)				264585
122	20457620 (243, 244)	Novel Protein sim. GBank gl 2052147 (emb CAB08137) - (294752) ksgA [Mycobacterium tuberculosis]	Contains protein domain (PF00398) - Ribosomal RNA adenine dimethylases	transferase	264605
123	8758278 (245, 246)				264604
124	79104017 (247, 248)	Novel Protein sim. GBank gl 2833385 (sp Q43134 UGST_SORBI - GRANULE-BOUND GLYCOPROTEIN (STARCH) SYNTHASE PRECURSOR		synthase	18108394, 18108397, 265006, 265007, 265008, 265010, 265011, 18108355, 18108378, 18108380, 18108384
125	87797888 (249, 250)	Novel Protein sim. GBank gl 475542 (U08255) - glutamate receptor delta-1 subunit [Rattus norvegicus]	Contains protein domain (PF00060) - Ligand-gated ion channel	misc_channel	264508, 264906, 265009, 264596, 22279002
126	56701283 (251, 252)	Novel Protein sim. GBank gl 5102785 (emb CAB45200.1) - (AL078308) putative transcriptional regulator [Streptomyces coelicolor]			264511
127	20467267 (253, 254)			UNCLASSIFIED	264605
128	80248473 (255, 256)	Novel Protein sim. GBank gl 130120 (sp P23820 PHOB_PSEAE - PHOSPHATE REGULON TRANSCRIPTIONAL REGULATORY PROTEIN PHOB	Contains protein domain (PF00072) - Response regulator receiver domain	phosphatase	264907, 264909, 264910, 264600, 264601, 264603, 264605, 18108351, 264693, 264557
129	95290543 (257, 258)	Novel Protein sim. GBank gl 2508493 (sp P38038 YGCB_ECOLI - HYPOTHETICAL 100.5 KD PROTEIN IN IAP-CYSH INTERGENIC REGION	Contains protein domain (PF00270) - DEAD/IDEAH box helicase	UNCLASSIFIED	35698423, 35695855, 264600, 264602, 264603, 264604, 264605, 264508, 264908, 264564, 264628, 264682, 264585, 264683
130	80085563 (259, 260)	Novel Protein sim. GBank gl 864065 (emb CAA56337) - (X83413) U88 [Human herpesvirus 6]			264634
131	94995022 (261, 262)	Novel Protein sim. GBank gl 1076036 (pir S54860 - ABC transporter PstC-2 chain - Mycobacterium tuberculosis	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	transport	18108376, 264769, 29331828, 264689, 22278996, 265021, 264600, 264511, 264601, 264602, 264605, 264905, 264636

132	10887892 (263, 264)	Novel Protein sim. GBank glj1877340[embjCAB07088] - (Z82771) accA3 [Mycobacterium tuberculosis]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	carboxylase	284638 284805, 284689
133	94630883 (265, 266)				
134	78834660 (267, 268)	Novel Protein sim. GBank glj4585838[embjCAB40932.1] - (AL048630) putative NADH dehydrogenase [Streptomyces coelicolor]		dehydrogenase	284905, 284805, 285021
135	18885057 (269, 270)	Novel Protein sim. GBank glj1460074[embjCAB01049] - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]			284634
136	79846083 (271, 272)	Novel Protein sim. GBank glj2125896[embjCAA7331.1] - (Y13070) folypolyglutamate synthase [Streptomyces coelicolor]		synthase	284508
137	79819770 (273, 274)				
138	78635971 (275, 276)	Novel Protein sim. GBank glj5420387[embjCAB46878.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284663, 284685, 284686, 284691, 284692, 284693
139	86686078 (277, 278)	Novel Protein sim. GBank glj5689912[embjCAB52075.1] - (AL109732) putative mutase [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01817) - Chorismate mutase	dehydrogenase	18108374, 18108385, 33657109, 33657182, 285010, 22278988, 285008, 285007, 285008, 285009, 284693
140	79825759 (279, 280)			UNCLASSIFIED	18108387
141	20700094 (281, 282)				284808
142	80028104 (283, 284)	Novel Protein sim. GBank glj3581916[embjCAA20855] - (AL031545) mutS family DNA mismatch repair protein [Schizosaccharomyces pombe]		nuclease	284602, 285017
143	11072274 (285, 286)				
144	95009102 (287, 288)	Novel Protein sim. GBank glj3334127[spjP87303]BAC2 MOUSE - TRANSCRIPTION REGULATOR PROTEIN BACH2 (BTB AND CNC HOMOLOG 2)		UNCLASSIFIED	284600
145	80027058 (289, 290)	Novel Protein sim. GBank glj3757569[embjCAA21315] - (AL031883) 1-evidence-predicted by content; 1-method=genefinder;084; 1-method_score=66.31; 1-evidence_end [Drosophila melanogaster]			283978, 284600, 284910, 284632, 284508, 284553, 284584, 284591, 284558, 284908, 284628, 284639
146	13085662 (291, 292)	Novel Protein sim. GBank glj140807[spjP24538]Y121_BURCE - INSERTION ELEMENT IS402 HYPOTHETICAL 24 KD PROTEIN	Contains protein domain (PF01675) - Transposase		22278986, 284602
147	94320366 (293, 294)	Novel Protein sim. GBank glj2827608[embjCAA16663] - (AL021646) uvrD2 [Mycobacterium tuberculosis]		helicase	284805, 284908, 284809, 284510, 285009, 60433356, 284600, 284601, 284604, 284605, 284887, 284769, 18108385, 85274791, 18108387
148	80248804 (295, 296)	Novel Protein sim. GBank glj2916947[embjCAA17585] - (AL021989) hypothetical protein Rv0888 [Mycobacterium tuberculosis]		transport	285009, 285010, 284600, 284602, 284603, 284604, 284605, 284693, 33657109, 284636

149	80249373 (297, 298)	Novel Protein sim. GBank gll172073jsp Q11040Y081_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.01	Contains protein domain (PF00005) - ABC transporter	transport	285010, 284600, 284601, 284603, 284604, 27486285, 284638
150	20284748 (289, 300)	Novel Protein sim. GBank gll3724125[emb]CAA11805] - (AJ224340) maltosephosphorylase [Lactobacillus sanfrancisco]			284600
151	20726388 (301, 302)	Novel Protein sim. GBank gll729312jsp P07651 DEOB_ECOLI - PHOSPHOPENTOMUTASE (PHOSPHODEOXYRIBOMUTASE)	Contains protein domain (PF01676) - Metalloenzyme superfamily	UNCLASSIFIED	284602
152	95002877 (303, 304)	Novel Protein sim. GBank gll2497852jsp P55687 Y4TM_RHISN - HYPOTHETICAL HYDROLASE/PEPTIDASE Y4TM		peptidase	284602
153	80256885 (305, 306)	Novel Protein sim. GBank gll3123021jsp Q80509 VT1_FUNHE - VITELLOGENIN I PRECURSOR (VTG I) (CONTAINS: LIPOVITELLIN 1 (LV1); PHOSVITIN (PV); LIPOVITELLIN 2 (LV2))		UNCLASSIFIED	284583
154	82305888 (307, 308)	Novel Protein sim. GBank gll418897 pir JUN0443 - transcription initiation factor sigma homolog hrdB - Streptomyces aureofaciens	Contains protein domain (PF00140) - Sigma-70 factor	mapolymerase	284910, 284782, 284691, 284634 284605
155	20429859 (309, 310)	Novel Protein sim. GBank gll828710 pir S41739 - hypothetical protein - Escherichia coli		UNCLASSIFIED	284585
156	39564742 (311, 312)	Novel Protein sim. GBank gll3695013 (AF052588) - CtrA (Pseudomonas aeruginosa)	Contains protein domain (PF00142) - 4Fe-4S iron sulfur cluster binding proteins, NifH/HnfC family	hydrolase	284691
157	10358887 (313, 314)	Novel Protein sim. GBank gll1073072 pir C55543 - cmaU protein - Pseudomonas syringae pv. syringae		UNCLASSIFIED	284805
158	79761936 (315, 316)	Novel Protein sim. GBank gll1073072 pir C55543 - cmaU protein - Pseudomonas syringae pv. syringae	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	285008 284605
159	78890376 (317, 318)	Novel Protein sim. GBank gll1173023jsp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30	Contains protein domain (PF00327) - Ribosomal protein L30p/L7e	ribosomal prot	22278996, 284600, 284603, 35695917, 32833986, 35698423, 284638
160	11075119 (319, 320)	Novel Protein sim. GBank gll5304869[emb]CAB46028.1] - (AL031685) dJ963K23.2 (novel protein) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukin	284112, 284532, 22278002
161	80055007 (321, 322)	Novel Protein sim. GBank gll1173023jsp P46789 RL30_STRCO - 50S RIBOSOMAL PROTEIN L30		UNCLASSIFIED	284639
162	80016371 (323, 324)	Novel Protein sim. GBank gll2681891[emb]CAA115785] - (AL009204) putative protease [Streptomyces coelicolor]		UNCLASSIFIED	284905, 284907, 284600 284891
163	11892308 (325, 326)	Novel Protein sim. GBank gll4418478 gb AAD20378] - (AF125988) transposase [Mycobacterium avium]		UNCLASSIFIED	284805, 284488
164	80077802 (327, 328)	Novel Protein sim. GBank gll78177 pir QCECT - hypothetical 38.8K protein (fla 5' region) - Escherichia coli		UNCLASSIFIED	285010
165	10856067 (328, 330)				284600
166	88095003 (331, 332)				
167	16395460 (333, 334)				
168	80078362 (335, 336)				
169	80239581 (337, 338)				284558, 284557, 284558, 284559

170	79612384 (339, 340)	Novel Protein sim. GBank gi 140888 sp P27847 YIGK_ECOLI - HYPOTHETICAL 15.4 KD PROTEIN IN RECQ-PLD8 INTERGENIC REGION (F139)	Contains protein domain (PF01810) - LysE type translocator	284908 284596, 284604	
171	95283073 (341, 342)				
172	37787007 (343, 344)	Novel Protein sim. GBank gi 4210905 gb AAD12048.1 - (AF045809) AgIG [Sinorhizobium meliloti]	Contains protein domain (PF00528) - Binding-protein-dependent transport systems inner membrane component	284769	
173	57529660 (345, 346)	Novel Protein sim. GBank gi 132854 sp P02387 RL2_ECOLI - 60S RIBOSOMAL PROTEIN L2	Contains protein domain (PF00181) - Ribosomal Proteins L2	284769	
174	95283078 (347, 348)	Novel Protein sim. GBank gi 1881350 db BAA18377 - (AB001488) PROBABLE TRANSPORT PROTEIN, SIMILAR TO ANTIOTIC TRANSPORT-ASSOCIATED PROTEIN ACTII IN STREPTOMYCES COELICOLOR. [Bacillus subtilis]		284510, 284593, 284602, 284603, 284605, 284762, 284693	
175	79758270 (348, 350)	Novel Protein sim. GBank gi 2072722 emb CAB08328 - (Z95121) manA [Mycobacterium tuberculosis]	isomerase	284565	
176	80058898 (351, 352)	Novel Protein sim. GBank gi 1055198 (U40187) - similar to PIR.A41724 chicken LD (limb deformity) gene product and to formin, also P-rich region similar to collagen [Caenorhabditis elegans]	UNCLASSIFIED	284807, 284810, 284681, 284558	
177	86884652 (353, 354)	Novel Protein sim. GBank gi 2328738 emb CAB10952 - (Z88268) hypothetical protein Rv1695 [Mycobacterium tuberculosis]	Contains protein domain (PF01513) - Domain of unknown function	284768, 60424179, 284687, 284688, 284768, 28331828, 60432289, 18108376, 284689, 18108387, 32833988, 22278988, 285020, 284800, 284801, 284802, 284603, 284604, 284805, 284635, 284782, 284636, 284908, 284864, 284837, 284638, 284486, 60433356, 284768	
178	79559528 (355, 356)	Novel Protein sim. GBank gi 1806596 (U81788) - kinesin-73 [Drosophila melanogaster]	struct	284693, 33857109, 284635	
179	20263112 (357, 358)		UNCLASSIFIED	284593	
180	80488658 (359, 360)	Novel Protein sim. GBank gi 1168367 sp P45256 DNAB_HAEIN - REPLICATIVE DNA HELICASE	helicase	284769	
181	79585369 (361, 362)	Novel Protein sim. GBank gi 3170615 (AF059485) - DOC4 [Mus musculus]	UNCLASSIFIED	21908767, 284635, 284636, 18108384	
182	80577899 (363, 364)		UNCLASSIFIED	284259, 35696052, 56182435, 284511, 285018, 33857109, 284595, 284566 284690	
183	11614017 (365, 366)	Novel Protein sim. GBank gi 1078627 pir J564172 - Inorganic pyrophosphatase (EC 3.6.1.1) - common tobacco	UNCLASSIFIED		
184	10174167 (367, 368)	Novel Protein sim. GBank gi 4371280 gb AAD18138 - (AC008280) hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	284510	

185	21680322 (369, 370)	Novel Protein sim. GBank gij300817[emb]CAA18398.1] - (AL022304) putative nima transport regulator [Schizosaccharomyces pombe]		UNCLASSIFIED	264604
186	80070329 (371, 372)	Novel Protein sim. GBank gij2828802[sp]P94408[YCLF_BACSU - HYPOTHETICAL 53.3 KD PROTEIN IN SPP-GERKA INTERGENIC REGION]		transport	264595
187	80186811 (373, 374)	Novel Protein sim. GBank gij3150280[emb]CAA19179] - (AL023634) cyclin [Schizosaccharomyces pombe]		UNCLASSIFIED	264369
188	20484942 (375, 376)	Novel Protein sim. GBank gij2145853[pir]S72938 - hix protein - Mycobacterium leprae		kinase	264605
189	82338215 (377, 378)	Novel Protein sim. GBank gij1881244[db]BAA18271] - (AB001488) SIMILAR TO PYRUVATE OXIDASE AND ACETOLACTATE SYNTHASE. [Bacillus subtilis]	Contains protein domain (PF00205) - synthase Thiamine pyrophosphate enzymes	UNCLASSIFIED	35696032, 264602, 264605, 264782, 264689, 35695917, 18108370, 18108372, 264638, 264565
190	80086621 (379, 380)	Novel Protein sim. GBank gij120226[sp]P28725[FKBP_STRCH - FK506-BINDING PROTEIN (PEPTIDYL-PROLYL CIS-TRANS ISOMERASE) (PPIASE) (ROTAMASE)]	Contains protein domain (PF00254) - isomerase FKBP-type peptidyl-prolyl cis-trans isomerases	UNCLASSIFIED	264563
191	88095012 (381, 382)	Novel Protein sim. GBank gij4980892[gb]AAD3474.1[AE00171] - (AE001718) ABC transporter, ATP-binding protein [Thermotoga maritima]		isomerase	264508, 264604, 264605, 264789, 264555
192	16333378 (383, 384)	Novel Protein sim. GBank gij1705481[sp]P33658[BIOA_ERWHE - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)]		transport	264587
193	79810127 (385, 386)	Novel Protein sim. GBank gij3122305[sp]Q2778[K6PF_SCHMA - 6-PHOSPHOFRUCTOKINASE (PHOSPHOFRUCTOKINASE)]			264605
194	20484949 (387, 388)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83899) and [Mycobacterium tuberculosis]			264638
195	13518389 (389, 390)	Novel Protein sim. GBank gij2842222 (AF030885) - telomere-associated recQ-like helicase [Usiligo maydis]			264600, 264689, 264638
196	95005568 (391, 392)	Novel Protein sim. GBank gij289437[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]			
197	80248665 (393, 394)	Novel Protein sim. GBank gij1781203[emb]CAB06110] - (Z83899) and [Mycobacterium tuberculosis]	Contains protein domain (PF00365) - kinase Phosphofructokinase		264602, 264682, 264692, 18108374
198	78163635 (395, 396)	Novel Protein sim. GBank gij2842222 (AF030885) - telomere-associated recQ-like helicase [Usiligo maydis]			
199	78890715 (397, 398)	Novel Protein sim. GBank gij289437[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]	Contains protein domain (PF00393) - 6-phosphogluconate dehydrogenases		264636
200	79413848 (399, 400)	Novel Protein sim. GBank gij2842222 (AF030885) - telomere-associated recQ-like helicase [Usiligo maydis]			265008
201	86945624 (401, 402)	Novel Protein sim. GBank gij289437[emb]CAA74911.1] - (Y14573) ring finger protein [Hordeum vulgare]		UNCLASSIFIED	264585, 264596
				UNCLASSIFIED	29331828, 265007, 264512, 33657402, 264596, 265017, 18108351, 264682, 264683, 264787, 264829, 55610764, 264834, 264835, 56182323, 80432113, 22278000

202	70588046 (403, 404)	Novel Protein sim. GBank, gij231772[sp]P30598[CHS1_USTMA - CHITIN SYNTHASE 1 (CHITIN-UDP ACETYL-GLUCOSAMINYL TRANSFERASE 1)]	Contains protein domain (PF01844) - synthase Chitin synthase	284600	
203	78843927 (405, 406)	Novel Protein sim. GBank gij1504042[dj]BAA132201 - (D86894) similar to yeast adenylate cyclase (S56776) [Homo sapiens]		22278995, 28331822, 28331825, 28331827, 284908, 21908754, 284883, 21908786, 21908789, 35886423, 284558	
204	78855188 (407, 408)	Novel Protein sim. GBank gij2633808[emb]CAB133101 - (Z88111) similar to hypothetical proteins [Bacillus subtilis]	UNCLASSIFIED	284809	
205	10090583 (409, 410)	Novel Protein sim. GBank gij2134381[pri]S60878 - polydromo 1 protein - chicken	transport	284909	
206	8758473 (411, 412)	Novel Protein sim. GBank gij2501040[sp]O05814[SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)]	UNCLASSIFIED	284604	
207	20764522 (413, 414)	Novel Protein sim. GBank gij2134381[pri]S60878 - polydromo 1 protein - chicken	UNCLASSIFIED	284556	
208	20289281 (415, 416)	Novel Protein sim. GBank gij2501040[sp]O05814[SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)]		284605	
209	80071089 (417, 418)	Novel Protein sim. GBank gij2501040[sp]O05814[SYP_MYCTU - PROLYL-TRNA SYNTHETASE (PROLINE-TRNA LIGASE) (PRORS)]		284605, 284688	
210	80188800 (419, 420)	Novel Protein sim. GBank gij5031809[trf]NP_005538.1[PSLR - Immunoglobulin superfamily containing leucine-rich repeat		284905, 284907, 284908, 284786, 284687, 284891, 284628, 18108374, 284638	
211	80034539 (421, 422)	Novel Protein sim. GBank gij5031809[trf]NP_005538.1[PSLR - Immunoglobulin superfamily containing leucine-rich repeat		263878	
212	82442474 (423, 424)	Novel Protein sim. GBank gij3122358[sp]O33123[LEU2 MYCLE - 3- ISOPROPYLMALATE DEHYDRATASE LARGE SUBUNIT (ISOPROPYLMALATE ISOMERASE) (ALPHA-IPM ISOMERASE) (IPMI)]	UNCLASSIFIED	284508, 284905, 284908, 284907, 284908, 284600, 284782, 284534, 284632, 284634, 284635, 284639, 284488	
213	80249562 (425, 426)	Novel Protein sim. GBank gij1173288[sp]P38108[IRSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	isomerase	22278996, 284508, 284600, 284602, 284603, 284605, 33657023, 284565, 284488	
214	80079381 (427, 428)	Novel Protein sim. GBank gij118236[sp]P18421[CH60_COX8U - 80 KD CHAPERONIN (PROTEIN CPN80) (GROEL PROTEIN) (HEAT SHOCK PROTEIN B)]	Contains protein domain (PF00330) - Aconitase family (aconitase hydratase)		
215	14973283 (429, 430)	Novel Protein sim. GBank gij1173288[sp]P38108[IRSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	Contains protein domain (PF00118) - TCP-1/cpn80 chaperonin family	284600, 284693	
216	80177716 (431, 432)	Unknown gene product [Homo sapiens]			
217	79603634 (433, 434)	Novel Protein sim. GBank gij2608924[sp]P48754[VP41_HUMAN - VACUOLAR ASSEMBLY PROTEIN VPS41 HOMOLOG (S53)]	UNCLASSIFIED	284629	
218	80258475 (435, 436)	Novel Protein sim. GBank gij1173288[sp]P38108[IRSEA_ECOLI - SIGMA-E FACTOR NEGATIVE REGULATORY PROTEIN	dna_ma_bind	284448	
219	20438787 (437, 438)	Novel Protein sim. GBank gij1781087[emb]CAB082311 - (Z83864) glib [Mycobacterium tuberculosis]		284508	
220	13499572 (439, 440)	Novel Protein sim. GBank gij2894703 (AF052427) - unknown [Trypanosoma cruzi]	mapolymerase	284594	
221	11287498 (441, 442)	Novel Protein sim. GBank gij4557313[db]BAA78708.1 - (AB025248) alpha-1,2-mannosidase [Bacillus sp. M-90]	synthase	284604	
			nucleaseinhib	284689	
			UNCLASSIFIED	284555	

222	79862802 (443, 444)	Novel Protein sim. GBank gi 1877268 emb CAB07049 - (Z82770) hypothetical protein Rv0143c [Mycobacterium tuberculosis]	UNCLASSIFIED	284805, 284769, 35698423
223	83053868 (445, 446)		UNCLASSIFIED	284808, 284907, 284603
224	79557920 (447, 448)		UNCLASSIFIED	284884, 284693
225	78558541 (448, 450)		UNCLASSIFIED	284692
226	78172397 (451, 452)	Novel Protein sim. GBank gi 2274851 db BAA21515 - (D84159) 3-7 gene product [Homo sapiens]	UNCLASSIFIED	22278998, 284112, 33657023, 283981
227	81777198 (453, 454)	Novel Protein sim. GBank gi 868245 (U29488) - C56C10.7 gene product [Caenorhabditis elegans]	UNCLASSIFIED	35685917, 284636, 284907
228	79872285 (455, 456)		UNCLASSIFIED	284768, 284907, 284908, 284692, 284593, 284639
229	78838288 (457, 458)		UNCLASSIFIED	284908, 284910
230	11013208 (459, 460)		UNCLASSIFIED	284831
231	20622207 (461, 462)	Novel Protein sim. GBank gi 1835114 emb CAA17133 - (Y10744) homoserine O-acetyltransferase [Leptospira meyeri]	UNCLASSIFIED	284908, 284600, 284603, 284692
232	80055035 (463, 464)		UNCLASSIFIED	284600, 284603, 284605, 284687, 284769
233	80083054 (465, 466)	Novel Protein sim. GBank gi 2842340 (AF032970) - imidazole propionate hydrolase [Pseudomonas putida]	UNCLASSIFIED	284604
234	7523968 (467, 468)	Novel Protein sim. GBank gi 3510505 (AF030881) - polypeptide [Fugu rubripes]	UNCLASSIFIED	284369
235	80203871 (469, 470)		UNCLASSIFIED	284108
236	78940001 (471, 472)	Novel Protein sim. GBank gi 2104009 emb CAB08805 - (Z95398) PckA [Mycobacterium leprae]	UNCLASSIFIED	284805
237	11755273 (473, 474)		UNCLASSIFIED	284681
238	78461401 (475, 476)		UNCLASSIFIED	284839
239	82435180 (477, 478)		UNCLASSIFIED	284908, 285010, 284603, 284762, 284682, 284636, 284638, 284486
240	21635575 (479, 480)	Novel Protein sim. GBank gi 2485617 sp Q57252 YDIJ_HAEIN - HYPOTHETICAL PROTEIN H11783	UNCLASSIFIED	284259, 284769
241	80377307 (481, 482)	Novel Protein sim. GBank gi 3183458 sp P75788 YLIA_ECOLI - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN YLIA	UNCLASSIFIED	284908, 284809, 284764, 284639
242	82148454 (483, 484)	Novel Protein sim. GBank gi 3875920 emb CAB04111 - (Z81503) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65450 comes from this gene; cDNA EST EMBL:D68888 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	284489, 284907, 284908, 284511, 284760, 284764, 284692, 284635, 284637
243	79633207 (485, 486)		UNCLASSIFIED	284908
244	80248682 (487, 488)	Novel Protein sim. GBank gi 2624302 emb CAA15575 - (AL008982) ald [Mycobacterium tuberculosis]	UNCLASSIFIED	284600, 284602, 284605, 284768, 284689
245	78883543 (489, 490)	Novel Protein sim. GBank gi 2820825 (AF044499) - vgrG protein [Escherichia coli]	UNCLASSIFIED	284907, 284758
246	79162828 (491, 492)	Novel Protein sim. GBank gi 5420387 emb CAB46879.1 - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	284637, 18108381, 18108387, 284585

247	79873185 (493, 494)	Novel Protein sim. GBank g 1839006 emb CAB0648 - (Z85982) argB [Mycobacterium tuberculosis]		Kinase	264909, 264691, 35696423, 18108387
248	80486983 (495, 498)	Novel Protein sim. GBank g 1168574 sp P42464 ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	35698286, 264907, 284511, 264602, 264768, 264688, 285021, 35695956, 18108385
249	78784845 (497, 498)			UNCLASSIFIED	264907, 264910, 265011, 264782, 264638
250	78619980 (499, 500)				21908768, 264692
251	84359489 (501, 502)			UNCLASSIFIED	52845156, 29331822, 29331824, 52644045, 285018, 21908768, 21908768, 265020, 27486281, 27486285, 35695763, 18108376, 264556, 264559, 264585
252	79737758 (503, 504)	Novel Protein sim. GBank g 3327166 db BAA31651 - (AB014576) KIAA0878 protein [Homo sapiens]			264685, 264687, 264632
253	20443124 (505, 508)	Novel Protein sim. GBank g 3036880 emb CAA18513 - (AL022374) putative ATP-dependent DNA helicase [Streptomyces coelicolor]		helicase	264604
254	80027421 (507, 508)	Novel Protein sim. GBank g 3915488 sp O34981 YJMB_BACSU - HYPOTHETICAL SYMPORTER IN COIT-RAPA INTERGENIC REGION		UNCLASSIFIED	284508, 264806, 264602, 264687, 265021, 264488
255	11398315 (509, 510)	Novel Protein sim. GBank g 1685720 db BAA04134 - (D17312) diarrheal toxin [Bacillus cereus]		UNCLASSIFIED	264593
256	80028158 (511, 512)	Novel Protein sim. GBank g 465787 sp P34422 YL31, CAEEL - HYPOTHETICAL 88.0 KD PROTEIN F4488.1 IN CHROMOSOME III	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	264602, 264692
257	20289282 (513, 514)	Novel Protein sim. GBank g 1172039 sp P42315 SCOA_BACSU - PROBABLE SUCCINYL-COA-3-KETOACID-COENZYME A TRANSFERASE SUBUNIT A (SUCCINYL COA:3-OXOACID COA-TRANSFERASE) (OXCT A)	Contains protein domain (PF01144) - Coenzyme A transferase	transferase	264605
258	20459484 (515, 516)	Novel Protein sim. GBank g 3127838 emb CAA18902 - (AL023498) hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264604
259	79910152 (517, 518)			collagen	264681, 264686, 264692
260	20378437 (519, 520)			UNCLASSIFIED	264692, 264556
261	20285683 (521, 522)	Novel Protein sim. GBank g 123781 sp P24221 HJTH_STRGR - HISTIDINE AMMONIA-LYASE (HISTIDASE)	Contains protein domain (PF00221) - Phenylalanine and histidine ammonia lyases	UNCLASSIFIED	264600
262	80189317 (523, 524)			UNCLASSIFIED	265017, 264389
263	88095045 (525, 528)	Novel Protein sim. GBank g 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nitrogen precursor protein (blast score 71); cDNA EST EMBL:702089 comes from this gene; cDNA EST EMBL:D76135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMBL:...		UNCLASSIFIED	264488, 264905, 264806, 264907, 264908, 264908, 264512, 264910, 264758, 264596, 264604, 265019, 264605, 264760, 18108351, 264763, 264764, 264286, 264768, 264768, 264769, 264691, 264692, 264693, 264628, 264634, 264635, 264555, 264636, 264638, 264639
264	87370826 (527, 528)	Novel Protein sim. GBank g 3043734 db BAA25531 - (AB011177) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	protease	264259, 264608, 21908754, 265018, 265019, 265020

265	95355648 (529, 530)	Novel Protein sim. GBank gl 4589624 gb BAA78034.1 - (AB023207) KIAA0980 protein [Homo sapiens]		kinase	284488, 35896286, 29331824, 56182181, 35898052, 264508, 264905, 264908, 264907, 68712502, 264908, 264909, 264511, 264512, 264910, 264592, 264595, 264758, 264596, 55811388, 264600, 265017, 264603, 264604, 264605, 264760, 18108351, 264762, 264681, 264764, 264288, 264766, 264768, 264769, 21908765, 21908767, 21908769, 265020, 264891, 33857023, 33857109, 33857182, 264828, 35898423, 35899855, 264830, 264831, 264632, 264634, 264635, 264636, 264555, 264638, 83373044, 56526486, 87168518, 264564, 264566, 264486
266	78588075 (531, 532)				264600
267	11382222 (533, 534)			UNCLASSIFIED	264828
268	78809568 (535, 536)			UNCLASSIFIED	264687, 264769, 264689
269	80025810 (537, 538)			UNCLASSIFIED	264602
270	84381144 (539, 540)	Novel Protein sim. GBank gl 4507367 ref NP_003182.1 pTARS - threonyl-tRNA synthetase		UNCLASSIFIED	264693
271	79552301 (541, 542)	Novel Protein sim. GBank gl 4980738 gb AAD35331.1 AE00170 - (AE001707) glucose-1-phosphate adenylyltransferase [Thermotoga maritima]		UNCLASSIFIED	264909, 264693
272	9874778 (543, 544)	Novel Protein sim. GBank gl 188224 sp P44589 5NTD_HAEIN - PROBABLE 5'-NUCLEOTIDASE PRECURSOR		synthase	264908
273	12840884 (545, 546)			UNCLASSIFIED	264688
274	39524248 (547, 548)	Novel Protein sim. GBank gl 3253159 (AF005335) - Translation initiation factor eIF2C [Oryctolagus cuniculus]			264564
275	82787041 (549, 550)	Novel Protein sim. GBank gl 134920 sp P21997 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)		UNCLASSIFIED	264807, 264908, 264909, 264766, 264768, 264691, 264632, 264636
276	68871073 (551, 552)	Novel Protein sim. GBank gl 128021 sp P20864 OBG_BACSU - SPOB-ASSOCIATED GTP-BINDING PROTEIN			265008, 60432229
277	80076735 (553, 554)	Novel Protein sim. GBank gl 128021 sp P20864 OBG_BACSU - SPOB-ASSOCIATED GTP-BINDING PROTEIN		ribosomal prot	264600, 18108387
278	12886847 (555, 556)	Novel Protein sim. GBank gl 79839 pir J03812 - uvrB protein - Micrococcus luteus		UNCLASSIFIED	264689
279	95282719 (557, 558)			nuclease	264508, 264604, 21808764, 264638, 264557, 264404
280	5603817 (559, 560)				264259
281	80249598 (561, 562)	Novel Protein sim. GBank gl 3123160 sp Q18884 YLN2_CAEEL - HYPOTHETICAL 48.2 KD-TRP-ASP REPEATS CONTAINING PROTEIN D2013.2 IN CHROMOSOME II			18108392, 264634, 264555, 264556, 264557, 264558
282	18598882 (563, 564)			UNCLASSIFIED	265019
283	20614211 (565, 566)			UNCLASSIFIED	264555

284	91212160 (587, 588)	Novel Protein sim. GBank gi2428094 (U58632) - acetyl xylan esterase; AxeA [Thermotoga neapolitana]	Contains protein domain (PF00300) - Phosphoglycerate mutase family	UNCLASSIFIED	35696032, 29331828, 264508, 264905, 264600, 264602, 264605, 264682, 264764, 56181562, 21908784, 18108378, 264636, 264559, 18108387
285	8757940 (569, 570)	Novel Protein sim. GBank gi2072674 (embjCAB08305) - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264603
286	80503235 (571, 572)	Novel Protein sim. GBank gi765323 (bba1157678 - (S74439) silk fibroin heavy chain (C-terminal) [Bombyx mori]-silkworms, Peptide Partial, 633 aa) [Bombyx mori]		UNCLASSIFIED	264688
287	12745921 (573, 574)	Novel Protein sim. GBank gi1870009 (embjCAB08660) - (Z92539) hypothetical protein Rv1019 [Mycobacterium tuberculosis]	Contains protein domain (PF00440) - Bacterial regulatory proteins, tetR family	UNCLASSIFIED	264557
288	20756502 (575, 576)	Novel Protein sim. GBank gi2506694 (spP40120) YDCG_ECOLI - 59.4 PROTEIN IN TRG-RIML INTERGENIC REGION PRECURSOR		UNCLASSIFIED	264601
289	80043604 (577, 578)	Novel Protein sim. GBank gi1625182 (L39015) - mitochondrial glutamyl-tRNA synthetase [Saccharomyces cerevisiae]		UNCLASSIFIED	264605
290	80430175 (579, 580)	Novel Protein sim. GBank gi1718095 (spP5328) UVRO_MYCLE - PUTATIVE DNA HELICASE II HOMOLOG	helicase	UNCLASSIFIED	264688, 264687, 264689, 264692
291	20747431 (581, 582)	Novel Protein sim. GBank gi117422 (spP10040) CRB_DROME - CRUMBS PROTEIN PRECURSOR (96F)	Contains protein domain (PF00008) - EGF-like domain	onco gene	35696032, 264606, 265011, 264628, 55611576
292	80052555 (583, 584)	Novel Protein sim. GBank gi1181619 (dbjBAA11565) - (D82364) a variant of TSC-22 [Gallus gallus]			52644507, 29331822, 264592, 265020, 264639
293	80082519 (585, 586)	Novel Protein sim. GBank gi3649789 (dbjBAA33403) - (AB012226) SecA [Vibrio alginolyticus]		synthase	264508
294	79830303 (587, 588)	Novel Protein sim. GBank gi5689967 (embjCAB52004.1) - (AL109683) putative membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	264905, 264687, 264638
295	79444180 (589, 590)				
296	79607078 (591, 592)				
297	79631297 (593, 594)				
298	80418688 (595, 596)				
299					

298	95293298 (597, 598)	Novel Protein sim. GBank gij220037[dbj BA014771] - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	284488, 283994, 56994075, 22278997, 22278998, 22278999, 20281099, 28931824, 28331825, 28931826, 60432289, 28931827, 28331828, 284905, 284906, 284907, 284908, 52644045, 284909, 284511, 265008, 284910, 284595, 284596, 284759, 33657084, 87188558, 265018, 265019, 284764, 284288, 284768, 284687, 58181562, 284769, 21908765, 21908768, 21908769, 33657023, 284692, 33657109, 27486281, 18108370, 284628, 284629, 53811578, 35685855, 284631, 284634, 284635, 284638, 284639, 83373044, 18108387, 87188518, 22279000, 22279002, 284565, 284588, 284587, 284602, 284687
300	20711340 (598, 600)	Novel Protein sim. GBank gij145922 (M20981) - Iron diferrate transport protein precursor [Escherichia coli]		
301	13511332 (601, 602)	Novel Protein sim. GBank gij1174881[sp P44594 TGT_HAEIN - QUELINE TRNA-RIBOSYLTRANSFERASE (TRNA-GUANINE TRANSGLYCOSYLASE) (GUANINE INSERTION ENZYME)]		
302	9875280 (603, 604)	Novel Protein sim. GBank gij67885[pir J HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus]	UNCLASSIFIED transport	284908
303	79574895 (605, 608)	Novel Protein sim. GBank gij67885[pir J HJNVAV - helicase (EC 3.6.1.-) - Autographa californica nuclear polyhedrosis virus]	helicase	284689 284602
304	20711344 (607, 608)	Novel Protein sim. GBank gij728887[sp P40802 APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN APG PRECURSOR]		284783
305	80412520 (609, 610)	Novel Protein sim. GBank gij1657554[gb AA818082.1] - (U73857) hypothetical protein [Escherichia coli]	UNCLASSIFIED	283878
306	8515878 (611, 612)	Novel Protein sim. GBank gij170012[sp Q10793 RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]	UNCLASSIFIED	285010, 21908768, 285020, 18108374, 283977
307	80222801 (613, 614)	Novel Protein sim. GBank gij8420387[emb CAB46878.1] - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01351) - Ribonuclease HII	284910, 284600, 284805, 284687, 284689, 284638, 18108387
308	80084305 (615, 616)	Novel Protein sim. GBank gij170012[sp Q10793 RNH2_MYCTU - PROBABLE RIBONUCLEASE HII (RNASE HII)]		284769
309	80504138 (617, 618)	Novel Protein sim. GBank gij1144522 (U34957) - phosphoribosylaminimidazole succinocarboxamide synthase [Mycobacterium tuberculosis]	synthase	284603 284602
310	80053816 (619, 620)			
311	11090659 (621, 622)			
312	80054347 (623, 624)			
313	80046768 (625, 626)		UNCLASSIFIED	284566 284603, 284567

314	187645112 (627, 628)	Novel Protein sim. GBank gij3661583 (AF092175) - Ikaros (Danto ref)	Contains protein domain (PF00320) - GATA zinc finger	dna_na_bind	264259, 60432289, 26331828, 264805, 264908, 264908, 264908, 264908, 264910, 60432229, 33857402, 60433438, 33109854, 265011, 265017, 264803, 265018, 264288, 264768, 264692, 35695763, 264628, 264629, 264639, 60170394, 22279002, 264589
315	82356091 (629, 630)	Novel Protein sim. GBank gij1652620dbj[BAA17540] - (D80907) pyridine nucleotide transhydrogenase beta subunit [Synecococcus sp.]			264508, 264600, 264762, 264687, 264768, 52844229, 264769, 264689, 264635, 264636, 264638, 264486
316	79811071 (631, 632)	Novel Protein sim. GBank		UNCLASSIFIED	264693
317	20468844 (633, 634)	gij118244jsp[P24176]DAPE, ECOLI - SUCCINYL-DIAMINOPIMELATE DESUCCINYLAASE (SDAP)		UNCLASSIFIED	264605
318	94141836 (635, 636)	Novel Protein sim. GBank gij4680229jpbIAAD27583.1(AF11827) Dnb-5 [Homo sapiens]	Contains protein domain (PF00526) - Dictyostellum (slime mold) repeats	transport	264908, 264908, 264910, 264593, 264594, 264780, 264288, 264768, 264769, 21908769, 264691, 264693, 264628, 65274791, 264635, 264636, 264638, 83373044, 22279002, 264589
319	17289360 (637, 638)	Novel Protein sim. GBank gij1149893jembj[CAA60220] - (X86498) rbsC [Clostridium perfringens]		transport	265018
320	13527675 (639, 640)	Novel Protein sim. GBank gij2811033jspIO5314jGLGC, MYCTU - GLUCOSE-1-PHOSPHATE ADENYLYLTRANSFERASE (ADP-GLUCOSE SYNTHASE) (ADP-GLUCOSE PYROPHOSPHORYLASE)		synthase	264687
321	94134387 (641, 642)	Novel Protein sim. GBank gij1680716 (U68234) - all-trans-retinoic acid 4-hydroxylase [Danto ref]		cyto450	264508, 264908, 264907, 264908, 265009, 264596, 264784, 264628, 264634, 264635, 264638, 264639, 83373044, 264567
322	68489053 (643, 644)	Novel Protein sim. GBank gij1180355 (U33058) - UNC-89 [Caenorhabditis elegans]		UNCLASSIFIED	55811150, 264691, 60431528, 55810784
323	94653725 (645, 646)			UNCLASSIFIED	264488, 265008, 264593, 264628, 264635
324	78174383 (647, 648)			UNCLASSIFIED	264687
325	79882691 (649, 650)			UNCLASSIFIED	264693
326	28774974 (651, 652)			UNCLASSIFIED	264288, 18108385
327	79776267 (653, 654)	Novel Protein sim. GBank gij451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264488, 264805, 264509, 264910
328	80253202 (655, 656)			UNCLASSIFIED	
329	10173821 (657, 658)			UNCLASSIFIED	264592
330	86597787 (659, 660)	Novel Protein sim. GBank gij180741jpirj[S20912] - regulatory protein whiB - Streptomyces coelicolor		UNCLASSIFIED	264510
331	79754888 (661, 662)	Novel Protein sim. GBank gij114049jspIP19480AHPPF - SALTY - ALKYL HYDROPEROXIDE REDUCTASE SUBUNIT F (ALKYL HYDROPEROXIDE REDUCTASE F52A PROTEIN)		UNCLASSIFIED	264259, 264908
332	80071440 (663, 664)			transcriptfactor	264910, 264687, 264689, 264638, 264567
333	13008555 (665, 666)			reductase	35698423, 264636, 264638, 264565
					264687

334	80230771 (667, 668)	Novel Protein sim. GBank glj322228[pir][S32227 - glutamate dehydrogenase (NADP+)] (EC 1.4.1.4) - Corynebacterium glutamicum	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264905, 264600, 264604, 264486
335	80037028 (669, 670)	Novel Protein sim. GBank glj219393[emb][CA808602] - (Z98800) glpQ2 [Mycobacterium tuberculosis]		esterase	264907, 264603, 264683, 18108374, 264636, 18108387
336	80414318 (671, 672)			UNCLASSIFIED	265009, 264768, 264686
337	11090829 (673, 674)				264602
338	95413134 (675, 676)	Novel Protein sim. GBank glj545074[ref][NP_008303.1pSMRT - silencing mediator for retinoid and thyroid hormone receptors	Contains protein domain (PF00249) - Myb-like DNA-binding domain	nucl_recp	264569, 18108397, 22278988, 26331822, 20281099, 29331824, 56182181, 68714117, 29331825, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 265008, 264910, 265009, 264758, 55812038, 65274444, 265011, 87186599, 265017, 265018, 265019, 264760, 55811150, 264681, 264782, 18108351, 264682, 264764, 264786, 264685, 264688, 264768, 52644228, 264689, 55811957, 35695917, 264692, 264693, 264628, 18108370, 18108374, 55811576, 35698423, 35695855, 264635, 264555, 264638, 264558, 264837, 264957, 18108380, 264638, 264558, 264639, 18108381, 83373044, 18108385, 87186518, 60432113
339	11398513 (677, 678)	Novel Protein sim. GBank glj4001713[db][BAA35087.1] - (AB015878) DnaK [Porphyromonas gingivalis]		eph	264593
340	80504149 (679, 680)	Novel Protein sim. GBank glj2842699[sp][Q82353]UBPC - PUTATIVE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE C6G9.08 (UBIQUITIN THIOLESTERASE) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE) (DEUBIQUITINATING ENZYME)		ubiquitin	264905, 265019, 264768, 18108374
341	11075198 (681, 682)	Novel Protein sim. GBank glj2688380 (AE001166) - conserved hypothetical protein [Borrelia burgdorferi]	Contains protein domain (PF00280) - Tryptophan synthase alpha chain	isomerase	264605
342	80054186 (683, 684)	Novel Protein sim. GBank glj1684738[emb][CAA70601] - (Y09452) Yed J hypothetical protein [Pseudomonas syringae]			264603, 264604
343	20468782 (685, 686)				
344	80428870 (687, 688)	Novel Protein sim. GBank glj2117275[emb][CA809104] - (Z95818) hypothetical protein Rv0807 [Mycobacterium tuberculosis]		UNCLASSIFIED	264605, 264605, 264768, 18108370, 18108374, 35695855
345	80258653 (689, 690)	Novel Protein sim. GBank glj3023317[sp][Q48935]APHA_MYCRA - ACETYL POLYAMINE AMINOHYDROLASE		histone	264593
346	79831058 (691, 692)	Novel Protein sim. GBank glj4239787[emb][CAA75437] - (Y15166) NADP-glutamate dehydrogenase [Pseudomonas aeruginosa]	Contains protein domain (PF00208) - Glutamate/Leucine/Phenylalanine/Va line dehydrogenase	dehydrogenase	264605

347	79158195 (693, 694)	Novel Protein sim. GBank gi 731675 sp P38785 YH4_YEAST - HYPOTHETICAL 80.7 KD PROTEIN IN ERG7-NMD2 INTERGENIC REGION		UNCLASSIFIED	285008, 285008, 285010, 285016, 263987, 263981
348	80020208 (695, 696)	Novel Protein sim. GBank gi 1073810 sp S47672 - ugpB protein - Escherichia coli		transport	284602, 18108351, 18108387
349	17282112 (697, 698)	Novel Protein sim. GBank gi 3261598 emb CA8009171 - (Z77137) hypothetical protein Rv1277 [Mycobacterium tuberculosis]		nuclease	285007
350	80502370 (699, 700)	Novel Protein sim. GBank gi 2959367 emb CAA179211 - (AL022117) hypothetical protein [Schizosaccharomyces pombe]		glycoprotein	285009, 284769, 284689, 18108370
351	80501805 (701, 702)	Novel Protein sim. GBank gi 4416302 gb AAD203071 - (AF105716) copia-type pol polyprotein [Zea mays]		protease	284769, 284805, 284808
352	11611583 (703, 704)	Novel Protein sim. GBank gi 1174887 sp P42873 URE1_STAXY - UREASE ALPHA SUBUNIT (UREA AMIDOHYDROLASE)	Contains protein domain (PF00449) - Urease	UNCLASSIFIED	284595
353	80081853 (705, 706)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA	Contains protein domain (PF00072) - Response regulator receiver domain	UNCLASSIFIED	284604
354	56626130 (707, 708)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	284628
355	80046344 (709, 710)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		UNCLASSIFIED	284909, 284595, 284883, 22279002
356	80043835 (711, 712)	Novel Protein sim. GBank gi 115157 sp P16574 BVGA_BORPE - VIRULENCE FACTORS PUTATIVE POSITIVE TRANSCRIPTION REGULATOR BVGA		transcriptfactor	284909, 284591, 284592
357	80070566 (713, 714)	Novel Protein sim. GBank gi 497637 J03839 - cytochrome oxidase d subunit I [Escherichia coli]		oxidase	284605
358	37032756 (715, 716)	Novel Protein sim. GBank gi 2280990 (AF006000) - Btg1 [Bordetella pertussis]		UNCLASSIFIED	284768
359	80501488 (717, 718)	Novel Protein sim. GBank gi 3510639 (AF049344) - UDP- GalNAc:polypeptide N-acetylgalactosaminyltransferase T5 [Rattus norvegicus]		UNCLASSIFIED	284604, 284769
360	80026748 (719, 720)	Novel Protein sim. GBank gi 113764 sp P25718 AMY1 - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		UNCLASSIFIED	284594
361	80584075 (721, 722)	Novel Protein sim. GBank gi 113764 sp P25718 AMY1 - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		transferase	22278996, 284259, 29331822, 29331824, 284605, 55811957, 265022
362	13089485 (723, 724)	Novel Protein sim. GBank gi 113764 sp P25718 AMY1 - ALPHA-AMYLASE PRECURSOR (1,4-ALPHA-D-GLUCAN GLUCANOHYDROLASE)		amylase	284688
363	79750145 (725, 726)	Novel Protein sim. GBank gi 2829818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)	Contains protein domain (PF00420) - NADH-ubiquinone/plastoquinone oxidoreductase chain 4L	dehydrogenase	284588
364	82443593 (727, 728)	Novel Protein sim. GBank gi 2829818 sp P95171 NUOK_MYCTU - NADH DEHYDROGENASE I CHAIN K (NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 11) (NUO11)			284769, 284602, 284604, 284508, 284762, 284638, 284488

365	88040288 (729, 730)	Novel Protein sim. GBank gij4929268jgb AAD33924.1 - (AF144237) LOMP protein [Homo sapiens]	Contains protein domain (PF00412) - LIM domain containing proteins	284488, 21906768, 21906767, 55811576, 21906769, 29146629, 22278995, 22278996, 285020, 285022, 284634, 284691, 284593, 33857023, 33857402, 284693, 284639, 284594, 29331824, 284758, 18108385, 29331827, 87168559, 285016, 22279000, 285019, 284482, 284761, 264681, 18108351, 285017, 284757
366	81821838 (731, 732)			
367	95357471 (733, 734)	Novel Protein sim. GBank gij4503843jre NP_003908.1 pG2AD - UNKNOWN	Contains protein domain (PF01602) - Glycoprotein Adaplin N terminal region	60424179, 65274572, 56182575, 22278994, 56994075, 22278998, 284259, 29331822, 29331824, 56182181, 60424289, 86714117, 29331825, 60432289, 29331826, 29331827, 29331828, 284805, 284828, 56182435, 285008, 284512, 265008, 284591, 55812038, 55811386, 285010, 87168559, 285017, 285018, 284604, 265019, 55811150, 284448, 284369, 284288, 284688, 284768, 56181562, 21906768, 21906768, 55811957, 35695917, 285022, 80170815, 33857023, 85274820, 18108385, 283987, 33657109, 33657349, 35895763, 264628, 18108376, 55811576, 65274791, 35695856, 56182323, 83373044, 60432113, 284563, 284584, 284587, 284509
368	79807289 (735, 736)	Novel Protein sim. GBank gij3813028jpp P84987 ALR_MYCSM - ALANINE RACEMASE	UNCLASSIFIED	284508, 284604, 284605, 284636
369	95262917 (737, 738)			
370	88090868 (739, 740)	Novel Protein sim. GBank gij3249559 (AF018261) - EH domain binding protein Epain [Rattus norvegicus]		284805, 284592, 284605, 284766, 284691
371	95292599 (741, 742)	Novel Protein sim. GBank gij2995299jemb CAA18328 - (AL022268) putative tRNA delta(2)-isopentenylpyrophosphate transferase [Streptomyces coelicolor]	Contains protein domain (PF01715) - transferase IPP transferase	284805, 284906, 284510, 284600, 284601, 284802, 284603, 265018, 284604, 284605, 285021, 284892, 284636, 284584
372	80021107 (743, 744)	Novel Protein sim. GBank gij2506393jpp P31576 FIXX_ECOLI - FERREDOXIN LIKE PROTEIN		284584
373	79863768 (745, 746)			
374	79847868 (747, 748)	Novel Protein sim. GBank gij3341840jemb CAA13184 - (AJ231122) z81f [Vibrio cholerae]	UNCLASSIFIED	284809
375	91230181 (749, 750)	Novel Protein sim. GBank gij5456834jgb AAD43716.1 - (AF182322) protocadherin gamma A2 [Homo sapiens]	UNCLASSIFIED	284905, 284808
376	80506214 (751, 752)	Novel Protein sim. GBank gij1805408jdbj BAA08970 - (D50453) homologues to nitrile hydratase region 3'-hypothetical protein P47K of P. chlororaphis [Bacillus subtilis]	cadherin	65274572, 284259, 29331826, 56182435, 60433356, 60433438, 284757, 55812038, 284758, 55811957, 284690, 33857023, 284769
377	10339083 (753, 754)		UNCLASSIFIED	284808

378	80058153 (755, 756)	Novel Protein sim. GBank gl 1078013 pir A48930 - carb	Contains protein domain (PF00289) - synthase	UNCLASSIFIED	265008, 264555
379	80503437 (757, 758)	protein homolog - Mycobacterium bovis (strain BCG) (fragment)	Carbamoyl-phosphate synthase (CPSase)		264769
380	80060937 (759, 760)	Novel Protein sim. GBank gl 216558 dbj BAA021741 - (O12851) glucose dehydrogenase [Escherichia coli]	Contains protein domain (PF01011) - dehydrogenase		264604
381	11769027 (761, 762)			UNCLASSIFIED	264684
382	80054377 (763, 764)				264592
383	83259025 (765, 766)	Novel Protein sim. GBank gl 3327136 dbj BAA31636 - (AB014581) KIAA0661 protein [Homo sapiens]			264595, 265017, 265021, 264638, 87168518, 22278002
384	95314255 (767, 768)			UNCLASSIFIED	264259, 26331822, 60432289, 26331827, 264286, 264766, 263967, 85274781, 35895855, 263981, 83373044, 264567
385	10237678 (769, 770)	Novel Protein sim. GBank gl 1073456 pir S47810 - probable alcohol dehydrogenase (EC 1.1.1.1) - Escherichia coli	Contains protein domain (PF00485) - dehydrogenase		264692
386	79633434 (771, 772)		iron-containing alcohol dehydrogenases		264906
387	17860637 (773, 774)	Novel Protein sim. GBank gl 1460074 emb CA010481 - (Z77250) hypothetical protein Rv2566 [Mycobacterium tuberculosis]	Contains protein domain (PF01841) - Transglutaminase-like superfamily	UNCLASSIFIED	264760
388	87741378 (775, 776)	Novel Protein sim. GBank gl 4240169 dbj BAA74863.1 - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00646) - homeobox		35686286, 264905, 68712502, 60432229, 264593, 80433356, 264686, 264688, 21908765, 264891, 22278000, 264482
389	79316971 (777, 778)			UNCLASSIFIED	18108394, 22278986, 264630, 264556, 22278002
390	80078949 (778, 780)	Novel Protein sim. GBank gl 854065 emb CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264600
391	7657302 (781, 782)				264482
392	79786056 (783, 784)	Novel Protein sim. GBank gl 3378523 emb CAA088671 - (AJ009832) cyclomalodextrinase glucanotransferase [Thermotoga neapolitana]		UNCLASSIFIED	264908
393	33208031 (785, 786)			synthase	264602, 21906764
394	10104463 (787, 789)				
395	80228010 (789, 790)				264693
396	20436224 (791, 792)	Novel Protein sim. GBank gl 2677780 (U70327) - unknown [Paratropus polyactis]	Contains protein domain (PF00047) - struct	UNCLASSIFIED	264508, 264563
397	80417014 (793, 794)	Novel Protein sim. GBank gl 4507809 ref NP_000388.1 pWAS - Wiskott-Aldrich syndrome (eczema-thrombocytopenia)	Immunoglobulin domain		264556
398	91230517 (795, 796)	Novel Protein sim. GBank gl 1518458 (U45998) - mitochondrial solute carrier [Onchocerca volvulus]	Contains protein domain (PF00153) - transport		265007, 265009, 264508, 264556, 264629, 264766
			Mitochondrial carrier proteins		18108398, 22278985, 22278998, 56994075, 22278999, 264289, 26331824, 26331828, 264905, 264908, 265007, 265008, 265009, 21908754, 33657084, 265017, 264448, 264286, 264766, 21908785, 21908786, 21908787, 265020, 265021, 33657023, 33657109, 264628, 35898423, 35895855, 264952, 18108380, 264587, 18108391

399	80055278 (797, 798)	Novel Protein sim. GBank gl 335809 db BAA31995 - (AB016974) glycerol kinase [Pseudomonas tolaasii]	Contains protein domain (PF00370) - FGGY family of carbohydrate kinases	kinase	284592, 284595
400	94117490 (799, 800)	Novel Protein sim. GBank gl 728835 ep P39192 ALU5_HUMAN - IIII ALU SUBFAMILY SC WARNING ENTRY IIII	Contains protein domain (PF00560) - Leucine Rich Repeat	cadherin	18108394, 56182575, 22278995, 22278997, 22278999, 284259, 29331824, 285008, 265007, 265009, 60432229, 33657402, 21908754, 285010, 285017, 285018, 285019, 18108351, 18108357, 21908765, 265021, 285022, 284691, 284692, 33657023, 18108370, 65274791, 284634, 284636, 60170394, 56182323, 284594
401	11397491 (801, 802)	Novel Protein sim. GBank gl 4928292 gb AAD33527.1 AF13211 - (AF132117) FhuA [Staphylococcus aureus]		transport	
402	95420284 (803, 804)	Novel Protein sim. GBank gl 5689487 db BAA83027.1 - (AB028999) KIAA1075 protein [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	phosphatase	65274572, 56182575, 35696286, 22278996, 22278998, 284093, 284259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 284908, 284907, 284909, 285008, 284511, 285007, 285008, 284910, 284591, 33657402, 60433356, 60433438, 284596, 21908754, 52844298, 285010, 285011, 87188559, 265017, 285018, 285019, 284681, 18108351, 284682, 284448, 284288, 284684, 284766, 284767, 284688, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 285020, 285021, 285022, 284690, 284693, 65274620, 35695763, 284628, 18108370, 284629, 18108379, 35898423, 55811576, 284635, 284636, 284557, 284639, 18108385, 22279002, 284563, 284564, 284585, 284586, 284768, 284632, 284639, 284563, 284682, 285008, 284682
403	80439913 (805, 806)			UNCLASSIFIED	
404	11809865 (807, 808)				
405	79471280 (809, 810)	Novel Protein sim. GBank gl 2661649 emb CAA15755 - (AL009198) dnaE2 [Mycobacterium tuberculosis]		polymerase	
406	79634172 (811, 812)		Contains protein domain (PF00159) - Pancreatic hormone peptides	UNCLASSIFIED	18108357, 284693
407	80478229 (813, 814)				
408	80079958 (815, 816)			UNCLASSIFIED	284769
409	5640527 (817, 818)	Novel Protein sim. GBank gl 3047117 (AF058919) - similar to ATP-dependent RNA helicases [Arabidopsis thaliana]		UNCLASSIFIED	284600
				helicase	284259

410	95357406 (819, 820)	Novel Protein sim. GBank gij475016[dbj BAA08184] - (D28601) Unknown [Mus musculus]	UNCLASSIFIED	284488, 52846365, 52846842, 56181686, 35898288, 52845080, 29331822, 29331824, 56182181, 29331825, 60424289, 35898052, 33656970, 284508, 284509, 284905, 284906, 284907, 284908, 52844045, 284909, 284510, 285007, 284512, 285008, 284910, 33657402, 284758, 52846317, 55811386, 285010, 285011, 285017, 284804, 285018, 55811150, 284782, 284764, 284766, 284887, 284788, 284788, 52844229, 21906786, 285020, 285021, 284534, 52844150, 284692, 33657023, 85274820, 33657109, 33657182, 27486281, 35895783, 284828, 284629, 60431528, 18108376, 283978, 35898423, 35898555, 284632, 284634, 284635, 284637, 284638, 284558, 284639, 56182323, 284559, 60432113, 22279002, 284563, 284565, 284486
411	80501670 (821, 822)		UNCLASSIFIED	284769
412	80241662 (823, 824)	Novel Protein sim. GBank gij3261784[embj CAB08997] - (Z8559) htpX [Mycobacterium tuberculosis]	eph	284807, 284910, 283873, 22279002, 284605
413	11076446 (825, 826)	Novel Protein sim. GBank gij128038[sp P20707 ODO1_AZOV1 - 2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE)]	dehydrogenase	18108374, 284760, 284769, 284602, 284638, 284603, 284909, 284605
414	82050554 (827, 828)	Novel Protein sim. GBank gij4868350[gb AAD31273.1 AF13202 - (AF132025) rhophilin [Drosophila melanogaster]	UNCLASSIFIED	284908, 87168518
415	84453144 (829, 830)	Novel Protein sim. GBank gij2555172 (AF025543) - ArcC; carbamate kinase [Rhizobium etli]	kinase	284488, 284800, 284802, 284764, 284636
416	80402775 (831, 832)	Novel Protein sim. GBank gij170917[sp P5231 MTX2_XANOR - MODIFICATION METHYLASE XORII (CYTOSINE-SPECIFIC METHYLTRANSFERASE XORII) (M.XORII)]	Contains protein domain (PF00145) - C-5 cytosine-specific DNA methylase	284605
417	20153797 (833, 834)	Novel Protein sim. GBank gij328165[embj CAB03751] - (Z81368) hypothetical protein Rv2419c [Mycobacterium tuberculosis]	UNCLASSIFIED	284689, 284693
418	84125841 (835, 836)		collagen	284908, 284910, 284784, 284639
419	85314273 (837, 838)		phosphatase	284769
420	37036349 (839, 840)	Novel Protein sim. GBank gij291694[embj CAA17580] - (AL021999) hypothetical protein Rv0981 [Mycobacterium tuberculosis]	phosphatase	284908, 284800, 284601, 284603, 284604, 284780, 284769
421	95282842 (841, 842)	Novel Protein sim. GBank gij231752[sp Q00787 CHB1_STRAL - 80 KD CHAPERONIN 1 (PROTEIN CPN80 1) (GROEL-PROTEIN 1) (HSP58)]	eph	22278896, 284682, 18108376, 18108387
422	78471263 (843, 844)		UNCLASSIFIED	284509
423	79604948 (845, 846)			

424	78866557 (847, 848)	Novel Protein sim. GBank glj4828614[re]NP_004977.1 pKTN1 - kinesin 1 (kinesin receptor)		struct	285019
425	80431450 (848, 850)	Novel Protein sim. GBank glj1703707 bbsj178482 - KRP5-kinesin-related protein [rats, testes, Peptide Partial, 167 aa]	Contains protein domain (PF00225) - Kinesin motor domain	struct	284908, 285007, 55811386, 284768, 55810764
426	80084522 (851, 852)				284605, 284559
427	80057232 (853, 854)	Novel Protein sim. GBank glj231828 pP28929 COBN_PSEDE - COBN PROTEIN		UNCLASSIFIED	284803, 284636
428	79487798 (855, 856)				284883
429	80091252 (857, 858)	Novel Protein sim. GBank glj81286 pJ522897 - extensin - Volvox carterii (fragment)		UNCLASSIFIED	35696423, 35695763, 35695855, 265017, 284584, 284782
430	80504192 (859, 860)	Novel Protein sim. GBank glj1808154 emb CAB08451 - (Z84385) hypothetical protein Rv0688 [Mycobacterium tuberculosis]	reductase		284508, 284905, 284509, 284908, 284909, 285008, 284600, 284687, 284789, 284889, 284636, 284638, 18108385, 284486
431	20824249 (861, 862)				284568
432	16525372 (863, 864)				285020
433	81494303 (865, 866)	Novel Protein sim. GBank glj3123552 emb CAA18608 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0268 LIKE) [Homo sapiens]		UNCLASSIFIED	284907, 284908, 284909, 284910, 284592, 284595, 284758, 284604, 284780, 284762, 284763, 284636, 284637, 22279002
434	84326323 (867, 868)	Novel Protein sim. GBank glj2495272 sp Q88828 CDX2_HUMAN - HOMEBOX PROTEIN CDX-2 (CAUDAL-TYPE HOMEBOX PROTEIN 2) (CDX-3)	Contains protein domain (PF00169) - PH domain	UNCLASSIFIED	55812038, 56182181, 56181562, 29331828, 35696092, 55810784, 55811576, 65274781, 35695855, 60432113, 55811150, 284636, 284768
435	80502738 (869, 870)	Novel Protein sim. GBank glj114105 pP08532 ARAH_ECOLI - L-ARABINOSE TRANSPORT SYSTEM PERMEASE PROTEIN ARAH		transport	284595, 284769
436	41085853 (871, 872)			UNCLASSIFIED	285020, 22279002
437	11399291 (873, 874)			UNCLASSIFIED	284593
438	11773835 (875, 876)			UNCLASSIFIED	284886
439	80018485 (877, 878)	Novel Protein sim. GBank glj3242702 (AC003040) - hypothetical protein [Arabidopsis thaliana]			284905, 284600, 284602, 284604
440	78841062 (879, 880)	Novel Protein sim. GBank glj2291232 gb AAB8531.1 - (AF016427) Contains similarity to Pfam domain: PF00004 (AAA), Score=288.1, E-value=3.7e-77, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00004) - ATPases associated with various cellular activities (AAA)		35696052, 284905, 284908, 284909, 265011, 35698423
441	20386935 (881, 882)	Novel Protein sim. GBank glj5639946 gb AAD45904.1 AF16132 - (AF161328) histidine kinase CuiS [Corynebacterium diphtheriae]			284805
442	85281058 (883, 884)	Novel Protein sim. GBank glj1184780 (U46088) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 284909
443	82458427 (885, 886)	Novel Protein sim. GBank glj5686993 emb CAB52056.1 - (AL109732) putative ATP-binding RNA helicase [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	35696052, 284508, 284908, 284512, 284604, 284762, 284769, 284689, 284636
444	11395887 (887, 888)	Novel Protein sim. GBank glj1783249 gb BAA11726 - (D83026) homologous to citrate-sodium symport (citrate transporters); hypothetical [Bacillus subtilis]		UNCLASSIFIED	284591

445	79552708 (889, 890)	Novel Protein sim. GBank gij5531272[embjCAB50897.1] - (AJ243800) WSC4 homologue [Kluyveromyces fragilis]		UNCLASSIFIED	284693 284509
446	79810937 (891, 892)	Novel Protein sim. GBank gij538413 (L36315) - zinc finger protein [Mus musculus]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcription factor	284788, 55811578
447	80438888 (893, 894)	Novel Protein sim. GBank gij1542814[embjCAB802185] - (Z80108) fms [Mycobacterium tuberculosis]	Contains protein domain (PF00551) - Formyl transferase	dehydrogenase	284508, 284600, 284603, 284605, 284682, 284788, 18108362, 284634, 18108387
448	80238110 (895, 896)	Novel Protein sim. GBank gij118784[spjP10443]DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	284605, 284559
449	20460634 (897, 898)	Novel Protein sim. GBank gij4589508[dbjBAA78775.1] - (AB023148) KIAA0931 protein [Homo sapiens]	Contains protein domain (PF00481) - Protein phosphatase 2C	phosphatase	65274572, 22278998, 29331824, 29331826, 284906, 284910, 284592, 52846317, 285017, 21908787, 55811957, 56528486, 22279002
451	21433609 (901, 902)	Novel Protein sim. GBank gij2850814 (AE001104) - conserved hypothetical protein [Archaeoglobus fulgidus]		UNCLASSIFIED	284682
452	10287278 (903, 904)	Novel Protein sim. GBank gij2493000[spjQ09450]SCOT_CAEEL - PROBABLE SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (3-OXOACID COA-TRANSFERASE)		UNCLASSIFIED	284907, 284800
453	52560098 (905, 906)	Novel Protein sim. GBank gij446889[embjCAB38153.1] - (AL035591) putative integral membrane export protein [Streptomyces coelicolor]		transferase	284603
454	38523922 (907, 908)	Novel Protein sim. GBank gij3411053 (AF034863) - synaptic scaffolding molecule [Rattus norvegicus]		UNCLASSIFIED	284887
455	13089682 (909, 910)	Novel Protein sim. GBank gij4508075[refjNP_002733.1]pPRKC - protein kinase C, mu	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	UNCLASSIFIED	284891
456	79563081 (911, 912)	Novel Protein sim. GBank gij113158[spjP25516]ACO1_ECOLI - ACONITATE HYDRATASE 1 (CITRATE HYDRO-LYASE 1) (ACONITASE 1)	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	UNCLASSIFIED	284905
457	79831273 (913, 914)	Novel Protein sim. GBank gij1168574[spjP42484]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		kinase	55812038, 265010, 265018, 284681
458	79581227 (915, 916)	Novel Protein sim. GBank gij1168574[spjP42484]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		kinase	22278997, 284259, 29331826, 265018, 284448, 284369, 21908785, 35696423
459	80587359 (917, 918)	Novel Protein sim. GBank gij1168574[spjP42484]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		kinase	284906
460	79245880 (919, 920)	Novel Protein sim. GBank gij1168574[spjP42484]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		UNCLASSIFIED	
461	95287618 (921, 922)	Novel Protein sim. GBank gij1168574[spjP42484]ATPB_CORGL - ATP SYNTHASE BETA CHAIN		synthase	284602, 284605, 284768, 284768, 265021, 33657023, 284559

462	79808589 (923, 924)	Novel Protein sim. GBank gi 1346891 sp P45971 TF1_XANCP. MULTIPHOSPHORYL TRANSFER PROTEIN (MTP) (CONTAINS: PHOSPHOENOLPYRUVATE-PROTEIN PHOSPHOTRANSFERASE (PHOSPHOTRANSFERASE SYSTEM, ENZYME I); PHOSPHOCARRIER PROTEIN HPR (PROTEIN H); PTS SYSTEM, FRUCTOSE-SPECIFIC IIA COMPONENT ...	Contains protein domain (PF00381) - PEP-utilizing enzymes	UNCLASSIFIED	284807
463	79798417 (925, 926)	Novel Protein sim. GBank gi 83413 U88 [human herpesvirus 6]		UNCLASSIFIED	284805, 284806, 284808, 284908, 284910, 284891, 284895, 285011, 284832, 284835, 284836, 284837, 284838, 284839
464	82340151 (927, 928)	Novel Protein sim. GBank gi 5689776 emb CAB52137.1 - (AJ242832) calpain [Homo sapiens]	Contains protein domain (PF00848) - Calpain family cysteine protease	UNCLASSIFIED	284834
465	83005730 (929, 930)	Novel Protein sim. GBank gi 1808175 emb CAB08470 - (Z64395) rpsC [Mycobacterium tuberculosis]	Contains protein domain (PF00417) - Ribosomal protein S3, N-terminal domain.	UNCLASSIFIED	285017, 21908784, 285020
466	20460845 (931, 932)	Novel Protein sim. GBank gi 1808175 emb CAB08470 - (Z64395) rpsC [Mycobacterium tuberculosis]		UNCLASSIFIED	284805, 284859
467	80408035 (933, 934)	Novel Protein sim. GBank gi 548705 sp P36949 RBSB_BACSU - D-RIBOSE-BINDING PROTEIN PRECURSOR		UNCLASSIFIED	284784
468	52562208 (935, 936)	Novel Protein sim. GBank gi 2114024 emb CAB08957 - (Z85958) grcC1 [Mycobacterium tuberculosis]		UNCLASSIFIED	284892
469	19520527 (937, 938)	Novel Protein sim. GBank gi 2809459 emb CAA17347 - (AL021929) cobQ [Mycobacterium tuberculosis]		UNCLASSIFIED	284488
470	80502758 (939, 940)	Novel Protein sim. GBank gi 14921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	synthase		284602, 284769
471	17937351 (941, 942)	Novel Protein sim. GBank gi 14921 sp P17447 BETT_ECOLI - HIGH-AFFINITY CHOLINE TRANSPORT PROTEIN	transport		285019
472	80047458 (943, 944)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	284586, 284885, 284557
473	20558793 (945, 946)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	284389
474	80593365 (947, 948)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	22278897, 284892, 284288
475	82454665 (949, 950)	Novel Protein sim. GBank gi 882343 (L10908) - Gcsp1 gene product [Mus musculus]		UNCLASSIFIED	284807, 284908, 284511, 285008, 284782, 284448, 284638, 284638
476	84143657 (951, 952)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	65274572, 60432048, 284259, 284508, 52844045, 55812038, 284758, 285011, 284288, 284886, 52844228, 65274791, 284638, 284586
477	79175833 (953, 954)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284638
478	79832483 (955, 956)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284889, 284693
479	80189746 (957, 958)	Novel Protein sim. GBank gi 543896 ref NP_006328.1 pGAC1 - glioma amplified on chromosome 1 protein (leucine-rich)		UNCLASSIFIED	284888, 35685855, 285008, 284631, 284810, 284832, 284638, 285018, 284389, 284909
480	79390729 (959, 960)	Novel Protein sim. GBank gi 1127551 (U18939) - orf2 [Batrachococcus baikalensis]		mapolymerase	284389
481	78624578 (961, 962)	Novel Protein sim. GBank gi 1127551 (U18939) - orf2 [Batrachococcus baikalensis]		UNCLASSIFIED	284683
482	83050811 (963, 964)	Novel Protein sim. GBank gi 4083042 (AF068065) - GP800; much-like glycoprotein [Cryptosporidium parvum]		UNCLASSIFIED	284909, 284888, 284768, 284893, 55811576, 56182323, 18108385

483	20203308 (965, 966)	Novel Protein sim. GBank gij2104303jemb[CAB08632] - (Z95387) hypothetical protein Rv2810c [Mycobacterium tuberculosis]	Contains protein domain (PF00634) - Glycosyl transferases group 1	284600	
484	11618046 (967, 968)	Novel Protein sim. GBank gij3450883 (AF083334) - fibrin [Anthraxa pernyi]	UNCLASSIFIED	284594	
485	80191234 (969, 970)	Novel Protein sim. GBank gij5042272jemb[CAB44528.1] - (AL078616) nuoF, NADH dehydrogenase subunit [Streptomyces coelicolor]	UNCLASSIFIED	284604	22279002
486	80059042 (971, 972)		dehydrogenase		
487	11613338 (973, 974)			284638	
488	81222363 (975, 976)	Novel Protein sim. GBank gij5724778jgb[AAC5522.2] - (AF012273) rho-type GTPase-activating protein rhoGAPX-1 [Mus musculus]	Contains protein domain (PF00620) - RhoGAP domain	284688, 68714117, 284768, 18108385, 55911576, 265008, 265008, 265009, 265019, 22279002, 284259, 16108370, 284907, 284784, 56182323, 264288, 284693	
489	10867710 (977, 978)	Novel Protein sim. GBank gij3882223jdb[BAA34471.1] - (AB018294) KIAA0751 protein [Homo sapiens]	kinase	284639	
490	85381124 (979, 980)	Novel Protein sim. GBank gij82091jpi[A25494 - hydroxyproline-rich glycoprotein - tomato (fragment)]	collagen	22278996, 29331822, 29331828, 264107, 284908, 284110, 265009, 284592, 284593, 60433356, 264288, 264683, 263974, 263976, 20281071, 60432113	
491	80498412 (981, 982)	Novel Protein sim. GBank gij2894206jemb[CAA17072] - (AL021840) hypothetical protein Rv2258c [Mycobacterium tuberculosis]	UNCLASSIFIED	284768	
492	87421264 (983, 984)			284600	
493	11692942 (985, 986)		UNCLASSIFIED	284638	
494	87726604 (987, 988)	Novel Protein sim. GBank gij5282605jemb[CAB45743.1] - (AL080150) hypothetical protein [Homo sapiens]	UNCLASSIFIED	284489, 35698286, 60432289, 29331828, 35698052, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 265008, 284910, 33857402, 264762, 264764, 264768, 284769, 284688, 21908765, 21908789, 35698917, 265020, 284693, 33857109, 284629, 35698423, 35698585, 284634, 284638	
495	80028598 (989, 990)	Novel Protein sim. GBank gij2781517jemb[CAA16054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]	Contains protein domain (PF00005) - ABC transporter	284602, 284682, 264638	
496	78985624 (991, 992)	Novel Protein sim. GBank gij230281jdbj[R69] - 434 Repressor (Amino-Terminal Domain) [R1-68]	Contains protein domain (PF01361) - Helix-turn-helix	284601, 265021	
497	78848681 (993, 994)	Novel Protein sim. GBank gij129738jpi[P28225]PDXH_ECOLI - PYRIDOXAMINE 5'-PHOSPHATE OXIDASE (PNP/PMP OXIDASE)	oxidase	265008	

498	88095408 (995, 996)	Novel Protein sim. GBank gl 1145789 (U41662) - neuroigin 2 [Rattus norvegicus]	Contains protein domain (PF00133) - Carboxylesterases	esterase	284259, 29331826, 35698052, 284508, 284508, 284805, 284808, 284907, 284908, 284909, 284510, 284511, 285008, 284910, 284591, 33657402, 284758, 285010, 285011, 284800, 284801, 284805, 284883, 284784, 284788, 284787, 284788, 284887, 284789, 21808787, 33657023, 284893, 284828, 284829, 35698423, 284630, 284832, 284834, 284835, 284837, 284838, 284558, 284839, 18108385, 284583, 284584, 284565, 284566, 284567
499	20438222 (997, 998)	Novel Protein sim. GBank gl 97480 pir S18739 - integral membrane protein - Rhodobacter capsulatus		UNCLASSIFIED	284805
500	11076810 (999, 1000)				284805
501	13418034 (1001, 1002)	Novel Protein sim. GBank gl 5708250 emb CAB52363.1] - (AL108747) putative integral membrane protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	284888
502	80021176 (1003, 1004)	Novel Protein sim. GBank gl 4488678 emb CAB38132.1] - (AL035591) glucose-6-phosphate isomerase [Streptomyces coelicolor]	Contains protein domain (PF00342) - Phosphoglucose isomerase	isomerase	22278996, 285011, 284802, 284605, 284635
503	20284463 (1005, 1006)			UNCLASSIFIED	284564
504	10887321 (1007, 1008)			UNCLASSIFIED	284687
505	95003068 (1009, 1010)			UNCLASSIFIED	284389
506	16454282 (1011, 1012)	Novel Protein sim. GBank gl 4033509 sp P02589 CALM_TETPY - CALMODULIN	Contains protein domain (PF00036) - EF hand	struct	285010
507	20451598 (1013, 1014)	Novel Protein sim. GBank gl 2501089 sp Q48127 SYW_CLOLO - TRYPTOPHANYL-TRNA SYNTHETASE (TRYPTOPHAN--TRNA LIGASE) (TRPRS)		UNCLASSIFIED	284604
508	79841424 (1015, 1016)	Novel Protein sim. GBank gl 468089 sp P34818 YO82_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN ZK1238.2 IN CHROMOSOME III		UNCLASSIFIED	284808
509	11776388 (1017, 1018)				284638
510	83373465 (1019, 1020)			UNCLASSIFIED	284887, 284639
511	16525578 (1021, 1022)				285007
512	20398484 (1023, 1024)	Novel Protein sim. GBank gl 2497418 sp P55635 Y4RB_RHISN - PUTATIVE INTEGRASE/RECOMBINASE Y4RB		UNCLASSIFIED	284565
513	79457404 (1025, 1026)	Novel Protein sim. GBank gl 1276897 (U41809) - cyclin J [Drosophila melanogaster]	Contains protein domain (PF00134) - Cyclin	cyclin	284683, 284688, 35698423, 284639
514	79813805 (1027, 1028)	Novel Protein sim. GBank gl 1184780 (U46088) - von Ebner minor salivary gland protein [Mus musculus]		UNCLASSIFIED	29331830, 284909
515	79462591 (1029, 1030)				22278999, 284690
516	9862020 (1031, 1032)	Novel Protein sim. GBank gl 2127400 pir S65770 - maltotriose trehalase trehalohydrolase - Arthrobacter sp. (strain Q38)		amylase	284910

517	95262994 (1033, 1034)	Novel Protein sim. GBank gll2983605 (AE000725) - ribose 5 phosphate isomerase B [Aquifex aeolicus]		isomerase	265018, 264605, 264764, 264766, 264687, 264691, 264585
518	8491831 (1035, 1036)	Novel Protein sim. GBank gll854085[emb]CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	264487
519	91877888 (1037, 1038)	Novel Protein sim. GBank gll5689365[db]BAA83073.1] - (AB024075) B120 [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	dna_bind	52644507, 22278897, 22278898, 60432049, 264259, 52645080, 29331824, 66714117, 60424269, 29331828, 35696052, 264905, 29331830, 66712502, 264511, 265007, 264591, 60432229, 33657402, 60433438, 21908754, 33109954, 52644298, 87188474, 87188559, 265017, 265018, 264604, 265019, 264681, 264448, 264369, 264288, 264685, 21908765, 21908766, 21908787, 21908789, 265021, 60170615, 33657023, 264692, 52645128, 33657109, 27486262, 27486264, 35695783, 18108370, 264629, 52644332, 56182323, 264639, 83373044, 18108385, 56528488, 60432113
520	78669188 (1039, 1040)				264769
521	11076821 (1041, 1042)	Novel Protein sim. GBank gll1169128[sp]P46839[CTPA_MYCLE - CATION-TRANSPORTING P-TYPE ATPASE A		transport	264605
522	80433608 (1043, 1044)	Novel Protein sim. GBank gll1172689[sp]P44331[RB5K_HAEIN - RIBOKINASE	Contains protein domain (PF00284) - pRB family carbohydrate kinase	kinase	264805, 264768
523	16356013 (1045, 1046)	Novel Protein sim. GBank gll2132243[pir]S81028 - hypothetical protein YPL238c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	264629
524	80261605 (1047, 1048)	Novel Protein sim. GBank gll4033608[db]BAA35136] - (AB012308) B2HC [Anthracidaria crassispine]		ATPase_associated	264092, 264596, 265011
525	79810048 (1049, 1050)				264807
526	38827630 (1051, 1052)	Novel Protein sim. GBank gll4106610[emb]CAA21365] - (AL031866) ORF42, len=386 aa, similarity to an aminotransferase, in P95957 Sulfolobus solfataricus, (401 aa), 33.1% identity in 393 aa overlap. Fasta scores: opt:468, E(): 8.5e-24, in Q64802 R. norvegicus, (425 aa), 28.6% ident...		UNCLASSIFIED	264758
527	80504729 (1053, 1054)				
528	85484134 (1055, 1056)			UNCLASSIFIED	264769
529	17936810 (1057, 1058)	Novel Protein sim. GBank gll731088[sp]P24215[UUA_ECOLI - MANNONATE DEHYDRATASE (D-MANNONATE HYDROLASE)		UNCLASSIFIED	56182575, 265017, 265018
530	10687336 (1059, 1060)	Novel Protein sim. GBank gll42144[emb]CAA25200] - (X00513) NusA protein (nusA) [Escherichia coli]		hydrolase	265019
531	80226576 (1061, 1062)			UNCLASSIFIED	264687
532	80933444 (1063, 1064)	Novel Protein sim. GBank gll5282840[emb]CAB45758.1] - (AL080170) hypothetical protein [Homo sapiens]	Contains protein domain (PF00822) - SPRY domain	UNCLASSIFIED	264555, 264556, 264557, 264558, 18108385
				UNCLASSIFIED	264488, 264490, 264259, 264592, 264760, 265021, 264690, 263976, 264558

533	87761531 (1085, 1088)	Novel Protein sim. GBank gij4883839 gb AAD31583.1 AF11229 - (AF11229) Integral inner nuclear membrane protein MAN1 (Homo sapiens)			284907, 284808, 284788, 35695917, 284630, 284555
534	82388284 (1087, 1088)	Novel Protein sim. GBank gij2895352 emb CAA04808.1 - (A001208) pep1 [Streptomyces coelicolor]	UNCLASSIFIED		284905, 265011, 284601, 284602, 284805, 284782, 284788, 285020, 284893, 284838 284906
535	78841850 (1088, 1070)	Novel Protein sim. GBank gij3878638 emb CAA88953 - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:700719 comes from this gene; cDNA EST yk465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST Y...	Contains protein domain (PF00069) - ATPase associated Eukaryotic protein kinase domain		
536	79807207 (1071, 1072)	Novel Protein sim. GBank gij2498628 sp P55757 YOH1_SERMA - HYPOTHETICAL 10.1 KD PROTEIN IN BIOA 5 REGION	reductase		18108376, 284905, 284906, 284907, 284909
537	84147448 (1073, 1074)				
538	87821863 (1075, 1076)	Novel Protein sim. GBank gij134820 sp P21897 SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)	collagen		285008, 284605, 65274781 28331822, 28331824, 28331825, 28331826, 28331827, 284908, 52844045, 33857402, 265017, 284782, 284883, 284288, 284885, 21908785, 35885783, 284558, 80170394, 284558, 22279002 284602, 265019
539	28398288 (1077, 1078)	Novel Protein sim. GBank gij2498433 sp Q12341 HAT1_YEAST - HISTONE ACETYLTRANSFERASE	histone		
540	79837077 (1079, 1080)				
541	87782288 (1081, 1082)	Novel Protein sim. GBank gij3882241 db BAA34480.1 - (AB018303) KIAA0760 protein (Homo sapiens)	Contains protein domain (PF00086) - Zinc finger, C2H2 type		284893 18108394, 22278997, 22278998, 284259, 284112, 265009, 33857402, 55812038, 52846317, 265017, 21908785, 284893, 55811576, 284635, 58528488, 284588 284910, 265018, 284889, 284638, 284486
542	85285638 (1083, 1084)	Novel Protein sim. GBank gij5042272 emb CAB4528.1 - (AL078618) nuof, NADH dehydrogenase subunit [Streptomyces coelicolor]	dehydrogenase		
543	79788290 (1085, 1086)				
544	20437181 (1087, 1088)	Novel Protein sim. GBank gij2791398 emb CAA15994 - (AL021184) hypothetical protein Rv1484 [Mycobacterium tuberculosis]	UNCLASSIFIED UNCLASSIFIED		284602, 284908 284605
545	80434504 (1089, 1090)				
546	80249016 (1091, 1092)	Novel Protein sim. GBank gij4887211 gb AAD32237.1 AF14744 - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]			284788, 284634, 284907, 284592, 284909 284600, 284602, 21908785
547	11077563 (1093, 1094)	Novel Protein sim. GBank gij1350855 sp P18176 RPOC_PSEPU - DNA-DIRECTED RNA POLYMERASE BETA' CHAIN (TRANSCRIPTASE BETA' CHAIN) (RNA POLYMERASE BETA' SUBUNIT)	mapolymerase		284604
548	82114938 (1095, 1098)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin- related protein; KRP; Costal2 [Drosophila melanogaster]	UNCLASSIFIED		284488, 284905, 284910, 284780, 284693, 284639, 284563, 284584

549	95421904 (1097, 1098)	Novel Protein sim. GBank gll4337460[gb AAD18133] - (AF056195) neuroblastoma-amplified protein [Homo sapiens]		UNCLASSIFIED	264488, 65274572, 18108398, 22278995, 22278998, 22278997, 22278998, 22278999, 264259, 29331824, 68714117, 29331825, 29331826, 35696052, 265007, 265008, 264910, 264592, 33857402, 33109954, 265017, 265018, 265019, 18108351, 264448, 264764, 264369, 264288, 264766, 264888, 264888, 21906765, 21906786, 21906787, 21906788, 21906789, 265020, 264691, 33857023, 264692, 264693, 65274620, 52845129, 33857108, 27486261, 27486262, 27488264, 33857349, 55811576, 18108387, 60432113, 22278002
550	10886616 (1098, 1100)	Novel Protein sim. GBank		UNCLASSIFIED	264688
551	60439980 (1101, 1102)	Novel Protein sim. GBank gll3122893[sp P94085 SYFB_MYCTU - PHENYLALANYL-TRNA SYNTHETASE BETA CHAIN (PHENYLALANINE--TRNA LIGASE BETA CHAIN) (PHERS)]		UNCLASSIFIED	264908, 264909, 264768
552	94672870 (1103, 1104)	Novel Protein sim. GBank gll501877[gb AAD37657.1 AF13326 - (AF133263) histidine protein kinase-response regulator hybrid protein CvgSY [Pseudomonas syringae pv. syringae]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264689, 264639, 264563
553	80106002 (1105, 1106)	Novel Protein sim. GBank		kinase	55811957, 264628
554	79818378 (1107, 1108)	Novel Protein sim. GBank gll131515[sp P02808 PTGA_SALTY - PTS SYSTEM, GLUCOSE-SPECIFIC IIA COMPONENT (EIIA-GLC) (GLUCOSE-PERMEASE IIA COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, A COMPONENT) (EIIA-GLC)]	Contains protein domain (PF00358) - phosphoenolpyruvate-dependent sugar phosphotransferase system, EIIA 1	transport	264762
555	78986347 (1109, 1110)	Novel Protein sim. GBank gll3914014[sp P98380 MFD_MYCTU - TRANSCRIPTION-REPAIR COUPLING FACTOR (TRCF)]		transcriptfactor	284508, 264605, 264559
556	20457127 (1111, 1112)	Novel Protein sim. GBank gll5042273[emb CAB44527.1 - (AL078618) nuoE, NADH dehydrogenase subunit (Streptomyces coelicolor)]		dehydrogenase	284488
557	19523405 (1113, 1114)	Novel Protein sim. GBank gll1170833[sp P45331 METE_HAEIN - 5-METHYLTETRAHYDROPTEROYLTRIGLUTAMATE--HOMOCYSTEINE METHYLTRANSFERASE (METHIONINE SYNTHASE, VITAMIN-B12 INDEPENDENT ISOZYME) (COBALAMIN-INDEPENDENT METHIONINE SYNTHASE)]		UNCLASSIFIED	264602
558	20724429 (1115, 1116)	Novel Protein sim. GBank gll4980567[gb AAD35173.1 AE001694] Iron(III) ABC transporter, permease protein [Thermotoga maritima]		UNCLASSIFIED	284634
559	80084353 (1117, 1118)	Novel Protein sim. GBank		UNCLASSIFIED	284634

560	80086533 (1119, 1120)	Novel Protein sim. GBank gi2492585 sp Q53183 Y4TR_RHISN - PROBABLE PEPTIDE ABC TRANSPORTER ATP-BINDING PROTEIN Y4TR	Contains protein domain (PF00005) - ABC transporter	transport	18108386, 284908, 284602, 284604, 18108374
561	20283187 (1121, 1122)			UNCLASSIFIED	284800
562	11688161 (1123, 1124)			UNCLASSIFIED	284889
563	79761420 (1125, 1126)	Novel Protein sim. GBank gi4104925 (AF042276) - poly(hydroxycarboxylate) granule associated protein GA2 [Pseudomonas putida]		UNCLASSIFIED	284910, 284691
564	58718380 (1127, 1128)	Novel Protein sim. GBank gi2792310 (AF040570) - unknown [Amycolatopsis mediterranei]		dehydrogenase	284582
565	58465618 (1129, 1130)	Novel Protein sim. GBank gi3449294 gb BAA32482 - (AB011532) MEGF8 [Rattus norvegicus]	Contains protein domain (PF00008) - EGF-like domain	synthase	285010
566	94323888 (1131, 1132)	Novel Protein sim. GBank gi4539568 emb CAB38487.1 - (AL035638) putative helicase [Streptomyces coelicolor]		helicase	284908, 284510, 285008, 284910, 284758, 284800, 284602, 284604, 284605, 284768, 284887, 284689, 35895917, 284693, 85274820, 284488
567	78560955 (1133, 1134)	Novel Protein sim. GBank gi100506 pir S17455 - Malate dehydrogenase (oxaloacetate-decarboxylating) (NADP+) (EC 1.1.1.40) - Flavaria trichervia (fragment)		UNCLASSIFIED	284881, 284691, 284593
568	94881793 (1135, 1136)	Novel Protein sim. GBank gi3915843 sp Q31212 IRS2_STRCO - 30S RIBOSOMAL PROTEIN S2	Contains protein domain (PF00380) - Malic enzyme	dehydrogenase	284889
569	39508897 (1137, 1138)	Novel Protein sim. GBank gi118122 sp P21827 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD	Contains protein domain (PF00318) - ribosomal prot		284565
570	78375927 (1139, 1140)			UNCLASSIFIED	18108378, 18108387, 284565
571	79783961 (1141, 1142)	Novel Protein sim. GBank gi118122 sp P21827 BRAD_PSEAE - HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID TRANSPORT PROTEIN BRAD		transport	284907, 284809
572	38988838 (1143, 1144)			UNCLASSIFIED	284782
573	20715521 (1145, 1146)	Novel Protein sim. GBank gi4539223 emb CAB38881.1 - (AL048487) putative integral membrane protein [Streptomyces coelicolor]		UNCLASSIFIED	285007, 284601
574	13521592 (1147, 1148)				284838
575	13078416 (1149, 1150)	Novel Protein sim. GBank gi118794 sp P10443 DP3A_ECOLI - DNA POLYMERASE III, ALPHA CHAIN		polymerase	284887
576	20482246 (1151, 1152)	Novel Protein sim. GBank gi15457625 emb CAB49116.1 - (AJ248283) PAB2227 [Pyrococcus abyssi]			284605
577	68727102 (1153, 1154)	Novel Protein sim. GBank gi5042274 emb CAB44528.1 - (AL078818) nuod, NADH dehydrogenase subunit [Streptomyces coelicolor]	Contains protein domain (PF00346) - Respiratory-chain NADH dehydrogenase, 49 Kd subunit	dehydrogenase	35896052, 284638
578	11804477 (1155, 1156)				284838
579	11794723 (1157, 1158)	Novel Protein sim. GBank gi11723081 sp Q11046 Y089_MYCTU - HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CY50.09		transport	284882, 284559

580	80059417 (1159, 1180)					22278999, 35696052, 264555, 264556, 264558, 264559
581	79230833 (1181, 1182)				UNCLASSIFIED	265008, 264564
582	80049617 (1183, 1184)			Contains protein domain (PF00047) - immunoglobulin domain	struct	265021, 264555, 264557
583	79321392 (1165, 1166)			Novel Protein sim. GBank gij3243131 (AF045777) - ilin [Drosophila melanogaster]	transport	264564
584	79845024 (1187, 1188)			Novel Protein sim. GBank gij2501182ispj77726jYAJR_ECOLI - HYPOTHETICAL 49.0 KD PROTEIN IN ABPA-CYOE INTERGENIC REGION		
585	79581454 (1168, 1170)			Novel Protein sim. GBank gij3882221dbjBAA34470.1] - (AB018283) KIAA0750 protein [Homo sapiens]	UNCLASSIFIED	264488, 264908, 264788, 264887, 35696423
586	39277496 (1171, 1172)			Novel Protein sim. GBank gij4467250[emb]CAB37575] - (AL035589) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]	UNCLASSIFIED	265018, 264684, 21806769
587	80497359 (1173, 1174)			Novel Protein sim. GBank gij5689518dbjBAA33043.1] - (AB028014) KIAA1091 protein [Homo sapiens]	UNCLASSIFIED	264908, 265007
588	79557239 (1175, 1176)			Novel Protein sim. GBank gij2143293[emb]CAB09380] - (Z95972) rpoB [Mycobacterium tuberculosis]	hydrolase	264600, 264602, 264605, 264769, 264690, 264557
589	79805828 (1177, 1178)			Novel Protein sim. GBank gij4511983jgJ/AA021843.1] - (AF088898) electrotransfer ubiquinone oxidoreductase [Zymomonas mobilis]	UNCLASSIFIED	265020, 264692
590	79815629 (1178, 1180)			Novel Protein sim. GBank gij1272368 (U51896) - LfGE [Vibrio parahaemolyticus]	MHC	22278998, 264907, 264909, 264510, 265009, 265010, 264687, 264769, 35695917, 18108376, 264634, 264636, 264638
591	10313540 (1181, 1182)			Novel Protein sim. GBank gij131480jgJ/P20968jPTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)	dehydrogenase	264691
592	13899767 (1183, 1184)			Novel Protein sim. GBank gij1272368 (U51896) - LfGE [Vibrio parahaemolyticus]	UNCLASSIFIED	264605
593	82348899 (1185, 1186)			Novel Protein sim. GBank gij131480jgJ/P20968jPTFB_ECOLI - PTS SYSTEM, FRUCTOSE-SPECIFIC IIBC COMPONENT (EIBC-FRU) (FRUCTOSE-PERMEASE IIBC COMPONENT) (PHOSPHOTRANSFERASE ENZYME II, BC COMPONENT) (EII-FRU)	UNCLASSIFIED	264769
594	20212382 (1187, 1188)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)		
595	10064064 (1188, 1190)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)	UNCLASSIFIED	264636
596	13085170 (1191, 1192)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)	UNCLASSIFIED	264592
597	80259003 (1193, 1194)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)	UNCLASSIFIED	264758, 65810784, 264555, 264556, 264637, 83373044
598	94140218 (1195, 1196)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)	UNCLASSIFIED	264603
599	20385137 (1197, 1198)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)		
600	10357883 (1198, 1200)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)		
601	79810404 (1201, 1202)			Novel Protein sim. GBank gij125329jgJ/P04951jKDSB_ECOLI - 3-DEOXY-MANNO-OCTULOSONATE CYTIDYL TRANSFERASE (CMP-KDO SYNTHETASE) (CMP-2-KETO-3-DEOXYOCTULOSONIC ACID SYNTHETASE) (CKS)	UNCLASSIFIED	264808, 264510

802	78250602 (1203, 1204)	Novel Protein sim. GBank gij3522981gjbAAC34243.1 - (AC004411) putative pto kinase [Arabidopsis thaliana]	Contains protein domain (PF00089) - kinase Eukaryotic protein kinase domain	265007	
803	11466087 (1205, 1206)		UNCLASSIFIED	284595	
804	81675420 (1207, 1208)			284758	
805	20438657 (1209, 1210)	Novel Protein sim. GBank gij1175322spjP44917Y883_HAEIN - HYPOTHETICAL PROTEIN H10883	UNCLASSIFIED	284605	
806	80334582 (1211, 1212)	Novel Protein sim. GBank gij5020284gjbAAD38043.1 AF15138 - (AF151383) Cdc42 GTPase-activating protein [Mus musculus]	UNCLASSIFIED	284764	
807	95381508 (1213, 1214)	Novel Protein sim. GBank gij188864 (M74027) - mucin [Homo sapiens]	UNCLASSIFIED	284508, 284908, 85658542, 284682, 284687, 284688, 284534, 18108378, 35998423, 284638, 284555, 284638	
808	11810888 (1215, 1216)		UNCLASSIFIED	284682	
809	80064775 (1217, 1218)	Novel Protein sim. GBank gij2498701spjP55552Y4LL_RHISN - HYPOTHETICAL 81.8 KD PROTEIN Y4LL	Contains protein domain (PF00989) - PAS domain	284605	
810	79629413 (1219, 1220)			284692	
811	87586208 (1221, 1222)			284508, 284908, 284907, 284908, 284909, 284511, 284910, 284758, 284604, 284684, 284786, 284888, 284892, 284628, 284635, 284636, 284637, 284558	
812	95287851 (1223, 1224)	Novel Protein sim. GBank gij1877386lmbjCAB07118 - (Z82772) recD [Mycobacterium tuberculosis]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	284600, 284601, 284604, 284789, 284558, 284565	
813	7523475 (1225, 1226)		UNCLASSIFIED	284389	
814	78969348 (1227, 1228)	Novel Protein sim. GBank gij5114231gjbAAD40238.1 AF13870 - (AF138709) histidine kinase YycG [Staphylococcus aureus]	kinase	18108372, 284563	
815	39586888 (1229, 1230)	Novel Protein sim. GBank gij1339850dbj BAA12741 - (D85230) large subunit of NADH-dependent glutamate synthase [Plectonema boryanum]	synthase	284600, 284602, 284629	
816	20465331 (1231, 1232)	Novel Protein sim. GBank gij544387spjP35673GALE_ERWAM - UDP-GLUCOSE 4- EPIMERASE (GALACTOWALDENASE) (UDP- GALACTOSE 4-EPIMERASE)	isomerase	284605	
817	91227222 (1233, 1234)	Novel Protein sim. GBank gij2498987spjO60789 TNP3_MOUSE - TUMOR NECROSIS FACTOR, ALPHA-INDUCED PROTEIN 3 (PUTATIVE DNA BINDING PROTEIN A20) (ZINC FINGER PROTEIN A20)	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	52845158, 21806785, 35698423, 21806788, 21808789, 22278994, 35698286, 22278998, 285020, 285021, 285007, 285008, 284636, 52844150, 33657023, 284692, 284693, 28331822, 28331824, 55812038, 83373044, 58182181, 60424269, 68714117, 28331825, 33657109, 28331826, 33657182, 28331827, 356986052, 28331828, 27486262, 33657349, 56528486, 285018, 285019, 22279002, 284482, 284448, 28331830, 68712502, 284909	

618	20632843 (1235, 1236)	Novel Protein sim. GBank gl 5459388 emb CAB50746.1 - (AL096839) putative aminotransferase [Streptomyces coelicolor]		isomerase	264603
619	91227224 (1237, 1238)				56994075, 29331826, 33656970, 265008, 33657402, 33109954, 87168559, 264448, 18108374, 83373044
620	61183143 (1239, 1240)	Novel Protein sim. GBank gl 46433 sp Q05922 DUS2_MOUSE - DUAL SPECIFICITY PROTEIN PHOSPHATASE 2 [DUAL SPECIFICITY PROTEIN PHOSPHATASE PAC-1]		phosphatase	29148498, 264756, 284389, 29148627
621	80239251 (1241, 1242)	Novel Protein sim. GBank gl 2633557 emb CAB13060 - (Z99110) yjdF [Bacillus subtilis]		UNCLASSIFIED	264556, 264558, 264639
622	20458427 (1243, 1244)	Novel Protein sim. GBank gl 1857710 gb AAB48482 - (U87224) contactin associated protein [Rattus norvegicus]		UNCLASSIFIED	264605
623	10131788 (1245, 1246)	Novel Protein sim. GBank gl 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK	Contains protein domain (PF00054) - laminin G domain	laminin	264908
624	19534127 (1247, 1248)	Novel Protein sim. GBank gl 1705703 sp P52225 CCMF_PSEFL - CYTOCHROME C-TYPE BIOGENESIS PROTEIN CYCK		cytochrome	264596
625	13084619 (1249, 1250)	Novel Protein sim. GBank gl 2894252 emb CAA17114.1 - (AL021841) hypothetical protein Rv3342 [Mycobacterium tuberculosis]		UNCLASSIFIED	264688
626	88062803 (1251, 1252)	Novel Protein sim. GBank gl 416592 sp P32323 JAGA1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR		UNCLASSIFIED	28331822, 264805, 264808, 33657023, 33657108, 264558
627	80255457 (1253, 1254)	Novel Protein sim. GBank gl 3098418 (AF040844) - P140 [Mus musculus]		UNCLASSIFIED	18108394, 264112, 264593, 265022, 264635
628	80077086 (1255, 1256)	Novel Protein sim. GBank gl 1711643 sp P50528 SSP1_SCHPO - SERINE/THREONINE-PROTEIN KINASE SSP1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264600
629	79851602 (1257, 1258)	Novel Protein sim. GBank gl 1143204 (U34305) - ORF2; Method: conceptual translation supplied by author. [Shigella sonnei]		isomerase	264608, 264807
630	39565158 (1259, 1260)	Novel Protein sim. GBank gl 3236368 (AF084748) - S3-12 [Mus musculus]		UNCLASSIFIED	264490
631	20598718 (1261, 1262)	Novel Protein sim. GBank gl 140687 sp P11686 YQGB_ECOLI - HYPOTHETICAL 30.9 KD PROTEIN IN SBM-FBA INTERGENIC REGION (ORF 4) (F286)			263978
632	27843890 (1263, 1264)			UNCLASSIFIED	264808, 264800, 264605, 264768, 264689, 264486
633	80477772 (1265, 1266)			UNCLASSIFIED	264769
634	17938808 (1267, 1268)			UNCLASSIFIED	265019
635	79574508 (1269, 1270)			UNCLASSIFIED	264889
636	79810981 (1271, 1272)			UNCLASSIFIED	264596, 264782, 264693

637	82455798 (1273, 1274)	Novel Protein sim. GBank g 12328739 emb CAB10853 - (Z98288) recN [Mycobacterium tuberculosis]		nuclease	264908, 264907, 264510, 264511, 264601, 264602, 264603, 264604, 264605, 18108351, 264762, 264766, 264687, 264789, 264688, 35695917, 264693, 264634, 264638, 264639, 264559, 18108385, 264636
638	14997457 (1275, 1276)	Novel Protein sim. GBank g 4678662 emb CAB41074.1 - (AL049845) putative large ATP-binding protein [Streptomyces coelicolor]			
639	80204210 (1277, 1278)	Novel Protein sim. GBank g 458828 db BAA76838.1 - (AB023209) KIAA0992 protein [Homo sapiens]		struct	264112, 263974
640	17928578 (1278, 1280)	Novel Protein sim. GBank g 11432083 (U60981) - homolog to Skp1p, an evolutionarily conserved kinetochore protein in budding yeast [Arabidopsis thaliana]		nuclease	265009, 265010
641	79836398 (1281, 1282)			UNCLASSIFIED	264693
642	19898737 (1283, 1284)			UNCLASSIFIED	264565
643	81516220 (1285, 1286)			UNCLASSIFIED	264908, 264908, 264758, 264288, 264632, 264635, 264638, 264584
644	11751367 (1287, 1288)			UNCLASSIFIED	264684
645	85010907 (1289, 1290)			UNCLASSIFIED	264908, 264762, 264693, 264639, 264559
646	80089083 (1291, 1292)			UNCLASSIFIED	264595, 264588
647	80257085 (1293, 1294)	Novel Protein sim. GBank g 4507813 ref NP_003738.1 pTNKS - TANKYRASE		transcript factor	264909, 264591
648	80077428 (1295, 1296)	Novel Protein sim. GBank g 1044863 bbs 169848 - protamine [Monodonta turbinata, gonads, Peptide, 108 aa]		UNCLASSIFIED	264600
649	80247447 (1297, 1298)			UNCLASSIFIED	263978
650	11798318 (1299, 1300)			UNCLASSIFIED	264688
651	11776832 (1301, 1302)	Novel Protein sim. GBank g 1346918 sp P12283 PURA_ECOLI - ADENYLOSUCCINATE SYNTHETASE (IMP-ASPARTATE LIGASE)			264602, 264638
652	85516704 (1303, 1304)	Novel Protein sim. GBank g 1722977 sp Q10638 Y03C_MYCTU - HYPOTHETICAL 82.8 KD PROTEIN CY130.12C		UNCLASSIFIED	264805, 264907, 264909, 263978, 264637
653	82124947 (1305, 1306)			UNCLASSIFIED	22278998, 264510, 264511, 264512, 264593, 21906754, 264803, 264760, 18108376, 264558
654	95010589 (1307, 1308)	Novel Protein sim. GBank g 130327 sp P26647 PLSC_ECOLI - 1-ACYL-SN-GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE (1-AGP ACYLTRANSFERASE) (1-AGPAT) (LYSOPHOSPHATIDIC ACID ACYLTRANSFERASE) (LPAAT)		UNCLASSIFIED	264908, 264595, 264632
655	79320892 (1309, 1310)			transferase	264592
656	80418738 (1311, 1312)				
657	20811010 (1313, 1314)			UNCLASSIFIED	264602, 264605, 264766, 264691
				UNCLASSIFIED	264557, 264558

659	87761915 (1315, 1316)	Novel Protein sim. GBank gij5689483jdbj BAA83030.1 - (AB029001) KIAA1078 protein [Homo sapiens]	UNCLASSIFIED	22278998, 60432049, 29331822, 29331824, 29331826, 285007, 285009, 33657402, 33657084, 285017, 264448, 21908785, 21908786, 283987, 20281148, 18108370, 18108374, 264482
659	87718663 (1317, 1318)	Novel Protein sim. GBank gij2137872jprj 48724 - zinc finger protein PZF - mouse	transcription factor	22278999, 60432049, 66714117, 29331827, 285007, 284786, 56181562, 18108359, 18108385, 18108370, 18108381
660	81897822 (1319, 1320)	Novel Protein sim. GBank	UNCLASSIFIED	284787
661	80026023 (1321, 1322)	gij134180jpr 15401 ISACV_BACSU - LEVANSUCRASE AND SUCRASE SYNTHESIS OPERON ANTI-TERMINATOR	UNCLASSIFIED	284604, 284605, 32833886, 18108376, 284636, 18108387, 22278000
662	20463731 (1323, 1324)	Novel Protein sim. GBank	UNCLASSIFIED	284605
663	20626080 (1325, 1326)	gij4544229jpb AAD22450.1 AF11618 - (AF116183) SecA homolog [Actinobacillus actinomycetemcomitans]	dehydrogenase	284605
664	80508512 (1327, 1328)	Novel Protein sim. GBank gij5689250jdbj BAA82881.1 - (AB024335) similar to orf3 [Comamonas testosteroni]	UNCLASSIFIED	284789
665	80078053 (1329, 1330)	Novel Protein sim. GBank gij1852848jdbj BAA17788 - (D90909) DNA photolyase [Synechocystis sp.]	isomerase	284600
666	79603142 (1331, 1332)	Novel Protein sim. GBank gij3261829jemb CAB10927 - (Z98280) hypothetical protein Rv1230c [Mycobacterium tuberculosis]	glycoprotein	284907, 265007
667	94631802 (1333, 1334)	Novel Protein sim. GBank gij5688851jdbj BAA82702.1 - (AB017438) Orf5 [Streptomyces coelicolor]	UNCLASSIFIED	284689, 284602, 264593
668	82051891 (1335, 1336)	Novel Protein sim. GBank gij3581853jemb CAA20809 - (AL031541) 50S ribosomal protein L20 [Streptomyces coelicolor]	ribosomal prot	284905, 284906, 284908, 284600, 264601, 284603, 284605, 284760, 284689, 284636, 284638, 284639
669	12987154 (1337, 1338)	Novel Protein sim. GBank gij2582531 (AF028444) - 2- isopropylmalate synthase [Streptomyces coelicolor]	UNCLASSIFIED	284637
670	80236549 (1339, 1340)	Novel Protein sim. GBank gij2582531 (AF028444) - 2- isopropylmalate synthase [Streptomyces coelicolor]	synthase	284905, 284906, 284908, 284601, 284762, 284788, 284689, 284638, 18108385, 264486
671	79601388 (1341, 1342)	Novel Protein sim. GBank gij2582531 (AF028444) - 2- isopropylmalate synthase [Streptomyces coelicolor]	UNCLASSIFIED	284690, 284692, 284693, 284636, 18108387
672	79834371 (1343, 1344)	Novel Protein sim. GBank gij2114430 (U92703) - Oil-1/EBF-like-3 transcription factor [Mus musculus]	transcription factor	284910, 265017
673	82285788 (1345, 1346)	Novel Protein sim. GBank gij4589285jpb AAD26430.1 AF13515 - (AF135154) ferric alkaligin siderophore receptor [Bordetella pertussis]		284759
674	79198259 (1347, 1348)		UNCLASSIFIED	284629

875	87895870 (1349, 1350)	Novel Protein sim. GBank gi 4980755 gb AA035347.1 AE001700 - (AE001700) D- alanine-D-alanine ligase [Thermotoga maritima]	Contains protein domain (PF01820) - D-ala D-ala ligase	UNCLASSIFIED	284488, 22278989, 88714117, 284508, 284511, 285008, 80433438, 284600, 284601, 284602, 284603, 284604, 284605, 284762, 284687, 284769, 80431602, 18108374, 284636, 284638 285010
876	78898807 (1351, 1352)	Novel Protein sim. GBank gi 1723568 sp Q10479 YDF7_SCHPO - PUTATIVE GLUCOSYLTRANSFERASE C17C8.07		ATPase-associated	284591, 284632
877	21644312 (1353, 1354)	Novel Protein sim. GBank gi 887208 (U03976) - dynein heavy chain isoform 5C [Tripneustes gratilis]			
878	84225200 (1355, 1356)	Novel Protein sim. GBank gi 158627 lprf 2203365A - laminin alpha5 [Mus musculus]	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	284758, 284682, 284557
879	79888855 (1357, 1358)	Novel Protein sim. GBank gi 3928723 emb CAA22219 - (AL034355) putative ABC transporter [Streptomyces coelicolor]		UNCLASSIFIED	22278988, 284693
880	20728424 (1359, 1360)	Novel Protein sim. GBank gi 5174483 ref NP_008050.1 pLAMC - laminin, gamma 3	Contains protein domain (PF00053) - Laminin EGF-like (Domains III and V)	laminin	284600, 284602 284102, 284907, 284908, 285006, 284693, 283872, 83373044, 284566
882	11392478 (1363, 1364)	Novel Protein sim. GBank gi 4768208 ref NP_004081.1 pDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VHI-related)	Contains protein domain (PF00762) - Dual specificity phosphatase, catalytic domain	UNCLASSIFIED phosphatase	284595 284634
883	80083680 (1365, 1366)	Novel Protein sim. GBank gi 5420387 emb CA46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]			284605
885	80248735 (1369, 1370)				284809, 283987, 283981
886	79208608 (1371, 1372)				284631
887	80085829 (1373, 1374)				284693, 284635
888	79853412 (1375, 1376)	Novel Protein sim. GBank gi 2688982 (AF027768) - LepA (Serratia marcescens)		peptidase	284807, 284638
889	88084258 (1377, 1378)	Novel Protein sim. GBank gi 3046931 (AF049330) - PPAR gamma coactivator [Mus musculus]	Contains protein domain (PF00076) - RNA recognition motif (e.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284808, 284907, 285007, 285009, 80433438, 21908754, 284760, 18108358, 21908766, 21908769, 285021, 18108361, 283974, 18108379, 284557, 18108385, 22278002 284510, 284511, 284764, 284769
890	80389750 (1379, 1380)	Novel Protein sim. GBank gi 2498941 sp Q15428 SP62_HUMAN - SPLICEOSOME ASSOCIATED PROTEIN 62 (SAP 62) (SF3A86)		UNCLASSIFIED	
891	81854392 (1381, 1382)			UNCLASSIFIED	284757
892	83088938 (1383, 1384)	Novel Protein sim. GBank gi 8420387 emb CA46679.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	55811957, 285018, 55811150, 18108351, 284908, 80431528, 284594
893	79588116 (1385, 1386)	Novel Protein sim. GBank gi 854085 emb CAA58337 - (X83413) U68 [Human herpesvirus 6]		UNCLASSIFIED	284635
894	82459983 (1387, 1388)	Novel Protein sim. GBank gi 287327 sp Q01033 VC48_HSVSA - HYPOTHETICAL GENE 48 PROTEIN			22278988, 284510, 284602, 284603, 284762, 284687, 284769, 284693

685	94147849 (1389, 1390)	Novel Protein sim. GBank glj4468339[emb]CAB38059.1] - (AJ010801) MUC4 [Homo sapiens]	Contains protein domain (PF000094) - von Willebrand factor type D domain	UNCLASSIFIED	56182575, 284508, 284905, 284907, 29331830, 284908, 284909, 284511, 285007, 284910, 284758, 284784, 284288, 85274791
686	78830982 (1391, 1392)	Novel Protein sim. GBank glj2849950 (AE001058) - glutamine ABC transporter, ATP-binding protein (gnc) [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	284905, 284595
687	11767869 (1393, 1394)	Novel Protein sim. GBank glj1731343[sp]Q10894[YY25_MYCTU - HYPOTHETICAL 24.4 KD PROTEIN CY48.25]	Contains protein domain (PF01836) - Transposase	UNCLASSIFIED	284682
688	66695862 (1395, 1396)			UNCLASSIFIED	284888, 35695917
689	79582558 (1397, 1398)			UNCLASSIFIED	284682
700	78830998 (1399, 1400)				284693
701	80230242 (1401, 1402)	Novel Protein sim. GBank glj1001238[db]BAA104771 - (DB4003) hypothetical protein [Synchocystis sp.]		UNCLASSIFIED	284488, 284510, 284511, 284602, 284605, 284689
702	78814789 (1403, 1404)	Novel Protein sim. GBank glj2498935[sp]Q46338[SOXG_CORSP - SARCOSINE OXIDASE GAMMA SUBUNIT]		UNCLASSIFIED	284604
703	20446820 (1405, 1406)	Novel Protein sim. GBank glj3150513 (AF067219) - contains similarity to the Ketch/MIPP family [Caenorhabditis elegans]	Contains protein domain (PF01344) - Kelch motif	UNCLASSIFIED	284288, 56181562, 33657109, 284628, 55811578
704	84312224 (1407, 1408)	Novel Protein sim. GBank glj421091[pr]S30730 - hypothetical protein o206 - Escherichia coli		UNCLASSIFIED	285008
705	17832141 (1409, 1410)	Novel Protein sim. GBank glj3024872[sp]Q55780[YY074_SYNYS3 - HYPOTHETICAL 52.8 KD PROTEIN SLR0074]			284600
706	20288062 (1411, 1412)	Novel Protein sim. GBank glj3420608[gb]AAC31907.1] - (AF075709) ABC transporter ATP-binding subunit [Pseudomonas putida]	transport		284603
707	20838065 (1413, 1414)	Novel Protein sim. GBank glj3649741[emb]CAA03985] - (AJ000281) mucin [Homo sapiens]	struct		284601, 284692
708	20708292 (1415, 1416)	Novel Protein sim. GBank glj3080425[emb]CAA18744.1] - (AL022804) putative protein [Arabidopsis thaliana]			18100398, 284637, 284908, 284909
709	88001439 (1417, 1418)	Novel Protein sim. GBank glj4758689[ref]NP_002323.1]pLRP1 - low density lipoprotein related protein 1 (alpha-2-macroglobulin receptor)			284369
710	11356683 (1419, 1420)	Novel Protein sim. GBank glj1703268[sp]Q11056[AM12_MYCTU - PUTATIVE AMIDASE CY50.19C]	Contains protein domain (PF000058) - apolipoprotein		265019
711	17831418 (1421, 1422)	Novel Protein sim. GBank glj4502351[ref]NP_001692.1]pBAAT - bile acid Coenzyme A: amino acid N-acyltransferase; glycine N-choyltransferase	Low-density lipoprotein receptor repeat class B		284591
712	80258164 (1423, 1424)				
713	78263126 (1425, 1426)		hydrolase		284906, 284607
714	27847851 (1427, 1428)				284508, 284555

715	78639423 (1429, 1430)	Novel Protein sim. GBank gl 178033 (AE000352) - ori, hypothetical protein [Escherichia coli]		UNCLASSIFIED	284807
716	78559072 (1431, 1432)	Novel Protein sim. GBank		dehydrogenase	284892
717	78481842 (1433, 1434)	gi 2484074 sp P55653 GABD_RHISN - PROBABLE SUCCINATE-SEMIALDEHYDE DEHYDROGENASE (NADP+) (SSDH)			284636
718	94319658 (1435, 1436)	Novel Protein sim. GBank gl 3873879 emb CAA94886 - (Z71176) similar to pro-collagen domains: cDNA EST EMBL:D27878 comes from this gene; cDNA EST EMBL:D27877 comes from this gene; cDNA EST EMBL:D34199 comes from this gene; cDNA EST EMBL:D84392 comes from this gene; cDNA EST EMBL... (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]	Contains protein domain (PF000093) - von Willebrand factor type C domain	kinase	18108392, 22278994, 22278998, 265008, 265018, 264681, 18108354, 264684, 264685, 264686, 264687, 264689, 21908789, 18108361, 264691, 264692, 55810764, 264635, 18108381, 18108382, 83373044, 18108388
719	17879564 (1437, 1438)	Novel Protein sim. GBank gl 2104302 emb CA08631 - (Z95387) hypothetical protein Rv2611c [Mycobacterium tuberculosis]		UNCLASSIFIED	285011
720	79841684 (1439, 1440)	Novel Protein sim. GBank			284808
721	15020180 (1441, 1442)	gi 123530 sp P04929 HRPX_PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR		UNCLASSIFIED	284629
722	9882603 (1443, 1444)	Novel Protein sim. GBank gl 498253 (U02372) - integrase [Vibrio cholerae]			264910
723	18755589 (1445, 1446)	Novel Protein sim. GBank gl 2263054 emb CAB10705 - (Z97559) hypothetical protein Rv2114 [Mycobacterium tuberculosis]		UNCLASSIFIED	284691
724	10126494 (1447, 1448)	Novel Protein sim. GBank gl 4063013 (AF063061) - protease PUA [Pseudomonas fluorescens]	Contains protein domain (PF00353) - Hemolysin-type calcium-binding proteins	protease	284909
725	7878678 (1449, 1450)			UNCLASSIFIED	284905, 284907
726	13066282 (1451, 1452)			UNCLASSIFIED	284636
727	13522872 (1453, 1454)				284634
728	20268471 (1455, 1456)	Novel Protein sim. GBank gl 2633910 emb CAB13411 - (Z99112) similar to hypothetical proteins [Bacillus subtilis]			284567
729	11293753 (1457, 1458)	Novel Protein sim. GBank		UNCLASSIFIED	284490
730	18900373 (1459, 1460)	gi 2484880 sp Q45291 GALE_BRELA - UDP-GLUCOSE 4-EPIMERASE (GALACTOWALDENASE) (UDP-GALACTOSE 4-EPIMERASE)		isomerase	284584
731	80058750 (1461, 1462)	Novel Protein sim. GBank gl 1146192 (L47638) - putative [Bacillus subtilis]		UNCLASSIFIED	284605
732	80258175 (1463, 1464)	Novel Protein sim. GBank gl 168396 sp P46881 AIP2_YEAST - ACTIN INTERACTING PROTEIN 2		struct	284591, 284584, 264595
733	20448839 (1465, 1466)	Novel Protein sim. GBank gl 3184080 emb CAA19338 - (AL023781) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284604
734	20435887 (1467, 1468)			ubiquitin	284604

735	11607959 (1469, 1470)	Novel Protein sim. GBank gi 401582 sp P27432 YICE_ECOLI - HYPOTHETICAL 48.9 KD PROTEIN IN GLTS-SELIC INTERGENIC REGION			284594
736	10878734 (1471, 1472)	Novel Protein sim. GBank gi 400831 sp P31135 POTH_ECOLI - PUTRESCINE TRANSPORT SYSTEM PERMEASE PROTEIN POTH	Contains protein domain (PF00528) - transport Binding-protein-dependent transport systems inner membrane component		284636
737	78945340 (1473, 1474)		Contains protein domain (PF00815) - UNCLASSIFIED Regulator of G protein signaling domain		285020
738	17895353 (1475, 1476)	Novel Protein sim. GBank			285008
739	78833670 (1477, 1478)	Novel Protein sim. GBank gi 2508867 sp P33225 TORA_ECOLI - TRIMETHYLAMINE- N-OXIDE REDUCTASE PRECURSOR (TMAO REDUCTASE) (TRIMETHYLAMINE OXIDASE)	oxidase		284910
740	19881557 (1479, 1480)	Novel Protein sim. GBank gi 3261828 emb CAB10925 - (Z98260) mmp [Mycobacterium tuberculosis]	Contains protein domain (PF01883) - UNCLASSIFIED		284907, 284764, 284634, 284637
741	78827273 (1481, 1482)	Novel Protein sim. GBank gi 3877484 emb CAA88472.1 - (Z48583) ATP binding protein with similarity to the CDC48/PAS1/SEC18 family; cDNA EST EMBL:D65037 comes from this gene; cDNA EST EMBL:D88340 comes from this gene; cDNA EST EMBL:D65048 comes from this gene; cDNA EST EMBL:D8845...	Domain of unknown function		284689, 35896286, 284510, 284808, 18108362
742	82393785 (1483, 1484)	Novel Protein sim. GBank gi 127420 sp P18888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	UNCLASSIFIED		28331822, 284910, 284762
743	82300051 (1485, 1486)	Novel Protein sim. GBank gi 127420 sp P18888 MTBA_BACAR - MODIFICATION METHYLASE BANI (CYTOSINE-SPECIFIC METHYLTRANSFERASE BANI) (M.BANI)	Contains protein domain (PF00145) - UNCLASSIFIED C-5 cytosine-specific DNA methylase		284488, 284259, 284508, 284905, 284906, 284907, 284808, 284909, 284510, 284511, 284512, 265008, 265009, 284910, 284591, 284596, 284759, 285010, 265011, 18108351, 284763, 284288, 284766, 284768, 284693, 18108370, 284829, 18108372, 284630, 284631, 284634, 284558, 18108385, 284482, 284564, 284567
744	80230421 (1487, 1488)				18108397, 284511, 284690, 284628, 284638, 284692, 284639, 284768
745	9841963 (1489, 1490)	Novel Protein sim. GBank gi 78921 pir S04846 - UDP-N- acetylmutamoylalanine-D-glutamate-2, 6-diaminopimelate--D- alanine-D-alanine ligase (EC 6.3.2.15) precursor - Escherichia coli	glycoprotein		284906
746	11073229 (1491, 1492)	Novel Protein sim. GBank gi 3386354 (AF074705) - pyochelin synthetase [Pseudomonas aeruginosa]	synthase		284600
747	94322044 (1493, 1494)	Novel Protein sim. GBank gi 2887411 db BAA24848 - (AB007878) KIAA0418 [Homo sapiens]	Contains protein domain (PF00018) - oxidase SH3 domain		66714117, 284905, 284509, 284906, 284907, 284908, 284909, 284511, 284910, 285011, 284881, 284288, 284766, 284687, 284768, 284769, 21906768, 35895917, 284691, 284693, 284628, 284634, 284635, 284639, 56182323, 83373044
748	11617923 (1495, 1496)				284690

749	20469119 (1497, 1498)	Novel Protein sim. GBank gi 1189727 sp P44848 FPQ_HAEIN - FORMAMIDOPYRIMIDINE-DNA GLYCOSYLASE (FAPY- DNA GLYCOSYLASE)		UNCLASSIFIED	284804 284800
750	20298427 (1499, 1500)				
751	21838169 (1501, 1502)	Novel Protein sim. GBank gi 5360088 gb AA042851.1 AF159888 - (AF159888) serine/threonine kinase PKN3 [Mycobacterium xanthus]	Contains protein domain (PF000089) - kinase Eukaryotic protein kinase domain		284805, 284559
752	82450388 (1503, 1504)	Novel Protein sim. GBank gi 1188862 sp P44428 BIOA_HAEIN - ADENOSYLMETHIONINE-8-AMINO-7-OXONONANOATE AMINOTRANSFERASE (7,8-DIAMINO-PELARGONIC ACID AMINOTRANSFERASE) (DAPA AMINOTRANSFERASE)	Contains protein domain (PF00202) - Aminotransferases class-III pyridoxal phosphate	UNCLASSIFIED	284508, 284907, 284510, 285011, 284782, 284889, 35695855, 284838, 18108387
753	80508718 (1505, 1506)	Novel Protein sim. GBank gi 2851330 sp P32399 YHGE_BACSU - HYPOTHETICAL 84.1 KD PROTEIN IN HEMY-GLTT INTERGENIC REGION (ORFB)		UNCLASSIFIED	284809, 284800, 284802, 284804, 284780, 284789, 284834
754	95083741 (1507, 1508)			UNCLASSIFIED	284508, 284806, 284907, 284908, 284909, 284759, 284802, 284784, 284789, 284828, 284829, 284830, 284832, 284834, 284835, 284837, 284838, 83373044, 18108385
755	80185449 (1509, 1510)	Novel Protein sim. GBank gi 3449278 emb CAA20420 - (AL031317) putative dehydrogenase [Streptomyces coelicolor]		UNCLASSIFIED	284448, 284890
756	94831888 (1511, 1512)				284769, 284689, 284638, 284639
757	78488533 (1513, 1514)	Novel Protein sim. GBank gi 458033 emb CAB40107.1 - (AJ001206) putative glycogen debranching enzyme [Streptomyces coelicolor]		UNCLASSIFIED	284882, 284885
758	78963178 (1515, 1516)			amylase	285007, 18108387, 265007, 18108387
759	79475687 (1517, 1518)	Novel Protein sim. GBank gi 2911858 (AF047659) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	284684, 284686
760	87628888 (1519, 1520)	Novel Protein sim. GBank gi 3451312 emb CAA20448 - (AL031324) membrane alipase [Schizosaccharomyces pombe]	Contains protein domain (PF00122) - transport E1-E2 ATPase		29331822, 284908, 52644045, 56182435, 80170831, 21906754, 265017, 265019, 284681, 284687, 284688, 21906768, 21908768, 285020, 285021, 285022, 284635, 22279000
761	78877988 (1521, 1522)	Novel Protein sim. GBank gi 3327158 dbj BAA31647 - (AB014572) KIAA0872 protein [Homo sapiens]		UNCLASSIFIED	284768
762	80023563 (1523, 1524)	Novel Protein sim. GBank gi 4981268 gb AAD35822.1 AE001744 - (AE001744) lipopolysaccharide core biosynthesis protein KdIB [Thermotoga maritima]		UNCLASSIFIED	284807, 284593, 265020
763	20294813 (1525, 1526)				284800
764	39515024 (1527, 1528)				284603

765	80025947 (1529, 1530)	Novel Protein sim. GBank gij3845093 (AE001371) - erythrocyte membrane protein PIEMP3 [Plasmodium falciparum]		struct	284905, 284908, 284594, 284686, 33657023
766	82417404 (1531, 1532)			UNCLASSIFIED	284605, 284762, 18108374
767	10296742 (1533, 1534)	Novel Protein sim. GBank gij541121 (pij)S40827 - hypothetical protein c300 - Escherichia coli		UNCLASSIFIED	284607
768	79418080 (1535, 1536)			UNCLASSIFIED	284592, 284585
769	80086554 (1537, 1538)	Novel Protein sim. GBank gij2982501 (emb)CAA06184 - (AJ004832) neuropathy target esterase [Homo sapiens]		esterase	55810764, 284559
770	80417847 (1539, 1540)	Novel Protein sim. GBank gij283437 (pij)S27850 - hypothetical protein - Trypanosoma cruzi (fragment)		UNCLASSIFIED	284903, 284907, 284828, 284909, 265010, 284786, 284628, 284629, 284634, 284636, 284555
771	95329509 (1541, 1542)	Novel Protein sim. GBank gij4769004 (gb)AAD29715.1 (AF140598) ring-box protein 1 [Homo sapiens]	Contains protein domain (PF000087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	58182575, 35696288, 284259, 66714117, 284107, 68712502, 58182435, 284112, 55812038, 87188559, 284288, 21908786, 33657023, 65274620, 65274791, 18108381
772	78971382 (1543, 1544)			UNCLASSIFIED	284910
773	78945383 (1545, 1546)			UNCLASSIFIED	285020
774	78856128 (1547, 1548)	Novel Protein sim. GBank gij5531324 (emb)CAB51045.1 - (AJ009579) putative alkane 1-monoxygenase [Pseudomonas fluorescens]		UNCLASSIFIED	284909
775	20620141 (1549, 1550)			UNCLASSIFIED	284555
776	78942693 (1551, 1552)			UNCLASSIFIED	285019
777	78960378 (1553, 1554)	Novel Protein sim. GBank gij4505461 (ref)NP_003824.1 (p)NRPB - nuclear restricted protein, BTB domain-like (brain)	Contains protein domain (PF01008) - Hepatitis C virus non-structural protein NS4a		
778	20691310 (1555, 1556)		Contains protein domain (PF01344) - Kelch motif	protease	21808754, 285020, 60170815, 284691
779	80054024 (1557, 1558)			UNCLASSIFIED	284511
780	85288987 (1559, 1560)	Novel Protein sim. GBank gij1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]		synthase	284807, 284600, 284601, 284602, 284603, 284604, 284605, 284486
781	80250049 (1561, 1562)				
782	8758529 (1563, 1564)	Novel Protein sim. GBank gij4155447 (AE001517) - proline/betaine transporter [Helicobacter pylori J99]		UNCLASSIFIED	284905, 284907, 265010, 284600, 284601, 18108382, 18108374, 284558
783	18410791 (1565, 1566)				284605
784	80051187 (1567, 1568)				265020
785	58073541 (1569, 1570)	Novel Protein sim. GBank gij3451335 (AC005525) - F22162.1 [Homo sapiens]		UNCLASSIFIED	284635, 33657023, 28331828, 265017, 284585, 284586
786	20436842 (1571, 1572)	Novel Protein sim. GBank gij138748 (sp)P10805 (UGPA, ECOLI - SN-GLYCEROL-3-PHOSPHATE TRANSPORT SYSTEM PERMEASE PROTEIN UGPA)	Contains protein domain (PF00047) - Immunoglobulin domain	struct	35696052, 284604
787	80258384 (1573, 1574)		transport		284603
787	80258384 (1573, 1574)			UNCLASSIFIED	284593

788	80507844 (1575, 1576)	Novel Protein sim. GBank gij2746079 (AF015310) - BTH1 [Brassica napus]		synthase	284908, 284602, 284803, 284769, 284638
789	17294715 (1577, 1578)	Novel Protein sim. GBank gij2351849 (U93357) - 40 kDa heat shock chaperone protein [Halobacterium salinarum]		UNCLASSIFIED	285007
790	86284406 (1579, 1580)	Novel Protein sim. GBank gij5706378 [dbj]BAA03089.1] - (AB026116) MALT1 [Homo sapiens]	Contains protein domain (PF000047) - Immunoglobulin domain	glycoprotein	22278999, 28331824, 284828, 87168559, 285018, 21908765, 21908767, 21908768, 21908769, 265020, 284692, 22279000, 284593
791	94651627 (1581, 1582)	Novel Protein sim. GBank gij5689948 [emb]CAB51985.1] - (AL109883) putative isoleucyl-tRNA synthetase [Streptomyces coelicolor A3(2)]			284601, 284605, 284636
792	80058788 (1583, 1584)	Novel Protein sim. GBank gij393184 (L02375) - S-antigen [Plasmodium falciparum]		struct	285021, 284631, 284635, 284558
793	79638730 (1585, 1586)	Novel Protein sim. GBank gij1345408 [dbj]BAA05046] - (D26046) AT motif-binding factor [Mus musculus]	Contains protein domain (PF00046) - Homeobox	homeobox	284693
794	81839294 (1587, 1588)	Novel Protein sim. GBank gij1059884 [pir]S24023 - dopamine receptor D4 - human (fragment)		UNCLASSIFIED	284603, 284604, 284910, 284762, 284808, 284638, 284809, 284757
795	80074988 (1589, 1590)	Novel Protein sim. GBank gij1877334 [emb]CAB07082] - (Z92771) b1rA [Mycobacterium tuberculosis]		carboxylase	284488, 35698052, 284905, 284907, 265010, 35698423, 284636
796	86669451 (1591, 1592)				60432228, 55811150, 284630, 284637, 284565
797	87771761 (1593, 1594)	Novel Protein sim. GBank gij2985447 [emb]CAA71519] - (Y10495) CDV-1R protein [Mus musculus]		struct	22278998, 284083, 284094, 66714117, 21908787, 21908769, 265020, 265022
798	79865209 (1595, 1596)			transcript factor	284887, 284788, 284693
799	79557816 (1597, 1598)	Novel Protein sim. GBank gij4467250 [emb]CAB37575] - (AL035568) probable Glu-tRNA Gln amidotransferase subunit [Streptomyces coelicolor]		hydrolase	284909, 284910, 284636, 284638
800	79970189 (1599, 1600)			UNCLASSIFIED	284488
801	80499389 (1601, 1602)	Novel Protein sim. GBank gij2791517 [emb]CAA18054] - (AL021246) hypothetical protein Rv2477c [Mycobacterium tuberculosis]		transport	284508, 284511, 265008, 265009, 284769, 284587, 284486
802	79834588 (1603, 1604)	Novel Protein sim. GBank gij4887211 [gb]AAD32237.1 [AF14744] - (AF14744) penicillin binding protein 1B [Pseudomonas aeruginosa]			284805, 284693
803	20467520 (1605, 1606)			struct	284605
804	10174239 (1607, 1608)	Novel Protein sim. GBank gij1176152 [sp]P44507 [YHAD_HAEIN - HYPOTHETICAL PROTEIN H10091]		kinase	284510
805	79599993 (1609, 1610)				
806	80484113 (1611, 1612)	Novel Protein sim. GBank gij2764612 [emb]CAA04683] - (AJ001330) ornithine transcarbamoylase [Lactobacillus sakei]	Contains protein domain (PF00185) - Aspartate/ornithine carbamoyltransferase	- transferase	284508, 284769
807	80381812 (1613, 1614)	Novel Protein sim. GBank gij2833311 [sp]Q21828 [YNFDCAEEL - HYPOTHETICAL 16.9 KD PROTEIN R07E5.13 IN CHROMOSOME III]			284764

808	35106817 (1615, 1616)	Novel Protein sim. GBank gi3913092ip1048170JARC_CLOPE - ARGININE/ORNITHINE ANTI-PORTER		transport	284809, 284802, 21806764, 18108374
809	81454254 (1617, 1618)	Novel Protein sim. GBank gi3913016ip174309JALF1_SNNY3 - FRUCTOSE- BISPHOSPHATE ALDOLASE CLASS I (FBP ALDOLASE)	Contains protein domain (PF00274) - Fructose-bisphosphate aldolase class-I	UNCLASSIFIED	284508, 284808, 284809, 285007, 284910, 284758, 284600, 284602, 284603, 284605, 284687, 284769, 284689, 284636, 284486
810	80192761 (1619, 1620)	Novel Protein sim. GBank gi401472ip130883YAFB_ECOLI - HYPOTHETICAL OXIDOREDUCTASE IN ASPU-MLTD INTERGENIC REGION	Contains protein domain (PF00248) - Aldolase reductase family	reductase	284389
811	80079280 (1621, 1622)			UNCLASSIFIED	284558
812	10287684 (1623, 1624)			UNCLASSIFIED	284692
813	79612280 (1625, 1626)			UNCLASSIFIED	284906
814	80473427 (1627, 1628)	Novel Protein sim. GBank gi1146168 (J01617) - glutaminyl- RNA synthetase [Escherichia coli]		synthase	284905, 284602, 284605, 284682, 284687, 284769, 284636
815	85419513 (1629, 1630)	Novel Protein sim. GBank gi4589652dbjBAA78848.11 - (A8023221) KIAA1004 protein [Homo sapiens]		UNCLASSIFIED	284488, 22278998, 22278999, 29331822, 29331824, 29331825, 29331827, 29331828, 29148499, 284905, 284908, 285007, 33857402, 80433358, 80433438, 284758, 285011, 285017, 285018, 285019, 284369, 284288, 284685, 21908765, 21908787, 285020, 285021, 284692, 85274620, 33657109, 284628, 18108376, 284635, 284636, 80170394, 58182323, 284584
816	19881810 (1631, 1632)				284600
817	95293316 (1633, 1634)	Novel Protein sim. GBank gi11781144embjCAB062541 - (Z83666) hypothetical protein Rv3089 [Mycobacterium tuberculosis]		UNCLASSIFIED	284595
818	80938190 (1635, 1636)	Novel Protein sim. GBank gi11477468 (U35244) - vacuolar protein sorting homolog r-vps33a [Rattus norvegicus]			65274572, 22278999, 80424269, 35696052, 55812038, 21908768, 55811957, 35695917, 33657023, 18108370, 18108374, 55810784, 35696423, 55811576, 284636
819	80254977 (1637, 1638)	Novel Protein sim. GBank gi11001352dbjBAA108381 - (D84008) ABC transporter [Synechocystis sp.]		transport	284585
820	80059688 (1639, 1640)	Novel Protein sim. GBank gi1486814ip137484IYYBT_BACSU - HYPOTHETICAL 74.3 KD PROTEIN IN RPLI-COTF INTERGENIC REGION		UNCLASSIFIED	284600, 284602, 284604
821	78782590 (1641, 1642)				
822	80215310 (1643, 1644)			UNCLASSIFIED	284810
823	84982289 (1645, 1646)	Novel Protein sim. GBank gi3878400embjCAA958281 - (Z71264) predicted using GeneFinder; Weak similarity to Mouse T-complex-associated-testes-expressed-1 protein (PIR Acc. No. A45841); cDNA EST EMBL.D32742 comes from this gene; cDNA EST EMBL.D33817 comes from this gene; cDNA EST...		UNCLASSIFIED	284510, 284594, 284637
				struct	284509, 284687, 284691
824	80411171 (1647, 1648)	Novel Protein sim. GBank gi1370076embjCAA668871 - (X98235) type I [Drosophila melanogaster]	Contains protein domain (PF01429) - Methyl-CpG binding domain		284910, 284763, 284769, 284693

825	20638600 (1649, 1650)	Novel Protein sim. GBank glj3025132[sp]P77391YEAG_ECOLI - HYPOTHETICAL 74.5 KD PROTEIN IN GAPA-RND INTERGENIC REGION		UNCLASSIFIED	264592
826	11075047 (1651, 1652)	Novel Protein sim. GBank glj3242281[emb]CAA16669] - (AL021846) hypothetical protein Rv3202c [Mycobacterium tuberculosis]			264605
827	80054207 (1653, 1654)	Novel Protein sim. GBank glj3417424[emb]CAA20312] - (AL031281) putative transport protein [Schizosaccharomyces pombe]			264603
828	95106322 (1655, 1656)	Novel Protein sim. GBank glj4336682[sp]AAD17897] - (AF101361) Abnormal X segregation [Drosophila melanogaster]		UNCLASSIFIED	52645080, 264508, 264805, 264805, 264509, 264906, 264807, 264908, 264909, 264512, 264910, 264591, 264758, 264600, 264768, 264768, 21908768, 35895917, 264691, 264628, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 264639, 83373044, 18108385, 264583, 264586, 264488
829	61742215 (1657, 1658)	Novel Protein sim. GBank glj3820539 (AF080002) - UDP-N- acetyl muramyl tripeptide synthetase MurC [Heliobacillus mobilis]		UNCLASSIFIED	264758, 264634
830	20396091 (1659, 1660)	Novel Protein sim. GBank glj1870004[emb]CAB08855] - (Z92539) hypothetical protein Rv1024 [Mycobacterium tuberculosis]		UNCLASSIFIED	66714117, 264910, 264639
831	87112435 (1661, 1662)	Novel Protein sim. GBank glj2500056[sp]Q46287[PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
832	19538322 (1663, 1664)	Novel Protein sim. GBank glj2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	UNCLASSIFIED	264600, 264602, 264769, 264689, 264636
833	20726654 (1665, 1666)	Novel Protein sim. GBank glj2500056[sp]Q46287[PFLA_CLOPA - PYRUVATE FORMATE-LYASE ACTIVATING ENZYME		UNCLASSIFIED	264602
834	21428762 (1667, 1668)	Novel Protein sim. GBank glj2497531[sp]Q46078[KPYK_CORGL - PYRUVATE KINASE (PK)	Contains protein domain (PF00224) - Pyruvate kinase	UNCLASSIFIED	264600, 264602, 264769, 264689, 264636
835	94140482 (1669, 1670)	Novel Protein sim. GBank glj699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		UNCLASSIFIED	264768, 263994, 21808767, 264910, 264632, 264635, 264259, 264639, 264693, 83373044, 264758, 35896052, 22279002, 264508, 264805, 264908, 264448, 263972, 264908, 264909
836	66128552 (1671, 1672)	Novel Protein sim. GBank glj699315 (U15184) - phosphate transport protein PSTC [Mycobacterium leprae]		UNCLASSIFIED	35895917, 264557
837	79450450 (1673, 1674)	Novel Protein sim. GBank glj728887[sp]P40602[APG_ARATH - ANTER-SPECIFIC PROLINE-RICH PROTEIN/AGG PRECURSOR		UNCLASSIFIED	264595
838	79184203 (1675, 1676)	Novel Protein sim. GBank glj2498533[sp]Q50598[Y0D8_MYCTU - HYPOTHETICAL 85.9 KD PROTEIN CYTA11.08		UNCLASSIFIED	264687
839	78641126 (1677, 1678)	Novel Protein sim. GBank glj2498533[sp]Q50598[Y0D8_MYCTU - HYPOTHETICAL 85.9 KD PROTEIN CYTA11.08		UNCLASSIFIED	264908
840	80059851 (1679, 1680)	Novel Protein sim. GBank glj4557753[ref]NP_000372.1[pm]DI1 - midline 1 protein [finger]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	264762, 264558

841	80376318 (1691, 1692)	Novel Protein sim. GBank gij139805[sp]P08045[XFIN_XENLA - XFIN PROTEIN (D86733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	284784
842	80078724 (1693, 1694)	Novel Protein sim. GBank gij2114321[dbj]BAA200371 - (D86733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00359) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	284905, 284908, 285008, 285009, 18108374, 58182323, 284558
843	87002847 (1695, 1696)	Novel Protein sim. GBank gij3882325[dbj]BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	struct	284091, 28331825, 284908, 284788, 284563
844	17841439 (1697, 1698)	Novel Protein sim. GBank gij2224721[dbj]BAA208441 - (AB002388) KIAA0390 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcription factor	285011
845	18348844 (1699, 1700)	Novel Protein sim. GBank gij825679[pir]A36929 - virulence regulatory protein VsrB - Pseudomonas solanacearum		kinase	284629 284907
846	78863441 (1691, 1692)				
847	78895348 (1693, 1694)				
848	78489365 (1695, 1696)			UNCLASSIFIED	284909
849	78756367 (1697, 1698)			UNCLASSIFIED	285020
850	78817649 (1699, 1700)	Novel Protein sim. GBank gij3183245[sp]P78061[JYCJL_ECOLI - PUTATIVE GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)	Contains protein domain (PF00120) - Glutamine synthetase	UNCLASSIFIED	284586 284909
851	95320333 (1701, 1702)	Novel Protein sim. GBank gij5454130[ref]NP_008280.1[ptLN] - talin	Contains protein domain (PF01608) - ILWEE domain		284488, 52844507, 284489, 18108388, 85274572, 56182575, 22278994, 22278995, 22278996, 35888286, 22278997, 22278998, 22278999, 20281171, 264480, 284259, 52845080, 28331822, 28331824, 66714117, 28331825, 60432289, 28331826, 28331827, 35896052, 28331828, 29146498, 29146499, 284107, 284905, 284906, 284907, 284908, 52844045, 56182435, 285008, 285007, 285008, 285009, 284910, 60432229, 60431735, 60433358, 33657402, 60433438, 284595, 284758, 284759, 21908754, 33109954, 52844288, 265010, 265011, 87189596, 285017, 285018, 285019, 284780, 284781, 284782, 284881, 18108351, 264763, 284448, 284682, 284784, 284883, 18108354, 284288, 284389, 284685, 284768, 284887, 284788, 284789, 21908785, 21908786, 21908787, 21908788, 29148627, 21908769, 28148629, 55811957, 35695917, 285020, 285021, 285022, 60170815, 52844150, 284891, 284892, 33857023, 284893, 283986, 33657109, 27486281, 27486282, 27486284, 27486285, 35895763, 60431602, 18108370, 20281089, 284629, 18108374, 18108376, 55811576, 35898423, 35895855, 284634, 284635, 284636, 284555, 60431850, 284556, 284681
852	10147366 (1703, 1704)				

853	13032587 (1705, 1708)	Novel Protein sim. GBank gll3402836[emb]CAA76082] - (Y18136) 2-enoate reductase [Moorella thermocella]		reductase	284838 284566
854	80052438 (1707, 1708)				
855	78641130 (1709, 1710)			UNCLASSIFIED	284682
856	11594238 (1711, 1712)			UNCLASSIFIED	284591
857	79210165 (1713, 1714)			UNCLASSIFIED	284630, 284634
858	80248910 (1715, 1716)				285008, 285009, 284601, 284602, 284603, 18108351
859	20296634 (1717, 1718)				284559
860	80041749 (1719, 1720)			UNCLASSIFIED	284489
861	65857045 (1721, 1722)			UNCLASSIFIED	33657023, 284630
862	80079487 (1723, 1724)				284600
863	80579831 (1725, 1726)	Novel Protein sim. GBank gll2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	284488, 18108398, 35696286, 284259, 18108351, 284288, 285021
864	94839904 (1727, 1728)				284259, 284112, 283974
865	80046310 (1729, 1730)	Novel Protein sim. GBank gll5689884[emb]CAB52047.1] - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]	Contains protein domain (PF01479) - S4 domain	UNCLASSIFIED	284635, 284600, 284636, 284591, 284602, 284693
866	80162031 (1731, 1732)	Novel Protein sim. GBank gll4657878[emb]NP_000341.1]pABCR - ATP binding cassette transporter		transport	284288, 284557, 284558
867	80082402 (1733, 1734)				284605
868	10075384 (1735, 1736)			UNCLASSIFIED	284909
869	80082406 (1737, 1738)				284605, 284687, 18108374
870	80248651 (1739, 1740)	Novel Protein sim. GBank gll828860[pil]S37755 - Adenylyl-transferase - Escherichia coli		transferase	284601, 284636
871	20378295 (1741, 1742)	Novel Protein sim. GBank gll1708180[sp]Q10602]HEMK_MYCTU - HEMK PROTEIN HOMOLOG		UNCLASSIFIED	284603
872	95197114 (1743, 1744)	Novel Protein sim. GBank gll1545959[emb]CAA67763] - (X98384) paladin [Mus musculus]		UNCLASSIFIED	35698286, 22278998, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 285008, 284511, 284512, 285007, 285008, 285009, 284910, 284591, 60433356, 284596, 52846317, 87188474, 285010, 284602, 284603, 285017, 285018, 284605, 18108351, 284764, 284766, 284768, 52844229, 284769, 21906765, 285021, 284534, 284691, 52845129, 284628, 284629, 35698423, 65274791, 284631, 284632, 284635, 284636, 284558, 284637, 284638, 284639, 60432113, 22279000, 22279002, 284584
873	20189728 (1745, 1746)	Novel Protein sim. GBank gll4156104 (AE001569) - putative Outer membrane protein [Helicobacter pylori J99]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	284595

874	80077682 (1747, 1748)	Novel Protein sim. GBank gi113418 sp P07818 SCRB_BACSU - SUCROSE-6- PHOSPHATE HYDROLASE (SUCRASE) (INVERTASE)			UNCLASSIFIED	284600
875	86608446 (1749, 1750)	Novel Protein sim. GBank gi1481000 p S37594 - mucin - human (fragment)				284258, 284448, 284288, 284557, 87168518
876	88465187 (1751, 1752)	Novel Protein sim. GBank gi13128283 (AF010498) - Iron(III) dichlorate transport ATP-binding protein [Rhodobacter capsulatus]	Contains protein domain (PF000005) - ABC transporter	transport		284807, 284601, 284602, 284605, 285020, 60431602
877	87802548 (1753, 1754)	Novel Protein sim. GBank gi1731074 sp P40348 URB1_USTMA - SIDEROPHORE BIOSYNTHESIS REGULATORY PROTEIN URBS1	Contains protein domain (PF003320) - GATA zinc finger	transcriptfactor		22278988, 284808, 284369
878	80187288 (1755, 1756)	Novel Protein sim. GBank gi11351614 sp Q09853 YAEI_SCHPO - HYPOTHETICAL 181.5 KD PROTEIN C23D3.13C IN CHROMOSOME I		ATPase-associated		284369, 284555
879	84328862 (1757, 1758)	Novel Protein sim. GBank gi13875304 emb CAA98434 - (Z74030) predicted using GeneFinder; cDNA EST EMBL-C07809 comes from this gene; cDNA EST EMBL-C09023 comes from this gene; cDNA EST yk505e8.3 comes from this gene; cDNA EST yk489h9.3 comes from this gene; cDNA EST yk489h9.5 com...				56182575, 29331824, 284508, 284808, 285018, 18108351, 284448, 284883, 21908768, 21908768, 60170815, 33857023, 65274820, 33857109, 18108374, 35895855, 284583
880	8491135 (1759, 1760)	Novel Protein sim. GBank gi1137120 sp P11214 UROT_MOUSE - TISSUE PLASMINOGEN ACTIVATOR PRECURSOR (TPA) (T- PLASMINOGEN ACTIVATOR)	Contains protein domain (PF00051) - Kingle domain	cathepsin		284508
881	11280122 (1761, 1762)	Novel Protein sim. GBank gi12632098 emb CAA75687 - (Y15513) Prodes protein [Drosophila melanogaster]		UNCLASSIFIED		284508
882	11077011 (1763, 1764)	Novel Protein sim. GBank gi1155088 emb CAA84425 - (X94978) cell wall-plasma membrane linker protein [Brassica napus]		UNCLASSIFIED		284688
883	79582989 (1765, 1766)	Novel Protein sim. GBank gi12078027 emb CAB08467 - (Z95208) hypothetical protein Ry2372c [Mycobacterium tuberculosis]		UNCLASSIFIED		284636
884	13517921 (1767, 1768)	Novel Protein sim. GBank gi12695634 emb CAA15904 - (AL021008) sucA [Mycobacterium tuberculosis]		UNCLASSIFIED		284680
885	80052457 (1769, 1770)	Novel Protein sim. GBank gi15689395 dbj BAA82881.1 - (AB028952) KIAA1029 protein [Homo sapiens]		UNCLASSIFIED		35898052, 284608, 284600, 284603, 35895917, 35895855, 284636
886	11685138 (1771, 1772)	Novel Protein sim. GBank gi1881338 dbj BAA19388 - (AB001488) PROBABLE INTEGRAL MEMBRANE PROTEIN, SIMILAR TO CHLORAMPHENICOL RESISTANCE PROTEIN OF STREPTOMYCES VENEZUELAE [Bacillus subtilis]		UNCLASSIFIED		284603
887	84315307 (1773, 1774)	Novel Protein sim. GBank gi1854085 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]				284629

891	13518679 (1781, 1782)	Novel Protein sim. GBank gi4959396 gb AAD34331.1 AF11248 - (AF112481) RAD54B protein [Homo sapiens]		UNCLASSIFIED	284636
892	57634157 (1783, 1784)	Novel Protein sim. GBank gi545526 bbs 143333 - LBP- 1b-transcription factor binding to initiation site of HIV-1 (alternatively spliced) [human, Nematode cells, Peptide, 541 aa]		transcription factor	22278986, 22278999, 29331828, 35696052, 284908, 284909, 285009, 285011, 284602, 285019, 284788, 21806765, 21908786, 21908789, 285020, 285021, 58526486 284688, 283987
893	78168037 (1785, 1786)	Novel Protein sim. GBank gi2829688 sp P80808 CYSK_MAIZE - CYSTEINE SYNTHASE (O-ACETYL SERINE SULFHYDRYLASE) (O- ACETYL SERINE (THIO)LYASE) (CSASE)		synthase	
894	11102240 (1787, 1788)				263978
895	80239868 (1789, 1790)			UNCLASSIFIED	284508, 284600, 284555, 284559
896	79747803 (1791, 1792)				284632
897	94991923 (1793, 1794)		Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	284686, 29331828, 284511
898	87895109 (1795, 1796)				58182575, 60432289, 58182435, 60432229, 55811957, 22278000, 284486
899	11100463 (1797, 1798)	Novel Protein sim. GBank gi1750127 (U86480) - YncC [Bacillus subtilis]		transport	284601 284789, 284691, 284563
900	80499768 (1799, 1800)	Novel Protein sim. GBank gi3122879 sp O07438 SYA_MYCTU - ALANYL-TRNA SYNTHETASE (ALANINE-TRNA LIGASE) (ALARS)	Contains protein domain (PF01411) - tRNA synthetases class II (A)	synthase	284907, 284602, 284605, 284769, 35685917, 18108376, 284563
901	80502410 (1801, 1802)	Novel Protein sim. GBank gi335570 emb CAA200011 - (AL031124) 3-Isopropylmalate dehydratase large subunit (Streptomyces coelicolor)	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	isomerase	284908, 285008, 284602, 284604, 284769, 284689, 284693
902	80503301 (1803, 1804)	Novel Protein sim. GBank gi2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00370) - FGG family of carbohydrate kinases	kinase	35696052, 284905, 284510, 284511, 284512, 284605, 284760, 18108351, 284762, 284687, 284788, 284769, 284888, 21908784, 35695917, 27486262, 35695855, 284634, 284636, 284486
903	82050208 (1805, 1806)	Novel Protein sim. GBank gi2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Contains protein domain (PF00491) - Arginase family	hydrolase	284604
904	20451078 (1807, 1808)	Novel Protein sim. GBank gi2860120 emb CAA18018.1 - (AL022121) glpK [Mycobacterium tuberculosis]	Arginase family	UNCLASSIFIED	284909
905	9398483 (1809, 1810)	Novel Protein sim. GBank gi4667200 gb AAD23616.1 AC00716 - (AC007168) hypothetical protein [Arabidopsis thaliana]			
906	80052628 (1811, 1812)	Novel Protein sim. GBank gi3736200 emb CAA21292 - (AL031855) putative vacuolar membrane protein [Schizosaccharomyces pombe]			284585, 284605
907	87913201 (1813, 1814)				
908	11754482 (1815, 1816)			UNCLASSIFIED	60432289, 284601, 284680
909	20727907 (1817, 1818)	Novel Protein sim. GBank gi3668940 db BAA34296 - (AB015054) Alg2 [Rhizomucor pusillus]		UNCLASSIFIED	284636
910	18776206 (1819, 1820)	Novel Protein sim. GBank gi4589728 db BAA76883.1 - (AB003137) DnaJ homolog protein [Salix glauca]	Contains protein domain (PF00884) - DnaJ central domain (4 repeats)	UNCLASSIFIED	284602
					285009

911	87454340 (1821, 1822)	Novel Protein sim. GBank gi 548774 sp P33685 RL7A_ORYSA - 60S RIBOSOMAL PROTEIN L7A		ribosomal prot	265010, 264604, 60432113
912	20448863 (1823, 1824)	Novel Protein sim. GBank gi 2314008 gb AAD07821.1 - (AE000597) CDP-diglyceride hydrolase (cdh) [Helicobacter pylori 26895]		hydrolase	264559
913	20469357 (1825, 1826)				
914	79183351 (1827, 1828)	Novel Protein sim. GBank gi 17857 sp Q03604 JIR1_CAEEL - PROBABLE RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE LARGE CHAIN (RIBONUCLEOTIDE REDUCTASE)	Contains protein domain (PF00317) - Ribonucleotide reductase	UNCLASSIFIED - reductase	264604 264636
915	87606703 (1828, 1830)	Novel Protein sim. GBank gi 5688571 dbj BAA83069.1 - (AB028040) KIAA1117 protein [Homo sapiens]			18108398, 22278998, 86714117, 264908, 264591, 21908786, 265020, 55811576, 264638 264595
916	79444081 (1831, 1832)	Novel Protein sim. GBank gi 4186110 emb CAA71790 - (Y10831) putative integrase [Ralstonia eutropha]		UNCLASSIFIED	264605
917	20185985 (1833, 1834)	Novel Protein sim. GBank gi 1855699 emb CAA89032 - (Y07782) phenolphthalein-S [Volvox carter]		UNCLASSIFIED synthase	264259, 28331826, 264808, 265018, 264448, 265020, 284835, 83373044
918	91228785 (1835, 1836)	Novel Protein sim. GBank gi 5688989 emb CAB52005.1 - (AL109663) putative membrane protein [Streptomyces coelicolor A3(2)]			265006, 264512, 264600, 264802, 264804, 264786, 18108370, 264563
919	80436785 (1837, 1838)				
920	78606095 (1839, 1840)	Novel Protein sim. GBank gi 1168448 sp Q05813 AMP1_STRLI - XAA-PRO AMINOPEPTIDASE I (X-PRO AMINOPEPTIDASE I) (AMINOPEPTIDASE P I) (APP) (PEPP I) (AMINOACYLPROLINE AMINOPEPTIDASE I)		peptidase	264508
921	19858834 (1841, 1842)	Novel Protein sim. GBank gi 3850084 emb CAA21911.1 - (AL033388) alcohol dehydrogenase [Schizosaccharomyces pombe]		UNCLASSIFIED	264600
922	78982605 (1843, 1844)				
923	86695830 (1845, 1846)	Novel Protein sim. GBank gi 267078 sp P29514 T896_ARATH - TUBULIN BETA-8 CHAIN		tubulin	265019, 22278002 264907, 265008, 265009, 265010, 18108351, 264689, 265021, 18108370, 18108374, 18108385 264510
924	21431341 (1847, 1848)				
925	20630332 (1848, 1850)	Novel Protein sim. GBank gi 2497688 sp Q60963 PAFA_MOUSE - PLATELET- ACTIVATING FACTOR ACETYLHYDROLASE PRECURSOR (PAF ACETYLHYDROLASE) (PAF 2- ACTYLHYDROLASE) (LDL-ASSOCIATED PHOSPHOLIPASE A2) (LDL-PLA(2)) (2-ACETYL-1- ALKYLGLYCEROPHOSPHOCHOLINE ESTERASE) (1- ALKYL-2-ACETYLGLYCEROPHO...		esterase	264603
926	76397657 (1851, 1852)	Novel Protein sim. GBank gi 3882325 dbj BAA34522.1 - (AB018345) KIAA0802 protein [Homo sapiens]			55811857, 263972, 264639
927	37036201 (1853, 1854)			UNCLASSIFIED	264769

928	80070810 (1855, 1856)	Novel Protein sim. GBank gl156146 (M30316) - xanthine dehydrogenase (AA at 2538) [Calliphora vicina]		dehydrogenase	264605
929	20830338 (1857, 1858)			UNCLASSIFIED	264603
930	5496348 (1859, 1860)	Novel Protein sim. GBank gl4115938[gbAA03446.1] - (AF116223) No definition line found [Arabidopsis thaliana]			264259
931	10245731 (1861, 1862)	Novel Protein sim. GBank gl4480609[embjCAB38642.1] - (AJ133495) ribonucleotide reductase major subunit [Staphylococcus aureus]	Contains protein domain (PF00317) - reductase		264486
932	80420813 (1863, 1864)	Novel Protein sim. GBank gl5459389[embjCAB50754.1] - (AL096839) putative integral membrane transport protein [Streptomyces coelicolor]		transport	264508, 264905, 264906, 264908, 264600, 264602, 264603, 264605, 264768, 264558, 18108387, 264488
933	94326010 (1865, 1866)	Novel Protein sim. GBank gl5689523[dbjBAA83045.1] - (AB029016) KIAA1093 protein [Homo sapiens]	Contains protein domain (PF00827) - UBA domain	UNCLASSIFIED	264508, 264686, 264693, 27486261, 18108370, 65274791, 264636, 264559, 22278002
934	80039105 (1867, 1868)	Novel Protein sim. GBank gl1191111[spjP12978]EBN2_EBV - EBNA-2 NUCLEAR PROTEIN			264369, 22278002
935	80063162 (1869, 1870)			UNCLASSIFIED	264604, 264605, 264693, 18108370, 18108374
936	80026632 (1871, 1872)	Novel Protein sim. GBank gl845866 (M32103) - ORF-27 [Staphylococcus aureus]		UNCLASSIFIED	22278995, 22278996, 264602, 264687, 32833986, 18108387
937	80250273 (1873, 1874)	Novel Protein sim. GBank gl1360689[prjCGHU1V] - collagen alpha 1(V) chain precursor - human		synthase	263978
938	80026633 (1875, 1876)	Novel Protein sim. GBank gl2226243[embjCAA74531.1] - (Y14083) hypothetical protein [Bacillus subtilis]		UNCLASSIFIED	264602
939	11071694 (1877, 1878)				264600
940	94144252 (1879, 1880)	Novel Protein sim. GBank gl3560186[embjCAA20878] - (AL031525) ubiquitin carboxyl-terminal hydrolase [Schizosaccharomyces pombe]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2	ubiquitin	264605, 264906, 264907, 264908, 264909, 264511, 264910, 264592, 33657402, 264596, 264758, 264760, 264683, 264768, 264768, 264768, 33657023, 33657109, 264628, 264629, 264630, 264635, 264636, 264555, 264637, 264556, 264638, 264639, 83373044, 18108385, 264565, 18108391
941	11389414 (1881, 1882)				264593
942	19484122 (1883, 1884)			UNCLASSIFIED	264760
943	80080258 (1885, 1886)	Novel Protein sim. GBank gl4033728 (AF038595) - apolipoprotein N-acyltransferase [Pseudomonas aeruginosa]		UNCLASSIFIED	264600, 264687, 264689, 264563
944	80216096 (1887, 1888)	Novel Protein sim. GBank gl2494784[spjQ50729]GJAA_MYCTU - GMP SYNTHASE (GLUTAMINE-HYDROLYZING) (GLUTAMINE AMIDOTRANSFERASE) (GMP SYNTHETASE)		synthase	264511, 264603
945	80052477 (1889, 1890)	Novel Protein sim. GBank gl732353[spjP39606]YWCH_BACSU - HYPOTHETICAL 38.6 KD PROTEIN IN QOXD-VPR INTERGENIC REGION	Contains protein domain (PF00818) - Ice nucleation protein repeat	UNCLASSIFIED	264906, 264604, 264605, 265020, 18108387
946	79248402 (1891, 1892)				265017

947	81802699 (1983, 1984)	Novel Protein sim. GBank gij2696770jemb[CAA17247] - (AL021899) hypothetical protein RV2033c [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	18108394, 22278998, 264907, 284809, 285008, 285009, 284910, 284758, 284600, 284802, 285018, 284805, 284759, 284889, 284693
948	88165538 (1995, 1998)	Novel Protein sim. GBank gij2827284 (AF041037) - novel antagonist of FGF signaling [Homo sapiens]		fgf	18108398, 58182575, 22278997, 22278999, 60432049, 28331822, 28331826, 284807, 56182435, 55811388, 285011, 284600, 285017, 285018, 285019, 18108351, 285020, 285021, 285022, 27486285, 283972, 55811578, 284638, 60170394, 284566
949	88081788 (1997, 1998)	Novel Protein sim. GBank gij4507985[re]NP_003427.1pZNF1 - zinc finger protein 135 (clone pHZ-17)	Contains protein domain (PF00098) - Zinc finger, C2H2 type	transcriptfactor	29331825, 21906764, 27488261, 21806768, 52844298, 33857349, 87188518, 56994075, 285020, 285021, 87188559, 52844150, 284637
950	78485672 (1999, 1990)	Novel Protein sim. GBank gij1079461prij[S43865 - Cytokeratin 8, type II - potoroo (fragment)]	Contains protein domain (PF00038) - Intermediate filament proteins	struct	284883, 18108381
951	20451411 (1901, 1902)	Novel Protein sim. GBank gij5420387[emb]CAB46879.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284604
952	78566854 (1903, 1904)	Novel Protein sim. GBank gij5305702[gb]AAD41779.1[AF12688] calpain-like protease [Mus musculus]		calhepsin	284910, 284691
953	10186003 (1905, 1906)	Novel Protein sim. GBank gij2495842[sp]Q47142[YFHS_ECOLI - HYPOTHETICAL 41.8 KD PROTEIN IN CSIE-GLYA INTERGENIC REGION]		transport	284510
954	8803326 (1907, 1908)	Novel Protein sim. GBank gij2360985 (AF016253) - D-amino acid dehydrogenase [Klebsiella aerogenes]		dehydrogenase	284508
955	95313410 (1909, 1910)	Novel Protein sim. GBank gij5454084[re]NP_006318.1pSIP1 - SYT Interacting protein	Contains protein domain (PF00078) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	rna_bind	56994076, 284509, 284805, 284806, 284907, 284808, 284809, 284510, 284910, 284758, 284759, 285010, 284801, 284760, 18108351, 284762, 284763, 284764, 284768, 284686, 284787, 284687, 284768, 284789, 284689, 284628, 284629, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 58182323, 284639, 18108388, 284563, 284584
956	80084224 (1911, 1912)	Novel Protein sim. GBank gij2052129[emb]CAB08155] - (Z84752) ftnJ [Mycobacterium tuberculosis]			284605
957	80058208 (1913, 1914)	Novel Protein sim. GBank gij1709787[sp]Q00451[PRF1_LYCES - 38.4 KD PROLINE-RICH PROTEIN]		UNCLASSIFIED	284603, 18108362
958	80038448 (1915, 1916)	Novel Protein sim. GBank gij2131050[emb]CAB09260] - (Z89944) opcA [Mycobacterium tuberculosis]		UNCLASSIFIED	284808, 284910, 284762, 283978, 284637
959	80026647 (1917, 1918)	Novel Protein sim. GBank gij2120478[pir]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	284602, 284692
960	37815408 (1919, 1920)	Novel Protein sim. GBank gij2120478[pir]S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	284259
961	20567383 (1921, 1922)				283978
962	11399318 (1923, 1924)				284593

963	80590374 (1925, 1928)				UNCLASSIFIED	284510, 284288, 284555, 284556, 284559, 284486
964	79832019 (1927, 1928)	Novel Protein sim. GBank gl 4589622 dbj BAA78833.1 - (AB023206) KIAA0989 protein [Homo sapiens]			UNCLASSIFIED	284112, 284910, 284689
965	91229465 (1929, 1930)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1 - (AL243459) proteophosphoglycan [Leishmania major]			UNCLASSIFIED	284488, 285017, 284448, 284634, 284558, 83373044
966	95292815 (1931, 1932)				UNCLASSIFIED	284906, 284592, 284598, 284604, 284788, 21908764, 284692, 284693, 284628, 284636, 284638
967	79255708 (1933, 1934)	Novel Protein sim. GBank gl 1731207 ep Q11156 RGX3_MYCTU - SENSORY TRANSDUCTION PROTEIN REG3	Contains protein domain (PF00072) - Response regulator receiver domain		phosphatase	284760
968	78560269 (1935, 1936)	Novel Protein sim. GBank gl 2681839 emb CAA751871 - (Y14984) putative transport protein [Methylophilus methylotrophus]			transport	284693
969	79919470 (1937, 1938)	Novel Protein sim. GBank gl 5419878 emb CAB46422.1 - (AL098747) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type		dna_ma_bind	35998286, 284885, 284886, 35685917, 284892, 18108374, 284635
970	95085947 (1939, 1940)				UNCLASSIFIED	18108392, 18108394, 18108398, 22278995, 22278996, 22278998, 22278999, 29147820, 284828, 285006, 285007, 285008, 285009, 18108348, 33109854, 265010, 265011, 18108351, 284288, 21908767, 21908768, 18108370, 18108374, 18108377, 284630, 284635, 18108380, 83373044, 18108387, 18108388
971	78919770 (1941, 1942)				UNCLASSIFIED	265007, 265020, 22279002
972	20710704 (1943, 1944)					284557
973	20370183 (1945, 1946)	Novel Protein sim. GBank gl 1723119 ep P53990 Y174_HUMAN - HYPOTHETICAL PROTEIN KIAA0174				284604
974	80057103 (1947, 1948)				UNCLASSIFIED	284585
975	10198018 (1949, 1950)				UNCLASSIFIED	284510
976	80205742 (1951, 1952)	Novel Protein sim. GBank gl 3881459 emb CAA92888.1 - (Z88753) predicted using GeneFinder; Similarity to Yeast hypothetical protein YIK9 (SW:YIK9_YEAST); cDNA EST EMBL:D27860 comes from this gene; cDNA EST EMBL:D27879 comes from this gene; cDNA EST EMBL:D84477 comes from this ge...			UNCLASSIFIED	284508, 284906, 284758, 284632, 284639, 284583
977	10355349 (1953, 1954)	Novel Protein sim. GBank gl 5494589 ep Q05335 XYS3_PSEPU - XYLDLEGF OPERON TRANSCRIPTIONAL ACTIVATOR 3			UNCLASSIFIED	284906
978	80025921 (1955, 1956)				UNCLASSIFIED	284600, 284602, 284603, 284604
979	80447820 (1957, 1958)	Novel Protein sim. GBank gl 3171904 emb CAA75868 - (Y15908) DIA-12C protein [Homo sapiens]			UNCLASSIFIED	284787, 284788, 285008, 265007, 284906
980	80025928 (1959, 1960)				UNCLASSIFIED	284600, 284602, 284605
981	80096550 (1961, 1962)	Novel Protein sim. GBank gl 3598940 (AF017368) - facitgenital dyoplasia protein 2 [Mus musculus]			UNCLASSIFIED	284692, 284555, 284556, 284557, 284559

982	80185670 (1983, 1984)	Novel Protein sim. GBank gij2950220[embjCAA71575] - (Y10545) fused-cdb [Escherichia coli]		UNCLASSIFIED	284404
983	90895041 (1985, 1986)	Novel Protein sim. GBank gij476389[piljB43402] - myosin heavy chain-B, neuronal - chicken		struct	65274572, 58162575, 284908, 284909, 285007, 285008, 284758, 285010, 55811150, 33657023, 284634, 284557, 284558
984	20486876 (1987, 1988)	Novel Protein sim. GBank gij3451504[embjCAA07680.1] - (AJ007747) hypothetical protein BbLP-S1.21 [Bordetella bronchiseptica]	Contains protein domain (PF00534) - Glycosyl transferases group 1	UNCLASSIFIED	284605
985	85461368 (1986, 1970)	Novel Protein sim. GBank gij3451504[embjCAA07680.1] - (AJ007747) hypothetical protein BbLP-S1.21 [Bordetella bronchiseptica]		transferase	58182435, 284600
986	87102888 (1971, 1972)			UNCLASSIFIED	284108, 284110, 265020, 60170615
987	78867231 (1973, 1974)			UNCLASSIFIED	284909
988	19858661 (1975, 1976)			UNCLASSIFIED	284600
989	88095329 (1977, 1978)			UNCLASSIFIED	284508, 265017, 264534, 264564
990	88057746 (1978, 1980)	Novel Protein sim. GBank gij5725506[gbjAAD48080.1] (AF060152) METH1 protein [Homo sapiens]	Contains protein domain (PF01421) - Reprolysin (M12B) family zinc metalloprotease	UNCLASSIFIED	284258, 284808, 285009, 284910, 284598, 284389, 284288, 284768, 284828, 284635, 284588
991	10108140 (1981, 1982)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z85436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]	Contains protein domain (PF00211) - Adenylate and Guanylate cyclase catalytic domain	UNCLASSIFIED	284809
992	78845694 (1983, 1984)	Novel Protein sim. GBank gij2105049[embjCAB08835] - (Z85436) hypothetical protein Rv3845 [Mycobacterium tuberculosis]		UNCLASSIFIED	284508, 284593
993	10814053 (1985, 1986)	Novel Protein sim. GBank gij3328297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]		reductase	284907
994	11080590 (1987, 1988)	Novel Protein sim. GBank gij3328297 (AE001355) - Ribonucleoside Reductase, Large Chain [Chlamydia trachomatis]			284602
995	94321911 (1989, 1990)	Novel Protein sim. GBank gij5108572[gbjAAD39780.1] (AF143948) transcriptional activator SRCAP [Homo sapiens]	Contains protein domain (PF00176) - SNF2 and other N-terminal domain	helicase	18108398, 65274572, 22278998, 284490, 60432049, 28331827, 28146498, 284508, 284905, 284907, 284908, 58182435, 285008, 284591, 284592, 60432228, 60431735, 33657402, 284595, 284758, 21906754, 285010, 285017, 265018, 284605, 284780, 284448, 284763, 284768, 21906765, 21908768, 21908789, 55811957, 284692, 284893, 284829, 35898423, 55811576, 35895855, 284638, 284555, 284558, 284558, 83373044, 22279002, 284583
996	91013745 (1991, 1992)	Novel Protein sim. GBank gij2811719 (AC004227) - KIA001LB [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF)	phosphatase	83373044, 28331824, 283978, 55811957, 58528488, 87188518, 284910, 284908, 284585, 284586, 284893, 284768
997	80503347 (1993, 1994)	Novel Protein sim. GBank gij2849101 (AE001001) - ABC transporter, ATP-binding protein [Archaeoglobus fulgidus]	Contains protein domain (PF00005) - ABC transporter	transport	35898286, 22278997, 22278999, 284508, 284905, 284908, 285010, 284600, 284602, 284605, 284888, 284769, 285021, 284585, 18108391
998	11397390 (1995, 1996)	Novel Protein sim. GBank gij123530[spjP04929] (HRPX, PLALO - HISTIDINE-RICH GLYCOPROTEIN PRECURSOR			284595

999	11768047 (1997, 1998)	Novel Protein sim. GBank gi 2508697 sp P46480 YFCA_HAEN - HYPOTHETICAL PROTEIN HI0198		UNCLASSIFIED	284682	
1000	20727944 (1999, 2000)			UNCLASSIFIED	284602	
1001	86673131 (2001, 2002)	Novel Protein sim. GBank gi 2224699 db BAA20833 - (AB002377) KIAA0379 (Homo sapiens)	Contains protein domain (PF00023) - Kinase Ank repeat	UNCLASSIFIED	60432049, 284907, 284908, 284511, 284603, 284683, 284684, 284687, 284688, 28148827, 21908769, 284692, 18108385, 22279000 285009, 284369, 285020	
1002	80186603 (2003, 2004)	Novel Protein sim. GBank gi 586121 sp P37709 TRHY_RABIT - TRICHOHYALIN		struct		
1003	17833491 (2005, 2006)				285019 284635	
1004	16314887 (2007, 2008)	Novel Protein sim. GBank gi 854065 emb CAA56337 - (X83413) U88 [Human herpesvirus 6]				
1005	79617144 (2009, 2010)	Novel Protein sim. GBank gi 114073 sp P07872 APT_ECOLI - ADENINE PHOSPHORIBOSYLTRANSFERASE (APRT)		UNCLASSIFIED	284508	
1006	37815429 (2011, 2012)					
1007	79620871 (2013, 2014)	Novel Protein sim. GBank gi 4082978 db BAA36210.1 - (AB017138) epsilon subunit of malonate decarboxylase [Pseudomonas putida]		UNCLASSIFIED	284259 284905	
1008	86094444 (2015, 2016)	Novel Protein sim. GBank gi 2808807 emb CAA04607.1 - (AJ001206) putative trehalase synthase [Streptomyces coelicolor]		synthase	285007, 284602, 284605, 284760, 284636	
1009	57451289 (2017, 2018)	Novel Protein sim. GBank gi 3639077 (AF090113) - AMPA receptor binding protein [Rattus norvegicus]	Contains protein domain (PF00595) - Kinase PDZ domain (Also known as DHR or GLGF).	Kinase	284102, 284288	
1010	94672537 (2019, 2020)	Novel Protein sim. GBank gi 3746332 (AF016307) - possible NADH-dependent oxidase, may function as a demethylase [Shorthizobium mellei]		dehydrogenase	284592	
1011	85546916 (2021, 2022)	Novel Protein sim. GBank gi 2342847 gb AA888591.1 - (U80853) DHC-domain-containing cysteine-rich protein [Homo sapiens]		UNCLASSIFIED	35896052, 284905, 284784, 284788, 35895917, 284629	
1012	95294458 (2023, 2024)	Novel Protein sim. GBank gi 3413411 emb CAA20272 - (AL031231) guanosine pentaphosphate synthetase/ polyribonucleotide nucleotidyltransferase [Streptomyces coelicolor]	Contains protein domain (PF00013) - KH domain	phosphorylase	35896052, 284905, 284600, 284601, 284602, 284605, 284762, 284788, 284789, 284689	
1013	86095772 (2025, 2026)			UNCLASSIFIED	284591, 21908768	
1014	86808828 (2027, 2028)				28331824, 285019, 285020	

1015	95418879 (2029, 2030)	Novel Protein sim. GBank gl 4158965 (AF083085) - SEUL [Mus musculus]	Contains protein domain (PF000040) - Fibronectin type II domain	struct	22278994, 22278995, 56984075, 22278996, 22278998, 284259, 29331825, 29331828, 284907, 56182435, 284510, 284591, 284593, 60433356, 284594, 55812038, 284759, 21908754, 33657084, 265010, 284600, 265017, 265018, 265019, 18108351, 21908765, 21908768, 21908767, 21908768, 55811957, 265022, 33657023, 65274620, 33657182, 32833988, 18108370, 18108377, 55811576, 35698423, 284630, 22279000, 284565 284688, 284693
1016	79559694 (2031, 2032)	Novel Protein sim. GBank gl 25089899 p 41407 ACPD_ECOLI - ACYL CARRIER PROTEIN PHOSPHODIESTERASE (ACP PHOSPHODIESTERASE)		esterase	
1017	11089213 (2033, 2034)	Novel Protein sim. GBank gl 5103943 db BAA79259.1 - (AP000059) 802aa long hypothetical oligopeptide-binding protein oppA [Aeropyrum pernix]	Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5	transport	284600
1018	80072430 (2035, 2036)	Novel Protein sim. GBank gl 4493973 emb CAB39032.1 - (AL034459) predicted using hexExon; MAL3P7.14 (PF0925w). Hypothetical protein, len: 489 aa [Plasmodium falciparum]			22278996, 28148627, 284563
1019	11703607 (2037, 2038)			UNCLASSIFIED	284686
1020	80234432 (2039, 2040)				284508, 284509, 264512, 284600, 284762, 284789, 284889, 18108370, 284636, 284638, 284486 284769
1021	37036243 (2041, 2042)	Novel Protein sim. GBank gl 4633807 gb AAD28859.1 AF12779 - (AF127795) trehalase biosynthetic enzyme TreY [Rhizobium leguminosarum bv. viciae]		synthase	
1022	80502627 (2043, 2044)	Novel Protein sim. GBank gl 1781230 emb CAB082771 - (Z83867) hypothetical protein RV3137 [Mycobacterium tuberculosis]	Contains protein domain (PF00459) - Inositol monophosphatase family	phosphatase	35698052, 284508, 265008, 265009, 264769, 18108387, 284563
1023	11398341 (2045, 2046)	Novel Protein sim. GBank gl 3777485 (U92083) - calcium transporting ATPase [Pichia angustia]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase associated	284593
1024	80057129 (2047, 2048)			UNCLASSIFIED	52846842, 33657402, 33657023, 18108379, 55811576, 284631, 284556, 284557, 284559, 18108388, 284586 284693
1025	78644200 (2049, 2050)	Novel Protein sim. GBank gl 348304 emb CAA20556 - (AL031371) putative transport system permease protein [Streptomyces coelicolor]		transport	
1026	80025946 (2051, 2052)	Novel Protein sim. GBank gl 117492 sp Q02322 UVRD_HAEIN - DNA HELICASE II		helicase	284602
1027	17659234 (2053, 2054)	Novel Protein sim. GBank gl 4767728 ref NP_004896.1 pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	285017

1028	20297928 (2055, 2056)	Novel Protein sim. GBank gl 2791409 emb CAA16003 - (AL021184) acn [Mycobacterium tuberculosis]	Contains protein domain (PF00330) - Aconitase family (aconitate hydratase)	UNCLASSIFIED	284600
1029	8465090 (2057, 2058)			UNCLASSIFIED	284595
1030	85095343 (2059, 2060)			UNCLASSIFIED	284907, 284908, 284510, 284512, 285009, 285010, 285011, 284600, 284602, 284603, 284605, 284769, 18108372, 18108374
1031	85289117 (2061, 2062)			UNCLASSIFIED	284905, 284908, 284909, 284595, 284692, 284630, 284634, 284638
1032	94673275 (2063, 2064)	Novel Protein sim. GBank gl 4503895 ref NP_000145.1 pGALK - galactokinase 1		UNCLASSIFIED	284689
1033	86484818 (2065, 2066)	Novel Protein sim. GBank gl 2882990 (AE000682) - hypothetical protein [Aquifex aeolicus]		UNCLASSIFIED	35886052, 284908, 284510, 18108354, 284687, 284769, 284688, 60431602, 18108385, 284486
1034	78245937 (2067, 2068)	Novel Protein sim. GBank gl 405895 (U00007) - methionyl-tRNA synthetase [Escherichia coli]		UNCLASSIFIED	284906
1035	79956355 (2069, 2070)			UNCLASSIFIED	284892
1036	85804998 (2071, 2072)				284905, 86712502, 284908, 284766
1037	87896058 (2073, 2074)			UNCLASSIFIED	29331824, 284909, 80433438, 285019
1038	20481015 (2075, 2076)	Novel Protein sim. GBank gl 780819 (L38891) - polycystic kidney disease-associated protein [Homo sapiens]	Contains protein domain (PF01477) - PLAT/LH2 domain		284804, 284634
1039	87260021 (2077, 2078)	Novel Protein sim. GBank gl 2605967 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	
1040	80026940 (2079, 2080)	Novel Protein sim. GBank gl 2352095 (U97022) - DNA topoisomerase I [Fervidobacterium islandicum]	Contains protein domain (PF01131) - Prokaryotic DNA topoisomerase		284082, 284093, 284094, 284693, 284689, 283987
1041	10156882 (2081, 2082)	Novel Protein sim. GBank gl 3256535 db BAA29218.1 - (AP000001) 301aa long hypothetical 2-phosphoglycerate kinase [Pyrococcus horikoshii]		isomerase	284585
1042	11084375 (2083, 2084)	Novel Protein sim. GBank gl 2058299 emb CAA68953 - (X98309) ARI protein [Drosophila melanogaster]		kinase	284907
1043	80057138 (2085, 2086)	Novel Protein sim. GBank gl 1870167 emb CAA70125 - (Y08921) melK [Streptomyces reticuli]			284605
1044	80025952 (2087, 2088)		Contains protein domain (PF00005) - ABC transporter	transport	284585, 284587
1045	52415482 (2089, 2090)	Novel Protein sim. GBank gl 5688890 emb CA852053.1 - (AL109732) hypothetical protein [Streptomyces coelicolor A3(2)]		UNCLASSIFIED	285006, 284602, 285017, 29331825, 284637
1046	11754862 (2091, 2092)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		helicase	284686
1047	37036258 (2093, 2094)	Novel Protein sim. GBank gl 421047 db BAA74535.1 - (AB019033) orfSA [Pseudomonas sp.]		UNCLASSIFIED	284769
1048	78186400 (2095, 2096)	Novel Protein sim. GBank gl 3413419 emb CAA20279 - (AL031232) hypothetical protein SC10H5.07 [Streptomyces coelicolor]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N-terminal Domain	UNCLASSIFIED	284687
1049	81755108 (2097, 2098)	Novel Protein sim. GBank gl 5051636 gb AAD38328.1 AF073727 (AF073727) EH domain-binding mitotic phosphoprotein [Homo sapiens]		UNCLASSIFIED	284805, 284634
1050	78471521 (2099, 2100)			UNCLASSIFIED	284686

1051	80475471 (2101, 2102)			UNCLASSIFIED	18108374, 264769, 265010, 265011, 264601, 265009, 264604, 264605, 264636, 18108351, 264692
1052	82442862 (2103, 2104)	Novel Protein sim. GBank glj3123275 sp P35136 SERA_BACSU - D-3- PHOSPHOGLYCERATE DEHYDROGENASE (PGDH- (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]	Contains protein domain (PF00389) - D-isomer specific 2-hydroxyacid dehydrogenases	dehydrogenase	264508, 264762, 264687, 264486
1053	94851640 (2105, 2106)	Novel Protein sim. GBank glj5441318 emb CAB46717.1 - (AL034396) dJ1158B12.1 (zinc finger, X-linked, duplicated A) [Homo sapiens]			264686, 18108374, 29331824, 83373044, 21908754, 52845156, 56182435, 264689, 29331827, 27488281, 35696052, 21908765, 35696423, 21908768, 56182575, 21908769, 55811857, 87168518, 35696286, 22278997, 285020, 285011, 285021, 285022, 285007, 285016, 22279000, 22279002, 264482, 264906, 52844150, 264909, 264288, 29331822, 52845080, 264766
1054	78580225 (2107, 2108)			UNCLASSIFIED	264686
1055	80594138 (2109, 2110)	Novel Protein sim. GBank glj9052508 sp AAD38584.1 AF14560 - (AF145609) BcDNA.GH02833 [Drosophila melanogaster]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	264907, 264602, 264681, 264288, 21908768, 33857108, 55810764, 35695855, 264631
1056	17882319 (2111, 2112)	Novel Protein sim. GBank glj3021676 dbj BA025358 - (D86033) RNA polymerase sigma-70 factor [Pseudomonas fluorescens]		mapolymerase	264906
1057	85867216 (2113, 2114)	Novel Protein sim. GBank glj1226281 (U50308) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264682
1058	80376576 (2115, 2116)				264764
1059	94682754 (2117, 2118)	Novel Protein sim. GBank glj1170016 sp P46808 GREA_MYCLE - TRANSCRIPTION ELONGATION FACTOR GREA (TRANSCRIPT CLEAVAGE FACTOR GREA)		transcriptfactor	35696052, 35695855, 265009, 264636
1060	79461169 (2119, 2120)	Novel Protein sim. GBank glj2499087 sp Q08332 UGGG_DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	29146498, 264681, 264683, 264687
1061	11034025 (2121, 2122)	Novel Protein sim. GBank glj90254 pir j28334 - protein- tyrosine-phosphatase (EC 3.1.3.48) Ly-5 precursor (B-cell variant) - mouse		phosphatase	264634
1062	39567837 (2123, 2124)	Novel Protein sim. GBank glj3334200 sp Q49954 GCSP_SOLTU - GLYCINE DEHYDROGENASE (DECARBOXYLATING) PRECURSOR (GLYCINE DECARBOXYLASE) (GLYCINE CLEAVAGE SYSTEM P-PROTEIN)		dehydrogenase	264593
1063	8490481 (2125, 2126)	Novel Protein sim. GBank glj2499868 sp Q41228 PSE1_NICSY - PHOTOSYSTEM I REACTION CENTRE SUBUNIT IV A PRECURSOR (PSI-E A)			264508
1064	78891783 (2127, 2128)	Novel Protein sim. GBank glj82654 pir JA0086 - 10K zein precursor - maize			265007, 265008, 18108351, 18108385

1065	80021208 (2128, 2130)	Novel Protein sim. GBank gij2120988[pij]ST0682 - glycosyltransferase homolog - Bordetella pertussis		transferase	284800, 284602, 284689
1066	17896879 (2131, 2132)	Novel Protein sim. GBank gij2808382[pij]P16042[DNLJ_ECOLI - DNA LIGASE (POLYDEOXYRIBONUCLEOTIDE SYNTHASE (NAD+))]		synthase	285009
1067	10132178 (2133, 2134)				284909
1068	82062057 (2135, 2136)	Novel Protein sim. GBank gij4007669[emb]CAA22355 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]	Contains protein domain (PF00248) - Aldol/keto reductase family	reductase	284888, 18108362, 284558, 284600, 284760
1069	83002854 (2137, 2138)	Novel Protein sim. GBank gij4589484[dbj]BAA76770.1 - (AB023143) KIAA0928 protein [Homo sapiens]		UNCLASSIFIED	284604
1070	82101892 (2139, 2140)	Novel Protein sim. GBank gij120304[spj]P15932[FLOK_SALTY - FLAGELLAR HOOK-ASSOCIATED PROTEIN 1 (HAP1)]		UNCLASSIFIED	284604, 284760
1071	20710569 (2141, 2142)	Novel Protein sim. GBank gij1750397 (U81261) - glutamate synthase large subunit [Pseudomonas aeruginosa]		synthase	284602
1072	82356540 (2143, 2144)			UNCLASSIFIED	284887, 284688, 21906784, 35888052, 35895817, 35895855, 284600, 284601, 284602, 285009, 284605, 284508, 284905, 284680, 284906, 284782, 284828, 284768
1073	78814400 (2145, 2146)				284809
1074	80105882 (2147, 2148)	Novel Protein sim. GBank gij477532[pij]A49175 - Motch B protein - mouse (fragment)	Contains protein domain (PF00008) - EGF-like domain	synthase	284808
1075	81850283 (2148, 2150)	Novel Protein sim. GBank gij3883109[emb]CAA76940 - (Y17920) CALO protein [Drosophila melanogaster]		UNCLASSIFIED	58984075, 22278898, 284594, 284757, 284586, 285018, 285019, 284681, 284389, 284688, 285020, 18108364, 18108374
1076	80477264 (2151, 2152)	Novel Protein sim. GBank gij1176203[spj]P48442[YHCM_ECOLI - HYPOTHETICAL 43.1 KD PROTEIN IN RPLM-HHOA INTERGENIC REGION (F375)]		ATPase-associated	284769
1077	79831334 (2153, 2154)	Novel Protein sim. GBank gij4033487[pij]Q44472[TUD4_AGRV1 - PUTATIVE HYDROXYPYRUVATE REDUCTASE]		kinase	284905
1078	20288874 (2155, 2156)				
1079	80494518 (2157, 2158)	Novel Protein sim. GBank gij3413828[emb]CAA20286 - (AL031260) hypothetical protein SC9A10.09 [Streptomyces coelicolor]		UNCLASSIFIED	284600
1080	11767188 (2159, 2160)			UNCLASSIFIED	18108394, 284769, 284634, 284636
1081	84747080 (2161, 2162)			UNCLASSIFIED	284684
1082	81480656 (2163, 2164)			UNCLASSIFIED	83373044, 285019, 22278002, 284482, 18108351, 284682, 284908, 284693, 284487, 284758, 284768, 284769, 21906787, 284511, 284910, 284634, 284635, 284905, 284636, 284908, 284637, 284907, 284908, 284764, 284638, 20281099, 284766, 284595

1083	87448717 (2185, 2186)	Novel Protein sim. GBank gll1722945[sp]Q10523Y01N_MYCTU - HYPOTHETICAL 44.6 KD PROTEIN CY427 23		UNCLASSIFIED	60424178, 284905, 284908, 284510, 60432229, 284759, 87188474, 284605, 284789, 284689, 18108364, 18108376, 35895855, 284638 284789
1084	37799308 (2187, 2188)	Novel Protein sim. GBank gll18384[sp]P32057WCAI - PUTATIVE COLANIC ACID BIOSYNTHESIS GLYCOSYL TRANSFERASE WCAI		UNCLASSIFIED	
1085	86475388 (2189, 2170)	Novel Protein sim. GBank gll1899180 (U80204) - heat shock protein 80 [Tsatamurella tyrosinosolvens]	Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family	eph	60432229, 284687
1086	79608269 (2171, 2172)	Novel Protein sim. GBank gll1172858[sp]P46176RL14_ACYKS - 50S RIBOSOMAL PROTEIN L14	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomalprot	284486
1087	79603978 (2173, 2174)	Novel Protein sim. GBank gll160188[emb]CAA154311 - (AL006583) dJ327J16.3 (novel CHROMObox family protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHROMatin Organization Modifier) domain	helicase	29331827, 284693
1088	79854963 (2175, 2176)	Novel Protein sim. GBank gll2883155 (AE000693) - phosphoglucosyltransferase/phosphomannomutase [Aquifex aeolicus]		UNCLASSIFIED	284905, 284601, 18108387
1089	80218800 (2177, 2178)	Novel Protein sim. GBank gll4981768[sp]AAD38290.1(AE00177) - (AE001778) NADH dehydrogenase, 30 kDa subunit, putative [Thermotoga maritima]	Contains protein domain (PF00329) - Respiratory-chain NADH dehydrogenase, 30 Kd subunit	UNCLASSIFIED	284488, 284511, 285011, 284882, 284788, 284689, 21908784, 35895917, 285020, 32633986, 18108370, 35895855
1090	11083925 (2178, 2180)	Novel Protein sim. GBank gll4007680[emb]CAA22368 - (AL034443) putative oxidoreductase [Streptomyces coelicolor]			284604
1091	12917471 (2181, 2182)	Novel Protein sim. GBank gll2485562[sp]P77239YLCD - ECOLI - HYPOTHETICAL 44.3 KD PROTEIN IN NFRB-PHEP INTERGENIC REGION PRECURSOR		UNCLASSIFIED	284637
1092	80252286 (2183, 2184)	Novel Protein sim. GBank gll286009[emb]CAA17998.1 - (AL022121) ntlh [Mycobacterium tuberculosis]	Contains protein domain (PF00730) - Endonuclease III	nuclease	284596 284789, 35895917, 35895855, 284600, 284602, 284603, 284605, 18108351 284686
1093	80496304 (2185, 2186)	Novel Protein sim. GBank gll1001642[sp]BAA103731 - (DB4002) dGTP triphosphohydrolase [Synecococcus sp.]		UNCLASSIFIED	
1094	10860972 (2187, 2188)	Novel Protein sim. GBank gll456557[emb]CAB40855.1 - (AL049828) putative adenine glycosylase [Streptomyces coelicolor]	Contains protein domain (PF00455) - Bacterial regulatory proteins, deoR family	nuclease	284908, 285007, 284595, 284600, 284602, 284603, 284604, 284605, 284782, 284786, 284789, 284638, 284558, 18108387, 60432113, 284482, 284486
1095	87457250 (2189, 2190)	Novel Protein sim. GBank gll15001[sp]P18206BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		synthase	284800, 284602, 284603, 284604, 284605, 35895917, 284692, 284631
1096	80025977 (2191, 2192)	Novel Protein sim. GBank gll115001[sp]P18206BIOB_BACSH - BIOTIN SYNTHASE (BIOTIN SYNTHETASE)		UNCLASSIFIED	285018 284687
1097	79239560 (2193, 2194)	Novel Protein sim. GBank gll114135[sp]P08205IARGA - ECOLI - AMINO-ACID ACETYL TRANSFERASE (N-ACETYLGLUTAMATE SYNTHASE) (AGS)		synthase	
1098	79186424 (2195, 2196)				

1099	39523638 (2197, 2198)	Novel Protein sim. GBank gi 3915144 sp O33017 TRMD_MYCLE - TRNA (GUANINE- N1)-METHYLTRANSFERASE (M1G- METHYLTRANSFERASE) (TRNA [GM37] METHYLTRANSFERASE)		UNCLASSIFIED	284603
1100	85736571 (2199, 2200)	Novel Protein sim. GBank gi 3023255 sp O84420 ACOD_MESAU - ACYL-COA DESATURASE (STEAROYL-COA DESATURASE) (FATTY ACID DESATURASE) (DELTA(9)-DESATURASE)		desaturase	284259, 284638
1101	80491857 (2201, 2202)	Novel Protein sim. GBank gi 1174735 sp P43012 TOP1_HAEIN - DNA TOPOISOMERASE I (OMEGA-PROTEIN) (RELAXING ENZYME) (UNTWISTING ENZYME) (SWIVELASE)	Contains protein domain (PF01396) - Topoisomerase DNA binding C4 zinc finger	isomerase	284769
1102	79777614 (2203, 2204)			UNCLASSIFIED	284810, 284809
1103	81897259 (2205, 2206)	Novel Protein sim. GBank gi 1174342 sp P43416 SECY_STRSC - PREPROTEIN TRANSLOCASE SECY SUBUNIT		struct	284757
1104	95003115 (2207, 2208)	Novel Protein sim. GBank gi 2835448 (AF048978) - synaptic ras GTPase-activating protein p135 SynGAP [Rattus norvegicus]		UNCLASSIFIED	29331822, 21906754, 284555, 284558, 284558, 22278002
1105	80255121 (2209, 2210)			UNCLASSIFIED	284566
1106	79314110 (2211, 2212)			UNCLASSIFIED	284555, 284389
1107	80470019 (2213, 2214)			UNCLASSIFIED	284908, 284769
1108	80440618 (2215, 2216)			transport	284807, 284510, 284511, 284600, 284602, 284605, 284768, 284769
1109	80084615 (2217, 2218)	Novel Protein sim. GBank gi 2895310 emb CAA19338 - (AL022268) putative ATP-dependent helicase [Streptomyces coelicolor]		helicase	284602, 284605, 284638
1110	80503554 (2219, 2220)				
1111	80071744 (2221, 2222)	Novel Protein sim. GBank gi 2822039 (AE000668) - type I restriction modification system, subunit S [Methanobacterium thermoautotrophicum]			284908, 284593, 285010, 284801, 284603, 284804, 284805, 284882, 284789, 284893, 284638
1112	95010088 (2223, 2224)				18108370, 284557
1113	82458352 (2225, 2226)	Novel Protein sim. GBank gi 3218379 emb CAA19628 - (AL023862) putative oxidoreductase [Streptomyces coelicolor]		UNCLASSIFIED	284808
1114	14988014 (2227, 2228)	Novel Protein sim. GBank gi 1083428 pir S54876 - NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) precursor - mouse		dehydrogenase	284600, 284602, 284604, 284605, 284762, 284769, 284585
1115	11765583 (2229, 2230)				284636
1116	78841152 (2231, 2232)			UNCLASSIFIED	284686
					284908

1117	95305465 (2233, 2234)	Novel Protein sim. GBank gll3255965[emb]CAA84089] - (Z70200) U5 snRNP-specific 200KD protein [Homo sapiens]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	18108382, 284488, 263994, 264489, 18108398, 56182575, 22278995, 22278998, 35698286, 59994075, 22278997, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 66714117, 29331825, 29331826, 80432289, 29331827, 29331828, 35698032, 33856970, 26146498, 264508, 264805, 264509, 264808, 264907, 264908, 66712502, 264909, 52844045, 58182435, 264510, 264511, 265008, 265007, 264512, 265008, 265009, 264910, 60170831, 264591, 264592, 264593, 80433356, 264594, 80433438, 264595, 59812038, 264596, 264758, 264759, 21908754, 33109954, 33657084, 265011, 87168559, 264600, 264601, 264602, 264603, 265017, 264804, 265018, 264605, 265019, 264760, 55811150, 264681, 264762, 18108351, 284448, 264682, 264784, 264683, 264288, 264389, 264684, 264685, 264786, 264787, 264686, 264687, 264788, 264789, 264688, 18108359, 264689, 21908765, 21908768, 21908767, 21908769, 55811957, 29148784, 35695917, 265020, 285021, 265022, 60170815, 264690, 264691, 33657023, 264692, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 264691
1118	79563328 (2235, 2236)		UNCLASSIFIED	
1119	79642463 (2237, 2238)		UNCLASSIFIED	
1120	79480463 (2239, 2240)	Novel Protein sim. GBank gll5420387[emb]CAB46678.1] - (AJ243459) proleophosphoglycan [Leishmania major]	collagen	284807
1121	78471718 (2241, 2242)	Novel Protein sim. GBank gll1644450 (U67864) - MEX-3 [Caenorhabditis elegans]	Contains protein domain (PF00013) - KH domain	29331827, 265018, 265019, 264681, 265021, 60170815, 18108367
1122	78458246 (2243, 2244)		UNCLASSIFIED	284683, 264632, 18108388
1123	78637119 (2245, 2246)	Novel Protein sim. GBank gll98800[pr]S17768 - 3- dehydroquinase synthase (EC 4.8.1.3) - Mycobacterium tuberculosis	UNCLASSIFIED synthase	284639, 264563, 284693, 27486265
1124	78611596 (2247, 2248)		UNCLASSIFIED	
1125	78757861 (2249, 2250)		UNCLASSIFIED	284909
1126	78758914 (2251, 2252)	Novel Protein sim. GBank gll138154[sp]P03643[VGG_BPPHX - MAJOR SPIKE PROTEIN (G PROTEIN) (GPG)]	UNCLASSIFIED eph	284910, 264805, 264809, 264910
1127	11800830 (2253, 2254)		UNCLASSIFIED	
1128	8364885 (2255, 2256)	Novel Protein sim. GBank gll5002704[emb]CAB44358.1] - (AJ242630) DNA polymerase I [Methylobacterium sp. DM4]	Contains protein domain (PF00476) - DNA polymerase family A	284682, 264511

1129	60422480 (2257, 2258)	Novel Protein sim. GBank glj5689485[jb]BAA83026.1] - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	265011, 264768
1130	79420151 (2259, 2260)	Novel Protein sim. GBank glj4981328[jb]AAD35981.1]AE00174 - (AE001747) bioY protein [Thermotoga maritima]		UNCLASSIFIED	264593
1131	80055391 (2261, 2262)	Novel Protein sim. GBank glj1841552 (U99338) - unknown [Homo sapiens]		UNCLASSIFIED	35686286, 22278998, 28331826, 264603, 264605, 264559
1132	82062248 (2263, 2264)	Novel Protein sim. GBank glj1841552 (U99338) - unknown [Homo sapiens]		UNCLASSIFIED	22278998, 264906, 265009, 284600, 284602, 264604, 264605, 264760, 32833986, 18108374
1133	17290437 (2265, 2266)			UNCLASSIFIED	265018
1134	80235376 (2267, 2268)			UNCLASSIFIED	264512, 264534
1135	80028393 (2269, 2270)	Novel Protein sim. GBank glj4539171[jemb]CAB39700.1] - (AL049485) conserved hypothetical protein [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264600, 264602, 284603, 18108376
1136	79842052 (2271, 2272)	Novel Protein sim. GBank glj4982454[jb]AAD36931.1]AE00182 - (AE001823) ATP-dependent protease LA, putative [Thermotoga maritima]		UNCLASSIFIED	264906, 264908
1137	90931557 (2273, 2274)	Novel Protein sim. GBank glj4972749[jb]AAD34786.1] - (AF132180) unknown [Drosophila melanogaster]	Contains protein domain (PF00515) - collagen TPR Domain		22278998, 22278999, 35686052, 264907, 265009, 80433358, 264598, 265010, 264448, 264682, 264767, 264689, 265020, 264692, 55811578, 35685855, 264631, 264632, 22279002
1138	79841163 (2275, 2276)	Novel Protein sim. GBank glj731607[jp]P38739[YHC8 YEAST - HYPOTHETICAL 63.8 KD PROTEIN IN GUT1-RIM1 INTERGENIC REGION PRECURSOR]			264908
1139	79833561 (2277, 2278)	Novel Protein sim. GBank glj3650031 (AC003398) - putative proline-rich cell wall protein [Arabidopsis thaliana]		UNCLASSIFIED	264693
1140	39480358 (2279, 2280)			UNCLASSIFIED	264593
1141	79838019 (2281, 2282)			UNCLASSIFIED	265019, 264693
1142	19635948 (2283, 2284)			UNCLASSIFIED	264631
1143	87762158 (2285, 2286)	Novel Protein sim. GBank glj382800[jemb]CAA05880] - (AJ003125) procollagen I N-proteinase [Homo sapiens]	Contains protein domain (PF00090) - oxidase Thrombospondin type 1 domain		56162575, 264908, 264600, 284632, 87168518
1144	80088988 (2287, 2288)			UNCLASSIFIED	264635, 264638, 264907, 284593, 264908, 264596, 264909
1145	14610262 (2289, 2290)			UNCLASSIFIED	264112
1146	82062092 (2291, 2292)			UNCLASSIFIED	264769, 264689, 35686286, 264760, 264905, 264486, 264559
1147	80071761 (2293, 2294)				264557
1148	80048433 (2295, 2296)	Novel Protein sim. GBank glj2499003[jp]P76422[THID_ECOLI - PHOSPHOMETHYL PYRIMIDINE KINASE (HMP-PHOSPHATE KINASE) (HMP-P KINASE)]	kinase		264591
1149	11607438 (2297, 2298)	Novel Protein sim. GBank glj2689734[jemb]CAA17213.1] - (AL021897) hypothetical protein Rv1087c [Mycobacterium tuberculosis]			264591

1150	81325074 (2299, 2300)	Novel Protein sim. GBank gll2895095 (AF011337) - putative E1-E2 ATPase [Mus musculus]		ATPase-associated	264488, 35696286, 264907, 264808, 264809, 264810, 264593, 264598, 264758, 264764, 264766, 264768, 264693, 264628, 60431850, 264584, 264566, 264587, 264595
1151	80070874 (2301, 2302)	Novel Protein sim. GBank gll4324655 (gbIAAD16978) - (AF108191) DNA polymerase III alpha subunit [Streptomyces coelicolor]		polymerase	
1152	80235547 (2303, 2304)	Novel Protein sim. GBank gll3874275 (embjCAB07311.1) - (Z92825) predicted using GeneFinder; Similarity to Yeast low affinity glucose transporter HXT4 (PS:32487); cDNA EST EMBL: C12955 comes from this gene; cDNA EST yk404c10.3 comes from this gene; cDNA EST yk404c10.5 comes from thi...		glycoprotein	264488, 22278988, 264905, 264628, 264486
1153	80027783 (2305, 2306)	Novel Protein sim. GBank gll4240315 (dbjBAA74938.1) - (AB020720) KIAA0913 protein [Homo sapiens]		UNCLASSIFIED	264910, 264555, 264557, 265008
1154	83002985 (2307, 2308)	Novel Protein sim. GBank gll37617 (ATZN_ECOLI - ZINC-TRANSPORTING ATPASE (ZN(II)-TRANSLCATING P. TYPE ATPASE)	Contains protein domain (PF00122) - E1-E2 ATPase	UNCLASSIFIED	264890, 264636, 264603
1155	78411098 (2309, 2310)	Novel Protein sim. GBank gll418480 (spjP32139) (VHR_ECOLI - HYPOTHETICAL 34.0 KD PROTEIN IN GLNA-RBN INTERGENIC REGION		UNCLASSIFIED	264908, 264907, 264758, 264766, 264769, 264689, 264638, 264566
1156	57147843 (2311, 2312)	Novel Protein sim. GBank gll2486481 (spjQ50724) (Y09S_MYCTU - HYPOTHETICAL 87.3 KD PROTEIN CY78.27C		UNCLASSIFIED	264908, 264762, 264687, 264769, 264689, 18108374, 35695855
1157	95287711 (2313, 2314)	Novel Protein sim. GBank gll1136406 (dbjBAA11490) - (D79899) similar to pig tubulin-tyrosine ligase. [Homo sapiens]		UNCLASSIFIED	264687, 26331822, 26331824, 68714117, 26331826, 60433356, 265018, 265019, 83373044, 18108385, 22279000, 22279002, 264563, 264389, 264693
1158	82454917 (2315, 2316)	Novel Protein sim. GBank gll4503375 (refjNP_001378.1) (pDPYS - dihydropyrimidinase		UNCLASSIFIED	26331827, 264808
1159	78188451 (2317, 2318)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		transport	18108398, 26331827, 26331828, 29146488, 29146498, 18108354, 21908768, 29146827, 21908769, 264693, 18108382, 18108385, 264602, 264605, 264769, 18108370, 18108374, 264395
1160	81229883 (2319, 2320)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	264488, 35696286, 22278988, 264259, 68714117, 60432289, 35696052, 264905, 56182435, 265006, 60433436, 264759, 21908754, 33109954, 265017, 265019, 264448, 264288, 264766, 264685, 35696423, 35695855, 264558, 18108385, 60432113
1161	7417143 (2321, 2322)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1162	78635357 (2323, 2324)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1163	78563186 (2325, 2326)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1164	78650828 (2327, 2328)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1165	80491888 (2329, 2330)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	
1166	88098456 (2331, 2332)	Novel Protein sim. GBank gll145089476 (dbjBAA78768.1) - (AB023139) KIAA0922 protein [Homo sapiens]		UNCLASSIFIED	

1167	79903882 (2333, 2334)	Novel Protein sim. GBank glj2680433[dbj BAA23138] - (D76414) ppGpp hydrolase [Staphylococcus aureus]		Kinase	284488
1168	88094878 (2335, 2336)			UNCLASSIFIED	284259, 28331827, 56182435, 60433438, 285019, 33657023, 35695855, 284586
1169	11805403 (2337, 2338)			UNCLASSIFIED	284881
1170	21832244 (2339, 2340)			UNCLASSIFIED	284802
1171	20434682 (2341, 2342)	Novel Protein sim. GBank glj2772814 (AF028249) - precollagen D [Mytilus edulis]		UNCLASSIFIED	284556
1172	78810113 (2343, 2344)	Novel Protein sim. GBank glj4757846[ref NP_004317.1 pBCL9 - B-cell CLL/lymphoma 9		UNCLASSIFIED	55810784, 35696052, 284634, 284488
1173	60235713 (2345, 2346)	Novel Protein sim. GBank glj2684053[dbj BAA22846] - (AB007832) Bm trachealless [Bombyx mori]			284508, 284906, 284907, 284909, 284591, 284632, 284638, 284639
1174	20283077 (2347, 2348)	Novel Protein sim. GBank glj281102[emb CAA17520] - (AL021858) mmsA [Mycobacterium tuberculosis]		dehydrogenase	284600
1175	20711847 (2349, 2350)	Novel Protein sim. GBank glj118333[sp P23234 DCIP_ENTCL - INDOLE-3-PYRUVATE DECARBOXYLASE (INDOLEPYRUVATE DECARBOXYLASE)]	Contains protein domain (PF00205) - Thiamine pyrophosphate enzymes	carboxylase	284601
1176	80252645 (2351, 2352)	Novel Protein sim. GBank glj1144520 (U34956) - phosphoribosylformylglycinamide synthase [Mycobacterium tuberculosis]	Contains protein domain (PF00588) - AIR synthase related protein	synthase	284508, 284805, 284593, 284602, 284605
1177	80084847 (2353, 2354)	Novel Protein sim. GBank glj119791[sp P28643 FABG_CUPLA - 3-OXOACYL-ACYL-CARRIER PROTEIN] REDUCTASE PRECURSOR (3-KETOACYL-ACYL CARRIER PROTEIN REDUCTASE)	Contains protein domain (PF00108) - short chain dehydrogenase	reductase	284605
1178	94128841 (2355, 2356)	Novel Protein sim. GBank glj5031697[ref NP_005594.1 pFIC1 - familial intrahepatic cholestasis 1, (progressive, Byler disease and benign recurrent)]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase, associated	65274572, 18108398, 22278998, 22278999, 28331828, 284508, 284908, 284828, 33657402, 33109954, 284768, 21808765, 21808788, 21808788, 55811957, 33657023, 284628, 55811576, 35698423, 284636, 284556, 58182323, 60432113, 22279000, 22279002
1179	80055576 (2357, 2358)	Novel Protein sim. GBank glj2880090[emb CAA17888.1] - (AL022121) dppA [Mycobacterium tuberculosis]	Contains protein domain (PF00498) - Bacterial extracellular solute-binding proteins, family 5	transport	284603
1180	11794448 (2359, 2360)	Novel Protein sim. GBank glj2558614[emb CAA04787] - (AJ001483) dehydroquinase dehydratase [Streptomyces coelicolor]	Contains protein domain (PF01220) - Dehydroquinase class II	synthase	284638
1181	17848382 (2361, 2362)			UNCLASSIFIED	265017
1182	81404264 (2363, 2364)	Novel Protein sim. GBank glj5420387[emb CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]			265007, 265009, 284584, 284909, 284683
1183	76574044 (2365, 2366)	Novel Protein sim. GBank glj4091877 (AF061331) - alpha galactosidase precursor [Saccharomyces cerevisiae]			284689, 35698423, 284638, 18108385
1184	52559933 (2367, 2368)	Novel Protein sim. GBank glj2128478[ref S51839] - chitinase (EC 3.2.1.14) precursor - beetle		UNCLASSIFIED	284602
1185	79491185 (2369, 2370)			glycoprotein	263987

1186	20224012 (2371, 2372)			UNCLASSIFIED	264559
1187	78248834 (2373, 2374)			UNCLASSIFIED	29331825, 265017, 18108351
1188	78831387 (2375, 2376)	Novel Protein sim. GBank gi 2896039 (AF054525) - hypothetical protein [Synecoccus PCC7002]		UNCLASSIFIED	264905, 264906
1189	79609367 (2377, 2378)				264892
1190	78930589 (2379, 2380)			UNCLASSIFIED	265018
1191	80310105 (2381, 2382)			UNCLASSIFIED	264600, 264605, 264764, 35695855, 264638, 264486
1192	13521641 (2383, 2384)		Contains protein domain (PF01581) - FMRFamide related peptide family		264636
1193	11103584 (2385, 2386)				
1194	7883947 (2387, 2388)	Novel Protein sim. GBank gi 8540851emb CAA583371 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	263978
1195	20445442 (2389, 2390)	Novel Protein sim. GBank gi 1780277 (AE000459) - putative oxidoreductase [Escherichia coli]		UNCLASSIFIED	265007, 265008
1196	13000888 (2391, 2392)			UNCLASSIFIED	264605
1197	11392317 (2393, 2394)	Novel Protein sim. GBank gi 2497360 sp Q50715 IMDH_MYCTU - INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE (IMP DEHYDROGENASE) (IMPDH) (IMPD)	Contains protein domain (PF00571) - CBS domain		264889 264594
1198	85280101 (2395, 2396)				
1199	81882011 (2397, 2398)	Novel Protein sim. GBank gi 1708825 sp P54673 P3K1_DICDI - PHOSPHATIDYLINOSITOL 3-KINASE 1 (PI3-KINASE) (PTDINS-3-KINASE) (PI3K)			264603 264259, 264757, 33109954, 21906768
1200	9848880 (2399, 2400)				
1201	80503751 (2401, 2402)	Novel Protein sim. GBank gi 249887 sp P70845 BLMH_RAT - BLEOMYCIN HYDROLASE (BLM HYDROLASE) (BMH)	UNCLASSIFIED calhepsin		264910 264766, 264769
1202	80082633 (2403, 2404)	Novel Protein sim. GBank gi 606342 (U18987) - ORF_0822; reading frame open far upstream of start; possible frameshift, linking to previous ORF [Escherichia coli]	ribosomalprot		264600, 264558
1203	82125373 (2405, 2406)				
1204	80503916 (2407, 2408)	Novel Protein sim. GBank gi 2500728 sp Q59912 SECY_STRGB - PREPROTEIN TRANSLOCASE SECY SUBUNIT	UNCLASSIFIED		264768, 264769, 35695917, 264910, 264760, 264908, 264907, 264629, 264908, 264909, 264786
1205	80053981 (2409, 2410)				264905, 264769, 264636
1206	80241985 (2411, 2412)			UNCLASSIFIED	264586
1207	79841192 (2413, 2414)			UNCLASSIFIED	264556, 264557, 264558
1208	87755217 (2415, 2416)	Novel Protein sim. GBank gi 2645560 (AF027954) - Bcl-2 related ovarian killer protein [Rattus norvegicus]	Contains protein domain (PF00452) - Apoptosis regulator proteins, Bcl-2 family		29331824, 264909, 265021, 18108370 29331824, 29331825, 29331827, 265007, 264764, 264683, 264769, 264688, 264689

1208	79185742 (2417, 2418)	Novel Protein sim. GBank gi 1175033 sp P44389 XYLA_HAEIN - XYLOSE ISOMERASE	Contains protein domain (PF00259) - Xylose isomerase	isomerase	284887, 284888
1210	56426884 (2419, 2420)			UNCLASSIFIED	284907, 284993
1211	94665855 (2421, 2422)	Novel Protein sim. GBank gi 421095 pir J30888 - hypothetical protein o248 - Escherichia coli		transferase	284591, 284592, 284595
1212	79187929 (2423, 2424)	(293785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf		284889, 283967
1213	79859633 (2425, 2426)	Novel Protein sim. GBank gi 226292 pir J1505375A - vir gene [Bordetella pertussis]		kinase	284909
1214	10144308 (2427, 2428)	Novel Protein sim. GBank gi 5728285 gb AA048398.1 AF12816 - (AF128162) HERV-H LTR associating protein 2 [Homo sapiens]		UNCLASSIFIED	284908
1215	80050108 (2429, 2430)	Novel Protein sim. GBank gi 2326739 emb CAB10953 - (Z99289) recN [Mycobacterium tuberculosis]		UNCLASSIFIED	265009, 284801, 284602, 284603, 33657109
1216	20438324 (2431, 2432)	Novel Protein sim. GBank gi 417328 sp P33038 MURA_ENTCL - UDP-N- ACETYLGLUCOSAMINE 1- CARBOXYVINYLTRANSFERASE (ENOYL-PYRUVATE TRANSFERASE) (UDP-N-ACETYLGLUCOSAMINE ENOYL-PYRUVYL TRANSFERASE) (EPT)		transferase	284604
1217	95011344 (2433, 2434)				
1218	11083680 (2435, 2436)	Novel Protein sim. GBank gi 1805460 dbj BAA08022 - (D50453) homologue of succinate semialdehyde dehydrogenase GabD of E. coli [Bacillus subtilis]		UNCLASSIFIED	284905, 284907, 284908, 284591, 284786, 284891, 284693, 284828, 284630, 284636, 284564
1219	91218252 (2437, 2438)			dehydrogenase	284801
1220	91241524 (2439, 2440)	Novel Protein sim. GBank gi 4240315 dbj BAA74936.1 - (AB020720) KIAA0913 protein [Homo sapiens]		oncogene	56181686, 28331822, 60432289, 284601, 284892, 284829
1221	83045055 (2441, 2442)	Novel Protein sim. GBank gi 2143886 pir J152523 - nucleoporin p82 homolog - rat (fragment)			52844507, 284905, 284909, 265008, 265019, 265020, 52844150, 33657023, 284693, 33657182, 35695763, 284634, 22279000, 22279002, 264482
1222	20711865 (2443, 2444)	Novel Protein sim. GBank gi 730805 sp P39663 SPHR_SYN7 - ALKALINE PHOSPHATASE SYNTHESIS TRANSCRIPTIONAL REGULATORY PROTEIN SPHR	Contains protein domain (PF00466) - Transcriptional regulatory protein, C terminal	UNCLASSIFIED	284788, 285020, 284906
1223	11615847 (2445, 2446)			phosphatase	284601
1224	80432845 (2447, 2448)	Novel Protein sim. GBank gi 1172827 sp P46546 PROB_CORGL - GLUTAMATE 5- KINASE (GAMMA-GLUTAMYL KINASE) (GK)	Contains protein domain (PF01472) - PUA domain	kinase	284593
					284593, 284600, 284601, 284603, 284605, 284788, 18108376, 284635, 18108387

1225	80434427 (2448, 2450)	Novel Protein sim. GBank gij2105050jemb CAB08838 - (Z95438) hypothetical protein Rv3844c [Mycobacterium tuberculosis]			polymerase	264768
1226	80237518 (2451, 2452)					264905, 264512, 264689
1227	78422138 (2453, 2454)	Novel Protein sim. GBank gij1708788 sp P88133 FBN1_BOVIN - FIBRILLIN 1 PRECURSOR (MP340)			UNCLASSIFIED	264908, 264637, 264639
1228	79208027 (2455, 2456)	Novel Protein sim. GBank gij1653901 dbj BAA18811 - (D90817) acriflavine resistance protein [Synecococcus sp.]		Contains protein domain (PF00873) - AcrB/AcrD/AcrF family		264605, 264634
1229	84329135 (2457, 2458)				UNCLASSIFIED	87168474, 265011, 87168559, 264681, 264689, 264693, 65274620, 18108374, 264909, 264605, 18108388
1230	80049357 (2459, 2460)	Novel Protein sim. GBank gij116230 sp P28598 CH60_BACSU - 60 KD CHAPERONIN (PROTEIN CPN60) (GROEL PROTEIN)		Contains protein domain (PF00118) - TCP-1/cpn60 chaperonin family		
1231	79843141 (2461, 2462)				UNCLASSIFIED	264908
1232	79853104 (2463, 2464)	Novel Protein sim. GBank gij1215733 (U48718) - OphC [Agrobacterium tumefaciens]			transport	264909
1233	80255179 (2465, 2466)	Novel Protein sim. GBank gij118298 sp P20730 CHHC_BOMMO - CHORION CLASS HIGH-CYSTEINE HCB PROTEIN 13 PRECURSOR (HC-B.13)			UNCLASSIFIED	265017, 264564
1234	79242158 (2467, 2468)	Novel Protein sim. GBank gij726871 sp P40280 H2A_MAIZE - HISTONE H2A		Contains protein domain (PF00125) - histone Core histone H2A/H2B/H3/H4		265008, 265010, 18108381
1235	79914423 (2469, 2470)					264634, 264762
1236	81927147 (2471, 2472)	Novel Protein sim. GBank gij3875133 jemb CAA94750 - (Z70750) similar to actin binding domain; cDNA EST EMBL:T00093 comes from this gene; cDNA EST EMBL:D34443 comes from this gene; cDNA EST EMBL:D37508 comes from this gene; cDNA EST EMBL:D84247 comes from this gene; cDNA EST EMBL:...			UNCLASSIFIED	265018, 55811150, 264565, 264757
1237	83371782 (2473, 2474)	Novel Protein sim. GBank gij3885470 (AF081443) - G protein-coupled receptor LGR4 [Rattus norvegicus]				264758, 264601, 264766, 264687, 18108372, 264555, 264559
1238	87411577 (2475, 2476)					
1239	82197449 (2477, 2478)	Novel Protein sim. GBank gij4007990 gb AAC95339 - (AF084383) DOK protein [Mus musculus]		Contains protein domain (PF00560) - glycoprotein Leucine Rich Repeat		264259, 28331822, 29331824, 35696052, 264508, 264908, 52844045, 52848317, 264288, 264769, 264693, 264632, 264634, 264558, 87168518, 264563
1240	80497259 (2479, 2480)	Novel Protein sim. GBank gij1178192 sp P45420 YHCD_ECOLI - HYPOTHETICAL OUTER MEMBRANE USHER PROTEIN IN GLTF-NANT INTERGENIC REGION PRECURSOR			oncogene	264509, 264511, 264759, 264760, 264764, 264557
1241	80020711 (2481, 2482)	Novel Protein sim. GBank gij121383 sp P18904 GLNA_VIBAL - GLUTAMINE SYNTHETASE (GLUTAMATE-AMMONIA LIGASE)		Contains protein domain (PF00120) - Glutamine synthetase		264769
1242	79775890 (2483, 2484)				UNCLASSIFIED	264601, 264604, 264638
						264908, 264907, 264908, 264634

1243	79779458 (2485, 2486)	Novel Protein sim. GBank glij355671embjCAA189711 - (AL031124) branched-chain amino acid aminotransferase [Streptomyces coelicolor]		UNCLASSIFIED	18108374, 35695917, 35695855, 265009, 264508, 264909
1244	10284821 (2487, 2488)	Novel Protein sim. GBank glij2970848 (AF051945) - Xin [Mus musculus]		UNCLASSIFIED	264691
1245	80437103 (2489, 2490)	Novel Protein sim. GBank glij4586338jdbjBAA76357.11 - (AB016787) cytochrome o ubiquinol oxidase B [Pseudomonas putida]	Contains protein domain (PF001115) - Cytochrome C and Quinol oxidase polypeptide I	oxidase	264768
1246	80059321 (2491, 2492)	Novel Protein sim. GBank glij3581849jembjCAA208051 - (AL031541) putative phenylalanyl-tRNA synthetase beta chain [Streptomyces coelicolor]		UNCLASSIFIED	264604, 264636, 264557, 264564
1247	80064831 (2493, 2494)	Novel Protein sim. GBank glij2621684 (AE000842) - adhesion protein [Methanobacterium thermoautotrophicum]			264758, 264605, 264639
1248	88070353 (2495, 2496)	Novel Protein sim. GBank glij1352403jpp09487f16P_HUMAN - FRUCTOSE-1,6-BISPHOSPHATASE (D-FRUCTOSE-1,6-BISPHOSPHATE 1-PHOSPHOHYDROLASE) (FBPASE)	Contains protein domain (PF00316) - Fructose-1,6-bisphosphatase	UNCLASSIFIED	18108392, 264259, 26331826, 264106, 264508, 264907, 264828, 265009, 60433356, 264757, 264758, 21908754, 265010, 265011, 265018, 265019, 264780, 18108351, 18108354, 265021, 18108376, 18108377, 264630, 18108385
1249	80056657 (2497, 2498)	Novel Protein sim. GBank glij2791407jembjCAA160011 - (AL021184) hypothetical protein Rv1473 [Mycobacterium tuberculosis]	transport		264908, 265010, 264600, 264603, 264691, 18108376
1250	12694385 (2498, 2500)	Novel Protein sim. GBank glij112785jpp051003MG1_ECOLI - DNA-3-METHYLADENINE GLYCOSIDASE I (3-METHYLADENINE-DNA GLYCOSYLASE I, CONSTITUTIVE) (TAG I)		UNCLASSIFIED	264689
1251	79850448 (2501, 2502)				264909
1252	79458087 (2503, 2504)			UNCLASSIFIED	264883, 263976
1253	80050121 (2505, 2506)	Novel Protein sim. GBank glij5670178jppAAD46616.11AF18131 - (AF181317) NRAMP manganese transport protein MntA [Salmonella typhimurium]	glycoprotein		264800, 264603, 18108376
1254	87716767 (2507, 2508)	Novel Protein sim. GBank glij103160jppjS22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	35696286, 264910, 264764, 264688, 21906787, 55811957, 264892, 264556, 264639
1255	79189728 (2509, 2510)				264636
1256	87889508 (2511, 2512)	Novel Protein sim. GBank glij2985353jembjCAA04608.11 - (AJ001206) pep2 [Streptomyces coelicolor]		UNCLASSIFIED	80432288, 264600, 264605, 264764, 264687, 264769, 264689, 27486285, 18108374, 18108378
1257	80201435 (2513, 2514)	Novel Protein sim. GBank glij3193308 (AF089300) - contains similarity to Arabidopsis membrane-associated salt inducible-like protein (GB:AL021637) [Arabidopsis thaliana]		UNCLASSIFIED	264094, 265019
1258	20708150 (2515, 2516)				
1259	80166012 (2517, 2518)			UNCLASSIFIED	264602, 263978
1260	80084808 (2519, 2520)			UNCLASSIFIED	264806, 264448, 264908
				UNCLASSIFIED	264634, 264639

1261	87412602 (2521, 2522)	Novel Protein sim. GBank gl 5688511 dbj GAA03039.1 - (AB028010) KIAA1087 protein [Homo sapiens]	Contains protein domain (PF01699) - Sodium/calcium exchanger protein	cadherin	29331824, 264906, 264908, 264768, 264769, 264889, 264693, 264639, 18108384, 264663
1262	13504589 (2523, 2524)	Novel Protein sim. GBank gl 95100 pir S21334 - hypothetical protein 4 - Agrobacterium tumefaciens		UNCLASSIFIED	264634
1263	20710997 (2525, 2526)				264602
1264	80083396 (2527, 2528)	Novel Protein sim. GBank gl 3550958 (AF004840) - CDO [Rattus norvegicus]		struct	264634
1265	80253578 (2529, 2530)				264663
1266	78914604 (2531, 2532)			UNCLASSIFIED	264768, 264838, 264639, 264587
1267	80558918 (2533, 2534)	Novel Protein sim. GBank gl 1085002 pir S55056 - mitochondrial carrier protein DIF-1 homolog - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	264259, 21908754, 264369
1268	88178473 (2535, 2536)	Novel Protein sim. GBank gl 4888445 emb CAB43370.1 - (AL050269) hypothetical protein [Homo sapiens]	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	UNCLASSIFIED	18108398, 22278895, 56994075, 60424269, 29331827, 264108, 264512, 265007, 265008, 265009, 264595, 33109954, 33657084, 87188559, 264600, 265018, 265019, 264369, 264688, 21908787, 265020, 52644150, 264691, 33657023, 33657349, 18108374, 264556, 18108385, 60432113, 22279002, 264488
1269	78821948 (2537, 2538)	Novel Protein sim. GBank gl 3334781 emb CAA19939 - (AL031107) hypothetical protein SC5A7.10c [Streptomyces coelicolor]		UNCLASSIFIED	264508, 264905, 264908, 264687, 264693
1270	80031420 (2539, 2540)	Novel Protein sim. GBank gl 2851634 sp Q50591 Y0D1_MYCTU - HYPOTHETICAL 50.0 KD PROTEIN CY1A11.01	Contains protein domain (PF01574) - IMP dehydrogenase / GMP reductase N terminus	dehydrogenase	265010, 264601
1271	78840499 (2541, 2542)			ATPase associated	35696052, 264908
1272	79462878 (2543, 2544)				264686, 264689
1273	80220315 (2545, 2546)	Novel Protein sim. GBank gl 1655665 emb CAB03731 - (Z81380) hypothetical protein Rv2395 [Mycobacterium tuberculosis]		UNCLASSIFIED	264509, 264639
1274	95010802 (2547, 2548)				
1275	20730763 (2549, 2550)	Novel Protein sim. GBank gl 123726 sp P10413 HTPG_ECOLI - HEAT SHOCK PROTEIN HTPG (HIGH TEMPERATURE PROTEIN G) (HEAT SHOCK PROTEIN C62.5)	Contains protein domain (PF00183) - Hsp90 protein	UNCLASSIFIED	264905, 264908, 264909, 264769
1276	21148644 (2551, 2552)	Novel Protein sim. GBank gl 2128476 pir S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	264602
1277	20438185 (2553, 2554)				264369
1278	11088385 (2555, 2556)	Novel Protein sim. GBank gl 1175473 sp P44555 YAAJ_HAEIN - HYPOTHETICAL PROTEIN H10183		UNCLASSIFIED	264558
1279	21658756 (2557, 2558)	Novel Protein sim. GBank gl 1929513 (U84318) - ATP synthase subunit beta [Moorella thermoacetica]		UNCLASSIFIED	264603
1280	79310959 (2559, 2560)	Novel Protein sim. GBank gl 4938504 emb CAB43882.1 - (AL078465) putative protein [Arabidopsis thaliana]		synthase	264605
				struct	283976

1281	94323988 (2561, 2562)	Novel Protein sim. GBank gll136501 (U39546) - surface protein MCA-32 [Rattus norvegicus]	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	28331825, 28331828, 284766, 83373044
1282	87537895 (2863, 2864)	Novel Protein sim. GBank gll3328190 (AF074266) - proto-oncogene AF4 [Mus musculus]		UNCLASSIFIED	285008
1283	20468305 (2565, 2566)	Novel Protein sim. GBank gll3261721 (emb CAB07057 - (Z92770) hypothetical protein Rv0153c [Mycobacterium tuberculosis]		UNCLASSIFIED	284605
1284	20638325 (2567, 2568)	Novel Protein sim. GBank gll3929022 (AF057696) - LspB [Haemophilus ducreyi]			284604
1285	80427330 (2569, 2570)	Novel Protein sim. GBank gll417154 (sp P33128 HS82_ORYSA - HEAT SHOCK PROTEIN 82	Contains protein domain (PF00183) - eph Hsp90 protein		284766, 284689, 283967
1286	20465254 (2571, 2572)	Novel Protein sim. GBank gll2078004 (emb CAB08451 - (Z95207) gorA [Mycobacterium tuberculosis]	reductase		284605, 284639
1287	80417530 (2573, 2574)			UNCLASSIFIED	285011, 284602, 284766, 284687, 284769, 284689, 18108370, 284638, 18108385, 284583
1288	95338101 (2575, 2576)	Novel Protein sim. GBank gll535351 (sp A042161.1 AF08891 - (AF088918) emilin precursor [Homo sapiens]	Contains protein domain (PF00386) - collagen C1q domain		35996052, 284107, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 265007, 284512, 284910, 285009, 33657402, 284595, 284758, 285011, 285019, 284760, 18108351, 284681, 284764, 284288, 284685, 284766, 284687, 284768, 284769, 285020, 285021, 284534, 284692, 18108370, 284628, 18108374, 35696423, 284555, 284556, 284557, 284558, 18108365, 284564, 284566, 284567, 284488, 18108391
1289	11813647 (2577, 2578)	Novel Protein sim. GBank gll116988 (sp P46023 GPCR_LYMST - G-PROTEIN COUPLED RECEPTOR GRL101 PRECURSOR	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	UNCLASSIFIED	284637
1290	19526027 (2579, 2580)	Novel Protein sim. GBank gll2072674 (emb CAB08305 - (Z95120) rhlE [Mycobacterium tuberculosis]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain		284583
1291	80470286 (2581, 2582)			helicase	285007, 285008, 284769
1292	94723316 (2583, 2584)	Novel Protein sim. GBank gll1835755 (U86338) - zinc finger protein Phg-1 [Mus musculus]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcript factor	284092, 284259, 29331822, 29331824, 284508, 284908, 284909, 284512, 285008, 285009, 284591, 285019, 284369, 284288, 284686, 284768, 284693, 18108374, 284632, 56182323, 284639, 83373044, 22276002, 284482, 284563
1293	80067538 (2585, 2586)	Novel Protein sim. GBank gll2129173 (p F64453 - oxaloacetate decarboxylase (EC 4.1.1.3) alpha subunit - Methanococcus jannaschii		UNCLASSIFIED	285008, 55812038, 284369, 284556
1294	82125908 (2587, 2588)	Novel Protein sim. GBank gll5441778 (emb CAB46803.1 - (AL086811) putative alcohol dehydrogenase (zinc-binding) [Streptomyces coelicolor A3(2)]	biolindp		284602, 284605, 284760, 18108351, 284689, 33857023, 284559
1295	11686851 (2589, 2590)		dehydrogenase		284689

1296	11887904 (2591, 2592)	Novel Protein sim. GBank glj4982191gb/AAD36886.1(AE001805) DNA-directed DNA polymerase I [Thermotoga maritima]	Contains protein domain (PF01367) - 5'3' exonuclease	UNCLASSIFIED	264591, 264639	
1297	79839300 (2593, 2594)	Novel Protein sim. GBank glj1843770 (U97181) - F53F10.1 gene product [Caenorhabditis elegans]		polymerase	264693	
1298	94238508 (2595, 2596)	Novel Protein sim. GBank glj3445181 (AC005498) - R31685 2 [Homo sapiens]		struct	18108348, 265017	
1299	80255378 (2597, 2598)	Novel Protein sim. GBank glj4082973dbjBAA36204.1 (AB017138) alpha subunit of malonate decarboxylase [Pseudomonas putida]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264488, 264908, 264909, 22278002, 264566	
1300	80084867 (2599, 2600)			UNCLASSIFIED	264605	
1301	17939614 (2601, 2602)			UNCLASSIFIED	264806	
1302	95418198 (2603, 2604)				85656542, 265020	
1303	9684121 (2605, 2606)				264908	
1304	78377188 (2607, 2608)			UNCLASSIFIED	264508	
1305	18905899 (2609, 2610)				264566	
1306	13069230 (2611, 2612)	Novel Protein sim. GBank glj3242273jembICAB070171 - (Z92689) hypothetical protein Rv0238c [Mycobacterium tuberculosis]		UNCLASSIFIED	264636	
1307	82201029 (2613, 2614)	Novel Protein sim. GBank glj1502421 (U59433) - 3-ketoacyl acyl carrier protein reductase [Bacillus subtilis]	Contains protein domain (PF00516) - Envelope glycoprotein GP120	UNCLASSIFIED	264907, 264592, 264764	
1308	21426814 (2615, 2616)	Novel Protein sim. GBank glj95618ipirIS16288 - ferric enterobactin transport protein fepC - Escherichia coli		reductase	264555	
1309	78263011 (2617, 2618)	Novel Protein sim. GBank glj5459220jembICAB48893.1 - (AL098837) putative iron-sulfur protein [Streptomyces coelicolor A3(2)]		transport	264906, 18108354	
1310	20466319 (2619, 2620)			UNCLASSIFIED	264605	
1311	87813142 (2621, 2622)				35686288, 29331827, 264908, 265008, 264764, 264766, 264688, 21908787, 21908769, 35695917, 264691, 264693, 22278895, 22278998, 22278999, 264905, 264908, 265011, 265017, 265019, 264687, 21908768, 265020, 265021, 33657023, 22278002, 264564	
1312	88081720 (2623, 2624)	Novel Protein sim. GBank glj4453118ipjAAD210841 - (AF125158) zinc finger DNA binding protein 99 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_ma_bind		
1313	91225458 (2625, 2626)	Novel Protein sim. GBank glj4929733ipjAAD34127.1(AF151890) CGI-132 protein [Homo sapiens]	Contains protein domain (PF00886) - Ribosomal protein S16	ribosomalprot	22278896, 22278999, 264259, 20281099, 29146498, 264508, 264908, 66712502, 60433356, 60433438, 265011, 265017, 264683, 264288, 21906785, 21908787, 29146827, 21906788, 35695917, 265021, 33657023, 33657109, 18108370, 18108377, 35695855, 60432113, 22279000, 264563, 18108390	
1314	56926053 (2627, 2628)				264693	
1315	84357182 (2629, 2630)	Novel Protein sim. GBank glj2589223 (AF026565) - ring finger protein [Mus musculus]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	interleukinrecept	264691	

1318	85361609 (2631, 2632)	Novel Protein sim. GBank glj5689407[dbj BAA82987.1] - (AB028958) KIAA1035 protein [Homo sapiens]		kinase	56182575, 56181886, 20281171, 29331822, 29331824, 60424269, 29331825, 35696052, 52644045, 284591, 60432229, 265018, 285019, 55811150, 56181562, 21906765, 21908787, 21908768, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 35695855, 18108387, 87188518, 60432113, 22279002, 284584
1317	88055187 (2633, 2634)	Novel Protein sim. GBank glj4936757[gb AAD30541.1]AF13491 - (AF134918) semaphorin subclass 4 member G [Mus musculus]		UNCLASSIFIED	264093, 284608, 264909, 264369, 264684
1316	95322893 (2635, 2636)	Novel Protein sim. GBank glj4680204[gb AAD27567.1]AF11417 - (AF114171) hypothetical protein [Sorghum bicolor]		UNCLASSIFIED	18108392, 18108348, 265011, 265017, 18108359, 18108362, 56182323, 18108385, 22279000
1319	84238546 (2637, 2638)				264908, 264909, 265008, 265008, 264592, 265019, 284786, 56181562, 18108388, 264628, 264629, 18108377, 264639
1320	86603587 (2639, 2640)	Novel Protein sim. GBank glj4240183[dbj BAA74870.1] - (AB020854) KIAA0847 protein [Homo sapiens]		UNCLASSIFIED	35696286, 55812038, 265018, 21906788, 265020, 263978, 22279002
1321	86676351 (2641, 2642)	Novel Protein sim. GBank glj4888505[embj CAB43377.1] - (AL050276) hypothetical protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	transcript factor	60432049, 29331828, 264907, 264908, 264909, 264910, 55812038, 264601, 264762, 264764, 264766, 264768, 264769, 264628, 18108374, 264634, 264635, 18108385
1322	87755272 (2643, 2644)	Novel Protein sim. GBank glj5282591[embj CAB45736.1] - (AL080143) hypothetical protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331828, 264908, 265020, 33657023, 264893, 264404
1323	84845931 (2645, 2646)	Novel Protein sim. GBank glj5459516[dbj BAA82407.1] - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	65274572, 56994075, 264259, 29331822, 29331827, 264104, 56182435, 87188474, 18108351, 264288, 21906766, 21906767, 35695917, 265020, 264693, 65274791, 56182323, 18108387
1324	87737614 (2647, 2648)	Novel Protein sim. GBank glj5031717[ref NP_005704.1]pGPBP - goodpasture antigen-binding protein	Contains protein domain (PF01852) - START domain		22278986, 22278998, 29331828, 264905, 264907, 29331830, 264908, 264510, 265008, 264595, 264759, 21906754, 285018, 264288, 264768, 264769, 21908768, 265022, 18108378, 264631, 264632, 264634, 264636, 264638, 264593, 264564, 264565, 264566
1325	94847471 (2649, 2650)	Novel Protein sim. GBank glj3294501 (U64857) - similar to the DPTUKunitz family of inhibitors; most similar to tissue factor pathway inhibitor precursor [Caenorhabditis elegans]	Contains protein domain (PF00090) - Thrombospondin type 1 domain	protease	35696286, 264905, 264906, 264907, 264908, 264909, 264910, 264593, 33657402, 264758, 85688542, 264760, 264768, 264769, 264691, 35698423
1326	87318289 (2651, 2652)	Novel Protein sim. GBank glj1397275 (U61947) - C06G3.8 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264259, 66712502, 284682, 264683, 264635

1327	95322897 (2653, 2654)	Novel Protein sim. GBank gi 278932 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF00279) - Plant lipid transfer protein family	UNCLASSIFIED	18108398, 22278996, 22278997, 22278999, 264091, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264105, 264905, 56182435, 264112, 265008, 265009, 21908754, 285010, 285011, 265017, 265019, 264681, 264448, 264764, 264684, 264288, 264885, 264768, 264688, 21908787, 21908789, 29148629, 265020, 264690, 264891, 264692, 264693, 263967, 33657109, 33657182, 27488282, 33657349, 18108370, 18108374, 55810764, 35895855, 264634, 56182323, 83373044, 87188518, 60432113, 22279000, 22279002, 264563, 264567, 264488, 22278997, 29331828, 264595, 18108351, 264766, 22278002, 264482, 264567
1328	87753493 (2655, 2656)			UNCLASSIFIED	
1329	87755278 (2657, 2658)	Novel Protein sim. GBank gi 4678224 gb AAD26968.1 AC00713 - (AC007135) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	22278996, 29331827, 264684, 264692, 33657109
1330	87727737 (2658, 2660)	Novel Protein sim. GBank gi 437310 (L23504) - nodulin [Medicago truncatula]		UNCLASSIFIED	264259, 29331825, 264512, 265018, 265021, 264555, 264558, 56526488
1331	87376764 (2661, 2662)	Novel Protein sim. GBank gi 4589586 db BAA76815.1 - (AB023188) KIAA0971 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331826, 29331827, 33696052, 29331828, 60170831, 264448, 264686, 21908765, 55811957, 265020, 33657023, 33657109, 263973, 55811578, 35896423, 35895855, 56182323
1332	94845937 (2663, 2664)	Novel Protein sim. GBank gi 5459516 db BAA82407.1 - (AB029821) phosphatidylethanolamine N-methyltransferase [Homo sapiens]		synthase	85274572, 22278996, 56894075, 22278999, 60432049, 264259, 29331822, 29331826, 60432289, 29331827, 33696052, 52644045, 56182435, 264510, 21908754, 87188559, 265018, 265019, 264448, 264288, 264369, 264686, 21908765, 21908786, 21908787, 21908768, 265020, 265021, 52644150, 33657023, 56182323, 18108387, 60432113, 22279002
1333	88098478 (2665, 2666)	Novel Protein sim. GBank gi 5689527 db BAA83047.1 - (AB029018) KIAA1095 protein [Homo sapiens]		UNCLASSIFIED	60432289, 66712502, 264591, 60433356, 60433438, 55812038, 265010, 264639, 56526488 264905
1334	87592388 (2667, 2668)	Novel Protein sim. GBank gi 2662538 (AF036685) - Similar to protein-tyrosine phosphatase [Caenorhabditis elegans]		phosphatase	
1335	87644788 (2669, 2670)	Novel Protein sim. GBank gi 4240285 db BAA74921.1 - (AB020705) KIAA0898 protein [Homo sapiens]	Contains protein domain (PF00643) B-box zinc finger.	UNCLASSIFIED	22278998, 22278999, 29331827, 264509, 264511, 265007, 265008, 265009, 60433438, 21908754, 87168559, 265017, 264288, 21908765, 21908787, 21908789, 265020, 33657109, 27488284, 18108374, 264558, 264638, 264557, 60170394, 264559, 18108385, 264563

1336	87787890 (2671, 2672)	Novel Protein sim. GBank gi465445 sp P33485 VNUA_PRVKA - PROBABLE NUCLEAR ANTIGEN				264509, 264905, 264512, 264764, 264693, 264635, 264637
1337	94312042 (2673, 2674)	Novel Protein sim. GBank gi4589471 dbj BAA83019.1 - (AB028990) KIAA1067 protein [Homo sapiens]	UNCLASSIFIED			5618575, 56994075, 22278998, 22278999, 284092, 284259, 60432289, 29331826, 284908, 284908, 284909, 264112, 265008, 285008, 60433358, 55812038, 33857084, 265011, 265017, 265018, 265019, 264682, 284448, 264883, 284369, 264688, 264689, 21808786, 21808789, 285020, 284691, 27488281, 20281089, 18108379, 55811576, 35895855, 56182323, 60432113, 22279002, 284587
1338	80368114 (2675, 2676)		UNCLASSIFIED			29331822, 265010, 264288, 264689, 18108370, 35895855
1339	80249231 (2677, 2678)	Novel Protein sim. GBank gi1176422 (U43194) - rhophilin [Mus musculus]	UNCLASSIFIED			35898052, 264809, 264688, 264556, 264556
1340	88316311 (2679, 2680)					
1341	88101485 (2681, 2682)					284681, 284685, 284886, 284682 284629
1342	80089017 (2683, 2684)	Novel Protein sim. GBank gi45019584 emb CAB44507.1 - (AL035542) dJ994E9.5 (hs6M1-17 (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor like) protein)) [Homo sapiens]	Im7	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
1343	80082862 (2685, 2686)	Novel Protein sim. GBank gi4557543 ref NP_001384.1 pECM2 - extracellular matrix protein 2		Contains protein domain (PF00560) - Leucine Rich Repeat	264910, 264686, 264534	
1344	20562559 (2687, 2688)					263978
1345	91225546 (2689, 2690)	Novel Protein sim. GBank gi12144101 pir I55210 - tricarboxylate carrier - rat (fragment)	glycoprotein		264809, 60170394	
1346	80255717 (2691, 2692)	Novel Protein sim. GBank gi13681052 emb CAA18523 - (AL023843) predicted using GeneFinder: similar to serine/threonine kinase; cDNA EST yk246a12.3 comes from this gene; cDNA EST yk358c10.5 comes from this gene; cDNA EST EMBL:M89047 comes from this gene; cDNA EST yk246a12.5 comes...	kinase	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	22278998, 264907, 264681, 264685, 264689, 265020, 264693, 22279000, 22279002, 284566	
1347	80417393 (2693, 2694)	Novel Protein sim. GBank gi4504379 ref NP_003858.1 pHG38 - orphan G protein- coupled receptor HG38	glycoprotein	Contains protein domain (PF00560) - Leucine Rich Repeat	264808, 264908, 264909, 265008, 264910, 265011, 265017, 264764, 264768, 264767, 264769, 264631, 264634, 264638, 264567, 264488	
1348	87352335 (2695, 2696)	Novel Protein sim. GBank gi13399720 dbj BAA32100 - (AB010998) peptidylarginine deiminase type IV [Rattus norvegicus]	UNCLASSIFIED			264488, 264489, 264508, 264509, 264510, 264511, 264512, 264591, 284592, 264601, 264684, 264685, 264769, 264532, 264534, 264555, 264556, 264557, 264558, 22279002, 264488

1349	91225548 (2697, 2698)	Novel Protein sim. GBank gij2144101 pir 55210 - l-tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	52846842, 35696266, 22278996, 22278998, 22278999, 264259, 29331822, 29331824, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265008, 264512, 264910, 60170831, 264581, 60433438, 264757, 21908754, 265017, 265018, 264605, 264760, 264762, 264288, 264766, 264689, 21908765, 21908766, 21908767, 21908768, 55811957, 35695917, 265020, 264534, 264691, 264692, 33657023, 264693, 33657349, 18108374, 18108376, 35696423, 60170394, 22278900, 22278902, 264563, 264564
1350	87093136 (2699, 2700)			UNCLASSIFIED	52846842, 264259, 29331825, 264908, 264511, 264804, 264288, 21908769, 265020, 33657182, 33657349, 18108374, 35695855, 264555, 264558, 18108385, 22278902, 264498
1351	87381327 (2701, 2702)	Novel Protein sim. GBank gij4887239 gb AAD32246.1 - (AF084584) BAW protein [Fugu rubripes]		UNCLASSIFIED	264906, 264907, 264638
1352	80076386 (2703, 2704)			UNCLASSIFIED	264693, 263981
1353	95345417 (2705, 2706)	Novel Protein sim. GBank gij2144101 pir 55210 - l-tricarboxylate carrier - rat (fragment)		UNCLASSIFIED	35698286, 60424269, 264905, 264509, 264906, 264907, 264908, 264909, 264511, 264512, 264910, 264758, 264598, 55811386, 265011, 264605, 55811150, 264762, 264764, 264766, 52644229, 56181562, 35695917, 265022, 33657023, 264693, 35695763, 60431528, 264629, 263978, 35696423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108385, 264563, 264584, 264586
1354	95350845 (2707, 2708)	Novel Protein sim. GBank gij4889108 gb AAD27763.1 AF07703 - (AF077030) hypothesized 43.2 kDa protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278998, 23331826, 264906, 265008, 33657402, 21908754, 265011, 87186559, 264684, 264389, 264769, 264689, 21908765, 21908768, 52844150, 33657023, 264692, 264693, 18108374, 83373044, 87186518, 22278900
1355	88260186 (2709, 2710)	Novel Protein sim. GBank gij1489199 db BAA09487 - (O50928) The KIAA0138 gene product is novel. [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	22278996, 22278997, 264259, 66714117, 264511, 21908754, 265010, 264769, 264689, 21908765, 21908768, 21908769, 264532, 27486262, 264629, 264636, 264558, 264638, 264639, 264482, 264484

1356	95313981 (2711, 2712)	Novel Protein sim. GBank gll113865 (U0342) - ninein [Mus musculus]			18108397, 22278985, 22278986, 22278988, 264094, 29331828, 264905, 265006, 265007, 265008, 265010, 265017, 265018, 265019, 264784, 18108354, 264689, 21906785, 265022, 18108384, 35698423, 83373044, 18108387
1357	88260268 (2713, 2714)	Novel Protein sim. GBank gll897993[emb]CAA90330] - (Z50026) phosphatidylcholine transfer protein [Bos taurus]	Contains protein domain (PF01852) - START domain		264256, 29331822, 29331825, 264510, 87168559, 265018, 264448, 264288, 21906785, 21906786, 21906788, 265021, 264693, 18108376
1358	38718455 (2715, 2716)	Novel Protein sim. GBank gll558219 (L36831) - transcription regulator [Mus musculus]			264757
1359	87771643 (2717, 2718)			UNCLASSIFIED	264907, 264909, 264510, 264511, 264512, 18108351, 264764, 264534, 33657023, 18108374, 264634, 264635, 264638, 264639, 18108385, 264488, 264567
1360	87738272 (2719, 2720)	Novel Protein sim. GBank gll2598282[emb]CAA75612] - (Y15417) acetate-CoA ligase [Coprinus chereus]		synthase	60432288, 264605
1361	87593527 (2721, 2722)	Novel Protein sim. GBank gll5689443[db]BAA83005.1] - (AB028876) KIAA1053 protein [Homo sapiens]	Contains protein domain (PF00536) - SAM domain (Sterile alpha motif)	UNCLASSIFIED	35698286, 22278987, 22278989, 264259, 29331826, 264508, 264509, 264905, 264907, 264908, 265007, 265009, 33109954, 21906754, 87168474, 265011, 264761, 264683, 264288, 264768, 264769, 264689, 21906788, 265020, 265021, 33657023, 55811578, 35698423, 264634, 60432113, 22279002, 264482, 264486
1362	95287981 (2723, 2724)	Novel Protein sim. GBank gll5689411[db]BAA82988.1] - (AB028960) KIAA1037 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	- eph	56182575, 56181886, 60432049, 264259, 29331822, 56182181, 29331827, 35698032, 29331828, 264905, 264908, 264909, 264955, 55812038, 85658542, 55811150, 264681, 264288, 264389, 56181562, 60431528, 55810764, 35698423, 60431850, 264558
1363	85758476 (2725, 2726)	Novel Protein sim. GBank gll130494 (U35776) - ADP-ribosylation factor 1-directed GTPase activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	264488, 29331826, 264907, 264687, 264689, 264693
1364	88179488 (2727, 2728)				
1365	83003108 (2728, 2730)	Novel Protein sim. GBank gll4568562[db]BAA76803.1] - (AB023178) KIAA0959 protein [Homo sapiens]		oncogene	60432289, 60433356, 60433438, 87168559, 264603, 18108351, 21908786, 35698423, 60432113
1366	87003262 (2731, 2732)	Novel Protein sim. GBank gll1084944[db]S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins	- transport	264766

1367	87721210 (2733, 2734)	Novel Protein sim. GBank gl 488408 emb CAB43240.1 - (AL050019) hypothetical protein (Homo sapiens)	Contains protein domain (PF01342) - SAND domain	UNCLASSIFIED	264488, 52646942, 52846365, 22278995, 56994075, 35698286, 22278996, 22278998, 22278999, 264259, 29331824, 66714117, 29331825, 60432289, 35698052, 264905, 264907, 264908, 264909, 264510, 265006, 265007, 264512, 264910, 265008, 60170831, 33657402, 55812038, 21908754, 265011, 67168559, 265017, 265019, 18108351, 264448, 264682, 264683, 264288, 264389, 264686, 264767, 264688, 21908765, 21908768, 21908769, 55811957, 265020, 265021, 265022, 264534, 60170815, 264690, 264691, 18108362, 33657023, 33657109, 33657349, 264628, 18108370, 18108374, 18108376, 55811576, 35698423, 35695855, 264635, 264555, 264637, 264556, 52644332, 60170394, 264558, 18108381, 18108385, 56526486, 22279000, 264563, 264567
1368	94320078 (2735, 2736)	Novel Protein sim. GBank gl 484561 sp P35289 RB15_RAT - RAS-RELATED PROTEIN RAB-15	Contains protein domain (PF00071) - Ras family	oncogene	264259, 29331822, 29331826, 60432289, 29331827, 35698052, 264508, 264905, 264906, 264908, 264909, 264510, 265007, 264910, 60433438, 264758, 85658542, 87188559, 264600, 264601, 264760, 264764, 264765, 264788, 52644229, 264689, 35695917, 265020, 265021, 264631, 264632, 264634, 264637, 52644332, 264558, 264639, 83373044, 264563, 264566, 264486, 264567, 265008, 60432228, 60433356, 33657084, 21908764, 21908768, 264555, 264638, 264559, 264567
1369	86634033 (2737, 2738)	Novel Protein sim. GBank gl 2062702 (U90550) - butyrophilin (Homo sapiens)		UNCLASSIFIED	
1370	95316810 (2739, 2740)	Novel Protein sim. GBank gl 5031823 ref NP_005823.1 pKCNM - potassium large conductance calcium-activated channel, subfamily M, beta member 2		potassium_channel	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 35698052, 264508, 264509, 264905, 264908, 264907, 264808, 264809, 264510, 264511, 264512, 264758, 265011, 265019, 264764, 264766, 264769, 21908767, 35695917, 18108362, 35698423, 264632, 264635, 264638, 264555, 264636, 264556, 264639, 18108385, 65274727, 264404, 264563, 264568, 264486
1371	95336512 (2741, 2742)	Novel Protein sim. GBank gl 5032203 ref NP_005714.1 pTSPA - tetraspan 5	Contains protein domain (PF00335) - 4 transmembrane segments integral membrane proteins	glycoprotein	22278996, 264259, 29331822, 29331824, 29331826, 29331827, 264905, 264509, 29331830, 66712502, 265008, 265009, 264758, 33657084, 85658542, 265010, 265018, 265019, 264762, 264448, 35695917, 33657109, 33657162, 33657349, 35698955, 264558, 22279002, 264563

1372	80248517 (2743, 2744)	Novel Protein sim. GBank gll840708[dbj BA093334] - (D50885) trans-aldolase [Trypanosoma cruzi]		collagen	263978	264769, 21908765, 21908767, 22278989, 264691, 264910, 55812038, 265010, 264681, 264684
1373	80469421 (2745, 2746)			UNCLASSIFIED		264684
1374	95087038 (2747, 2748)	Novel Protein sim. GBank gll111878[pir JC1241] - beta-interferon-induced protein - rat		interferon		264907, 264510, 265007, 264512, 265008, 60432229, 264689, 85274781, 264555, 264556, 264557, 83373044, 60432113
1375	94238942 (2749, 2750)	Novel Protein sim. GBank gll594917[gb AAD03500.2] - (AF051155) G beta-like protein GBL [Rattus norvegicus]	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat			52644507, 52645156, 52646842, 52646365, 56182575, 56181686, 22278986, 56994075, 35698288, 22278987, 22278988, 22278989, 264259, 29331822, 52645080, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35698052, 33658970, 264905, 264909, 264908, 264907, 264908, 29331830, 265009, 33657402, 60433356, 52646317, 33109854, 33657084, 52644298, 87168474, 87168559, 264600, 265017, 265018, 265019, 55811150, 18108351, 264448, 264764, 264288, 264369, 264768, 52644228, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 52644150, 33657023, 264693, 85274620, 52645129, 33657109, 27488261, 33657349, 27488265, 35695783, 18108378, 55810784, 35698423, 35695855, 264630, 264631, 264634, 264636, 264638, 18108385, 87168518, 60432113, 22279000, 22279002, 264583, 264584, 264586, 264587, 264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35698032, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526486, 265010, 265011, 264600, 264583, 264762, 264584, 264585, 264764, 264486, 264768
1376	87399050 (2751, 2752)	Novel Protein sim. GBank gll138350[sp P28868 VGLX_HSVEB - GLYCOPROTEIN X PRECURSOR		UNCLASSIFIED		22279002, 264583, 264584, 264586, 264587, 264768, 264769, 35695917, 22278997, 264691, 264259, 29331822, 264693, 35698032, 264508, 264509, 264905, 264906, 264628, 264908, 264629, 18108372, 264809, 264510, 264511, 264512, 265008, 264630, 264631, 264910, 264632, 264634, 264635, 264636, 264591, 264592, 264637, 264638, 264558, 264639, 33657402, 264595, 18108385, 56526486, 265010, 265011, 264600, 264583, 264762, 264584, 264585, 264764, 264486, 264768
1377	86964242 (2753, 2754)	Novel Protein sim. GBank gll1663648 (U75321) - chromaffin granule ATPase II homolog [Mus musculus]	Contains protein domain (PF00122) - E1-E2 ATPase	ATPase-associated		29331824, 264591, 265019, 264686, 264768, 55811957, 264693, 22278002

1376	87595071 (2755, 2756)	Novel Protein sim. GBank gij4107015[db][BAA36283] - (AB001772) PEM-5 [Clona savigny]			22278994, 22278998, 264093, 264094, 264259, 29331824, 29331827, 265009, 265018, 265019, 18108351, 264389, 264288, 28148827, 55811957, 264891, 18108366, 33657109, 18108368, 264635, 263981, 18108385
1379	85679344 (2757, 2758)	Novel Protein sim. GBank gij3252872 (AF035620) - BRCA1-associated protein 2 [Homo sapiens]			265020
1380	87627962 (2759, 2760)	Novel Protein sim. GBank gij4837737[gb]/AAD30682.1 - (AF086834) germ cell specific Y-box binding protein [Homo sapiens]	nucL_rept		264510, 264512, 265009, 264288, 264564
1381	88178656 (2761, 2762)	Novel Protein sim. GBank gij4731580[gb]/AAD28508.1[AF12538 - (AF125384) L82A [Drosophila melanogaster]	UNCLASSIFIED		87168559, 265017, 264628, 22279002
1382	84847576 (2763, 2764)		UNCLASSIFIED	Contains protein domain (PF00583) - Acetyltransferase (GNAT) family	22278994, 22278997, 22278999, 29331822, 29331824, 29331826, 265007, 60432229, 60433396, 85858542, 265017, 265018, 264685, 264768, 21906766, 35695917, 33657023, 27486281, 27486282, 35695763, 35695855, 87168518, 22279002
1383	87860598 (2765, 2766)		UNCLASSIFIED		18108396, 264692
1384	86915895 (2767, 2768)		UNCLASSIFIED		264488, 264508, 264509, 264905, 264908, 264908, 264909, 264511, 264512, 264910, 284760, 18108351, 284766, 264769, 35695855, 264630, 264638, 264555, 264638, 264483, 264584, 264486
1385	86378788 (2769, 2770)	Novel Protein sim. GBank gij2384732 (AF015911) - NAC-1 protein [Rattus norvegicus]	UNCLASSIFIED		35696052, 55811388, 264688, 21906765, 265020, 33657023, 18108385
1386	91013049 (2771, 2772)	Novel Protein sim. GBank gij2384910 (AF022882) - contains similarity to the A-type potassium current class of channel proteins [Caenorhabditis elegans]	Inf		60432288, 29331828, 264906, 264907, 56182435, 265011, 264681, 60170615, 33657023, 83373044, 264568
1387	87797958 (2773, 2774)	Novel Protein sim. GBank gij4160304[emb]/CAA10600 - (AJ132192) HS1 binding protein 3 [Mus musculus]	UNCLASSIFIED		264591
1388	95101652 (2775, 2776)	Novel Protein sim. GBank gij4895184[gb]/AAD32753.1[AC00723 - (AC007231) putative disease resistance protein [Arabidopsis thaliana]	glycoprotein		65274572, 22278999, 264259, 29331826, 29331827, 35696052, 264509, 264907, 264908, 264909, 265008, 265008, 60170831, 33657402, 60433438, 264596, 21906754, 87168559, 264600, 265017, 264683, 18108354, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 264692, 33657023, 33657109, 35695855, 264558, 60170394, 83373044, 22279000

1388	91256016 (2777, 2778)	Novel Protein sim. GBank gij5689387[dbj BAA82977.1] - (AB028948) KIAA1025 protein [Homo sapiens]	Contains protein domain (PF00841) - Zn-finger in Ran binding protein and others.	UNCLASSIFIED	65274572, 22278899, 264259, 29331822, 29331824, 29331825, 60432289, 29331828, 29148499, 264908, 68712502, 55812038, 265017, 265018, 265019, 18108351, 264369, 21908765, 21908768, 21908767, 21908769, 265020, 265021, 264692, 33657023, 33657348, 18108370, 18108374, 55811576, 264555, 264556, 264557, 60170394, 83373044, 22279000, 264563, 264564
1389	94111916 (2779, 2780)	Novel Protein sim. GBank gij3702295 (AC005783) - R33063_1 [Homo sapiens]	peptidase		52645156, 52646365, 264259, 52645080, 29331825, 29331826, 264908, 52644045, 265009, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264760, 264682, 264288, 264686, 264687, 56181562, 52644228, 21908765, 21908769, 35695917, 265020, 265021, 60170615, 52644150, 33657023, 27486281, 27486284, 65274791, 264631, 264555, 52644332, 87168518, 22279000, 264567
1391	91227345 (2781, 2782)	Novel Protein sim. GBank gij1346910[sp P28650]PUA1_MOUSE - ADENYLOSUCCINATE SYNTHETASE, MUSCLE ISOZYME (IMP-ASPARTATE LIGASE)	Contains protein domain (PF00709) - Adenylosuccinate synthetase		29331826, 29331828, 29331830, 264448, 264288, 33657023, 18108365, 264555, 264556, 83373044
1392	94311097 (2783, 2784)	Novel Protein sim. GBank gij726286 (U22394) - mSin3A [Mus musculus]			52646842, 65274572, 22278894, 22278895, 35696286, 56994075, 22278897, 22278898, 22278899, 60432049, 264259, 52645080, 29331822, 29331824, 60432289, 29331826, 29331827, 35696052, 29331828, 33656870, 264907, 52644045, 265006, 265007, 265008, 60431735, 60433356, 52646317, 55811386, 52644296, 265010, 87168559, 265017, 264604, 265018, 265019, 264448, 264288, 264369, 264766, 21906784, 21906767, 35695917, 265020, 265021, 33657109, 52645129, 27486281, 27486282, 27486285, 33657348, 35695763, 18108370, 18108374, 18108376, 55811576, 35696423, 35695855, 264636, 52644332, 18108382, 18108385, 87168518, 60432113, 22279000, 264484, 264566, 18108381
1393	80408472 (2785, 2786)		Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	264763, 264631
1394	15028819 (2787, 2788)			UNCLASSIFIED	264629
1395	95361471 (2789, 2790)	Novel Protein sim. GBank gij2274845[dbj BAA21534] - (D88461) N-WASP [Rattus rattus]		UNCLASSIFIED	265009, 18108361

1386	95363253 (2791, 2792)	Novel Protein sim. GBank gi 2135604 pir 54810 - pHLEIF1 - human			22278997, 22278998, 264259, 29331825, 60432289, 29331828, 29148498, 29148499, 284907, 284908, 29331830, 284909, 265006, 285007, 265008, 265009, 60433356, 265010, 284602, 265017, 285018, 285019, 18108354, 52944229, 18108358, 21908767, 29148627, 21908768, 21908769, 29148629, 29148784, 285021, 285022, 18108368, 18108374, 58182323, 18108385, 284563, 284567, 35898286, 284907, 66712502, 284510, 35895917, 284692, 264693, 35898423
1397	87631317 (2793, 2794)			UNCLASSIFIED	
1398	91233667 (2795, 2796)	Novel Protein sim. GBank gi 5420389 emb CAB46880.1 - (AJ243460) proteophosphoglycan [Leishmania major]			284259, 29331822, 29331824, 29331825, 29331827, 35898052, 33656970, 87168474, 285018, 265019, 284682, 284768, 21908767, 265020, 33857023, 27486261, 55811576, 264632, 284639, 83373044, 87168518, 22279002
1399	87631078 (2797, 2798)	Novel Protein sim. GBank gi 2498887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III chicken		UNCLASSIFIED	284768, 18108370, 264555, 264557
1400	95418084 (2799, 2800)	Novel Protein sim. GBank gi 283920 pir S27839 - tensin - chicken	Contains protein domain (PF00017) - Src homology domain 2	UNCLASSIFIED	58182575, 22278994, 22278997, 284259, 29331822, 29331825, 29331826, 29331827, 29331828, 284908, 56182435, 264112, 265009, 265011, 265017, 285018, 265019, 284760, 264762, 264765, 264288, 264685, 264687, 56181582, 264769, 21908768, 21908767, 55811957, 264691, 264692, 264628, 264629, 55811578, 264634, 264555, 264637, 264557, 264638, 18108381, 264558, 18108384, 60432113, 22279000
1401	91226378 (2801, 2802)	Novel Protein sim. GBank gi 3256185 emb CAA15485 - (AL008635) dJ510H18.1 [Homo sapiens]	Contains protein domain (PF00790) - VHS domain	UNCLASSIFIED	65274572, 60432289, 284909, 264758, 264768, 21908769, 22279002
1402	95361475 (2803, 2804)	Novel Protein sim. GBank gi 1515427 (U57523) - nei homolog [Homo sapiens]	Contains protein domain (PF00008) - Igf EGF-like domain		264905, 264907, 264908, 284909, 284112, 284693, 33857109, 284634
1403	94147933 (2805, 2806)	Novel Protein sim. GBank gi 5262615 emb CAB45747.1 - (AL080158) hypothetical protein [Homo sapiens]			65274572, 66712502, 265017, 264448, 264288, 21908765, 21908769, 264693, 55811576, 65274791, 60432113
1404	90835393 (2807, 2808)			UNCLASSIFIED	85274572, 22278998, 29331822, 29331828, 66712502, 285008, 60433436, 265017, 284693, 18108385

1405	95095068 (2809, 2810)	Novel Protein sim. GBank gij1854065[emb]CAA58371] - (X83413) U88 [Human herpesvirus 8]			264488, 56994075, 35696288, 29331822, 29331824, 29331826, 29331828, 35696052, 264508, 264908, 264907, 264908, 264510, 264511, 264910, 33857402, 264594, 264758, 264600, 264604, 264762, 18108351, 264764, 33857023, 33857109, 264628, 264634, 83373044, 22279002, 264563, 264482, 264488, 264567, 264907, 264605
1406	87612369 (2811, 2812)	Novel Protein sim. GBank gij1624076[gb]AAC98425.1] - (U42580) contains Pro-rich Px motifs: SPKPP (20X), PEPPA (9X), similar to soybean pro-rich cell wall protein, corresponds to Swiss-Prot Accession Number P13953 [Paramedum bursaria Chlorella virus 1]	collagen		
1407	84129872 (2813, 2814)	Novel Protein sim. GBank gij2827886 (AF015037) - endooligopeptidase A related protein; EOPA related protein [Oryctolagus cuniculus]	UNCLASSIFIED		35696288, 22278999, 264094, 264259, 66714117, 29331826, 29331827, 29331828, 26146498, 264107, 264908, 265008, 265008, 264910, 60433438, 265011, 265017, 18108351, 264448, 264288, 264886, 21908785, 21908789, 264692, 33857109, 18108370, 264628, 263972, 18108374, 35696423, 55811578, 264631, 264557, 264558, 83373044, 18108385, 87168518, 60432113, 22279002
1408	95381477 (2815, 2816)	Novel Protein sim. GBank gij2564653 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - oncogene EGF-like domain		264488, 264489, 35696286, 264109, 264508, 264905, 264509, 264908, 264907, 264908, 264909, 265008, 265009, 264910, 33657402, 264757, 264758, 265011, 264601, 265017, 264760, 264762, 264683, 264685, 264768, 264887, 264689, 21908787, 265021, 264690, 264691, 33857023, 264692, 264693, 33857109, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 56182323, 264639, 264563, 264564, 264565, 264566, 264567, 264693
1408	66644385 (2817, 2818)	Novel Protein sim. GBank gij2662165[db]BAA23714] - (AB007902) H-0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]			
1410	86612587 (2819, 2820)	Novel Protein sim. GBank gij2463780[sp]Q80994[ACR3_MOUSE - 30 KD ADIPOCYTE COMPLEMENT-RELATED PROTEIN PRECURSOR (ACRP30) (ADIPOCYTE SPECIFIC PROTEIN ADIPOQ)]	Contains protein domain (PF00366) - complement C1q domain		29331826, 264112, 264512, 265008, 265010, 264601, 264686, 264769, 21906787, 263974, 264631, 264566

1411	87818641 (2821, 2822)	Novel Protein sim. GBank gi 3123155 sp P91343 YM3M_CAEEL - HYPOTHETICAL 49.0 KD TRP-ASP REPEATS CONTAINING PROTEIN F55F8.5 IN CHROMOSOME 1	Contains protein domain (PF00400) - WD domain, G-beta repeat	Kinase receptor	22278995, 22278997, 22278999, 28331822, 60432289, 28331828, 284907, 285017, 285019, 284682, 21906787, 21906768, 21906769, 285020, 284690, 284691, 33657023, 33657109, 27486284, 284628, 283972, 284634, 284558, 18108385 284757
1412	84390919 (2823, 2824)			UNCLASSIFIED	
1413	95418558 (2825, 2826)	Novel Protein sim. GBank gi 3879121 emb CAA94370 - (270310) predicted using GeneFinder. Similarity to Mouse ankyrin (PIR Acc. No. S37771); cDNA EST EMBL: T01823 comes from this gene; cDNA EST EMBL: D32335 comes from this gene; cDNA EST EMBL: D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	homeobox	56994075, 28331822, 35686052, 28331828, 28331830, 284909, 52644045, 284510, 52644298, 85658542, 87168474, 285017, 285018, 284681, 284687, 21906768, 35895917, 285020, 52644150, 284692, 283987, 27486264, 35695763, 284639, 18108387, 284566 284682, 284683, 285022, 284636
1414	94675860 (2827, 2828)	Novel Protein sim. GBank gi 3252981 (AF068921) - Ras- binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	
1415	94326948 (2829, 2830)	Novel Protein sim. GBank gi 1871187 (U90439) - unknown protein [Arabidopsis thaliana]			52646365, 58182575, 22278994, 22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 284259, 28331822, 28331824, 28331825, 28331826, 28331827, 28331828, 29146498, 66712502, 28331830, 52644045, 284113, 284511, 33657402, 284757, 21906754, 55811388, 265017, 265018, 265019, 264761, 284683, 284369, 284288, 284686, 284689, 21906768, 21806767, 29148627, 21906769, 55811857, 265020, 285021, 284690, 33657023, 65274620, 52645129, 27486262, 27486284, 60431528, 284629, 35695855, 58182323, 284559, 60432113, 284404, 22278002, 284482

1416	84325977 (2831, 2832)	Novel Protein sim. GBank gi15106557gb AAD39749.1 AF123052 MLL septin-like fusion protein [Homo sapiens]	Contains protein domain (PF00735) - struct Cell division protein	18108392, 18108394, 18108397, 18108398, 22278995, 22278998, 35686286, 22278997, 22278998, 22278999, 29331822, 35696052, 29331828, 29146498, 284905, 264907, 284908, 284828, 264909, 264113, 265006, 265007, 265008, 265009, 60170831, 264595, 18108348, 21908754, 87168474, 265010, 265011, 87188599, 265017, 265018, 265019, 264762, 18108351, 264681, 264763, 264882, 264683, 264766, 52644229, 264686, 264689, 21908765, 21908766, 21908767, 29148827, 21908768, 55811957, 29148829, 265020, 52644150, 18108381, 33657023, 18108382, 18108368, 264828, 18108370, 264829, 18108374, 18108378, 55811576, 65274791, 264634, 264638, 56182323, 18108381, 60170394, 18108385, 56526486, 87168518, 22278900 264107, 264448
1417	87826663 (2833, 2834)	Novel Protein sim. GBank gi14958935 gb BAA78095.1 - (AB027570) suppressor of potassium transport defect 3 [Rattus norvegicus]	ATPase_associated	
1418	87594276 (2835, 2836)		UNCLASSIFIED	264258, 264808, 265010, 52644229, 21908784, 21908768, 264690, 264639, 18108388
1419	87757188 (2837, 2838)	Novel Protein sim. GBank gi12072294 (U95097) - mitotic phosphoprotein 43 [Xenopus laevis]	struct	264259, 60432289, 265006, 87168474, 264288
1420	87288628 (2838, 2840)	Novel Protein sim. GBank gi15174421 ref NP_008023.1 pCPNE - copine VI (neuronal) (Z69635) Similarity to Yeast uridine kinase (SW URK1_YEAST); cDNA EST EMBL:Z14695 comes from this gene; cDNA EST CEMSE17F comes from this gene; cDNA EST EMBL:D67355 comes from this gene; cDNA EST yk209h1.5 comes from this gen...	ATPase_associated	29331824, 265007, 264563
1421	94746986 (2841, 2842)		kinase	18108358, 18108398, 18108397, 21908766, 18108398, 21908767, 56182575, 21908768, 21908769, 56181686, 55811957, 35695917, 35696286, 22278996, 22278997, 22278998, 22278999, 265021, 265022, 60170615, 264259, 33657023, 29331822, 56182181, 29331824, 66714117, 29331825, 33657109, 29331826, 27488261, 29331828, 35696052, 33657349, 264905, 264509, 20281149, 18108370, 264907, 60431528, 66712502, 263972, 55811576, 35696423, 35695855, 264512, 265007, 60431850, 60432229, 80431735, 56182323, 264558, 60170394, 83373044, 55812038, 264758, 18108385, 21908754, 55811386, 87168518, 87168559, 60432113, 265017, 265018, 265019, 22278900, 55811150, 264563, 264682, 264763, 264448, 264566, 264486, 18108391

1422	85178777 (2843, 2844)	Novel Protein sim. GBank gi 4505939 ref NP_000928.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide A (220kD)		mapolymerase	56994075, 35698286, 87168559, 55611957, 55811576, 264555, 264557, 87168518
1423	86997762 (2845, 2846)			UNCLASSIFIED	264686, 264489, 264692, 264594, 264603, 265018, 264908
1424	95201610 (2847, 2848)	Novel Protein sim. GBank gi 437181 (U02289) - GTPase- activating protein [Caenorhabditis elegans]	Contains protein domain (PF00520) - struct RhoGAP domain		29331822, 29331825, 29331827, 29146498, 264905, 264908, 264908, 264908, 264909, 265007, 264910, 265009, 33109954, 265010, 87168559, 265019, 264768, 264887, 21808765, 21908766, 21908767, 21908768, 29148627, 55811957, 29148629, 265021, 264691, 264692, 56526486, 22278002, 264563
1425	21662314 (2849, 2850)	Novel Protein sim. GBank gi 100798 pir S14959 - proline- rich protein - wheat		UNCLASSIFIED	265007, 264558
1426	94322115 (2851, 2852)	Novel Protein sim. GBank gi 2078441 (U56964) - weak similarity to S. cerevisiae intracellular protein transport protein US1 (SP:P25386) [Caenorhabditis elegans]		UNCLASSIFIED	264488, 60424179, 35698286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331827, 56182435, 264910, 60433356, 60433438, 21908754, 265018, 264288, 21908765, 21908766, 21908767, 21908769, 265020, 265022, 33657109, 18108370, 18108376, 264558, 83373044, 18108385, 56526486, 22279002, 264482
1427	91227510 (2853, 2854)	Novel Protein sim. GBank gi 5616074 gb AAD45816.1 AF08194 - (AF081943) prolactin- derived STE20-like kinase PSK [Homo sapiens]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain		22278994, 56994075, 22278997, 29331828, 29331830, 264828, 265006, 265007, 265008, 265009, 264883, 264288, 18108354, 21908765, 21908768, 29148629, 33657023, 18108374, 35698555, 83373044, 22279002, 264564
1428	94323008 (2855, 2856)	Novel Protein sim. GBank gi 138350 sp P28968 VGLX_HSVB - GLYCOPROTEIN X PRECURSOR		glycoprotein	55181686, 264259, 264807, 265007, 265009, 264595, 265010, 264688, 65274620, 264629, 85274791, 22279002, 264566
1429	87888689 (2857, 2858)			UNCLASSIFIED	264112, 264595, 265017, 265019, 21906765, 263977, 264555
1430	94735021 (2859, 2860)	Novel Protein sim. GBank gi 1181619 gb BAA11565 - (D82364) a variant of TSC-22 [Gallus gallus]			264094, 29331824, 264591, 264593, 265018, 264881, 21906765, 21906767, 85274620, 55811578, 264639, 87168518, 22279002
1431	80429081 (2861, 2862)	Novel Protein sim. GBank gi 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264768, 265020, 264691, 264693, 264638
1432	67463004 (2863, 2864)	Novel Protein sim. GBank gi 414787 (L18966) - pyruvate dehydrogenase phosphatase [Bos taurus]		phosphatase	18108394, 29146498, 265007, 60433438, 264763, 29148629, 263969
1433	87605403 (2865, 2866)	Novel Protein sim. GBank gi 2460318 (AF022147) - uterus- ovary specific putative transmembrane protein [Rattus norvegicus]	Contains protein domain (PF00100) - Zona pellucida-like domain	UNCLASSIFIED	264259, 264510, 264591, 264603, 264565
1434	85713730 (2867, 2868)			UNCLASSIFIED	264882, 264691

1435	94708213 (2868, 2870)	Novel Protein sim. GBank gi 3970850 dbj BAA34789.1 - (AB015330) HRIHFB2007 [Homo sapiens]		Transcript factor	22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331826, 33856970, 264508, 264905, 66712502, 29331830, 264909, 265007, 265008, 264910, 265009, 60433356, 60433438, 264596, 21906754, 265010, 265017, 265018, 265019, 18108351, 264762, 264448, 264288, 264769, 21906767, 21906768, 21906769, 265020, 265021, 265022, 264690, 264691, 33657109, 264628, 18108374, 18108376, 55811576, 264636, 60170394, 56182323, 264559, 83373044, 87168518, 60432113, 22278000, 22279002, 264563, 264482, 264585, 263978, 264557, 264559
1436	86635024 (2871, 2872)	Novel Protein sim. GBank gi 3183977 emb CAA39515 - (X56044) protein H19C [Mus musculus]		UNCLASSIFIED	
1437	87631082 (2873, 2874)	Novel Protein sim. GBank gi 2496887 sp Q09232 YQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C08F5.2 IN CHROMOSOME III		UNCLASSIFIED	22278997, 66714117, 29331826, 264907, 56182435, 265009, 18108351, 264892, 264893
1438	85544280 (2875, 2876)	Novel Protein sim. GBank gi 1905908 (AD000092) - hypothetical human serine-threonine protein kinase R31240.1 [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	264488, 264508, 264906, 264909, 264757, 264600, 264801, 264605, 264788, 264769, 264690, 35696423, 264558, 264563, 264566
1439	91231894 (2877, 2878)	Novel Protein sim. GBank gi 3676299 emb CAA94892 - (Z71180) similar to BPTIKUNITZ inhibitor domain; cDNA EST EMBL:D68293 comes from this gene; cDNA EST yk448h4.5 comes from this gene; cDNA EST yk249a6.5 comes from this gene; cDNA EST yk448h4.3 comes from this gene [Caenorhabditis...]	Contains protein domain (PF00450) - Serine carboxypeptidase	cathepsin	22278994, 18108394, 65274572, 56182575, 22278998, 22278999, 264259, 60432049, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 33856970, 264107, 264508, 264509, 264907, 66712502, 29331830, 56182435, 264511, 265006, 265007, 265009, 60432229, 60433438, 264595, 55812038, 55811386, 265011, 18108354, 264288, 18108355, 264767, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 265022, 33657109, 18108370, 18108374, 55810764, 35695855, 264634, 264636, 56182323, 83373044, 18108387, 87168518, 60432113, 22279000, 264486
1440	87423843 (2879, 2880)	Novel Protein sim. GBank gi 2662165 dbj BAA23714 - (AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo sapiens]		UNCLASSIFIED	264909, 265008, 265010, 265017, 265018, 265019, 18108351, 264369, 265020, 33657023, 33657109, 60431528, 55811576, 264635

1441	95317662 (2881, 2882)	Novel Protein sim. GBank gij4403956[embjCAB11123.2] - (Z88551) predicted using hexExon; MAL3P8.28 (PFC0845c). Hypothetical protein, len: 167 aa; Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe), C.elegans protein ZK287.5 (TR:....	Contains protein domain (PF00846) - helicase F-box domain.	18108392, 264488, 263994, 264489, 56182575, 22278994, 22278995, 56994075, 35698286, 22278997, 22278999, 60432049, 264259, 29331822, 29331824, 56182181, 66714117, 29331826, 29331827, 29331828, 35698052, 29146498, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264910, 264592, 264593, 33657402, 60433438, 264595, 264758, 21906754, 85858542, 87188474, 265010, 87188559, 264800, 264802, 265017, 264604, 265018, 264605, 265019, 264760, 264761, 264762, 264681, 264448, 264764, 264683, 264288, 264766, 264768, 264769, 52644229, 264689, 21908765, 21808766, 21906767, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170815, 52844150, 264691, 264692, 33657023, 65274620, 33857109, 35695763, 264628, 18108370, 264629, 18108374, 55811578, 35696423, 65274791, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 56182323, 264558, 60170394, 264639, 264559, 83373044, 18108385, 18108388, 56526486, 22279000, 22279002, 264563, 264483, 264564, 264566, 264567, 264488, 264906, 265007, 264693, 264558
1442	83387491 (2883, 2884)	Novel Protein sim. GBank gij5103027[dbjBAA78785.1] - (AB023419) mSox7 [Mus musculus]	transcription factor	
1443	87108935 (2885, 2886)	Novel Protein sim. GBank gij4887228[gbjAAD32244.1]AF15075 - (AF150755) microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	52845080, 264691, 264628, 264555
1444	87620478 (2887, 2888)	Novel Protein sim. GBank gij3874447[embjCAB02772] - (Z81039) predicted using GeneFinder; cDNA EST EMBL: T01209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...	UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 29331828, 264288, 35695917, 33657023, 264635, 60170394
1445	94980470 (2889, 2890)	Novel Protein sim. GBank gij289888[embjCAA11022] - (AJ222988) L-peritaxin [Mus musculus]	UNCLASSIFIED	264369
1446	85079268 (2891, 2892)	Novel Protein sim. GBank gij5081610[gbjAAD39494.1]AF13544 - (AF135440) huntington yeast partner C [Mus musculus]	Contains protein domain (PF01646) - FF domain	264369
1447	86945392 (2893, 2894)	Novel Protein sim. GBank gij3880411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	18108398, 35696286, 22278997, 66714117, 29331828, 265009, 264758, 265018, 264288, 21906766, 21906767, 264692, 264634, 264566
1448	94990477 (2895, 2896)	Novel Protein sim. GBank gij3880411 (AC004561) - putative proline-rich protein [Arabidopsis thaliana]	Contains protein domain (PF00439) - Bromodomain	29331827, 264509, 264909, 265008, 264595, 18108397, 18108398, 264566, 264486

1449	87860858 (2887, 2898)				UNCLASSIFIED	66714117, 264908, 264908, 264908, 264591, 264601, 264764, 264632
1450	87458698 (2889, 2900)	Novel Protein sim. GBank gl 1707074 (U80450) - M01E11.2 [Caenorhabditis elegans]			UNCLASSIFIED	35686286, 35696052, 265008, 265009, 60170831, 33109954, 264683, 264689, 35686423, 35695855, 56328488
1451	87787970 (2901, 2902)	Novel Protein sim. GBank gl 4160304(emb CAA10600) - (AJ132192) HS1 binding protein 3 [Mus musculus]			UNCLASSIFIED	29331826, 264683, 264693, 263978, 264630
1452	85892899 (2903, 2904)	Novel Protein sim. GBank gl 2832809(dbl BAA24608.1) - (C89340) dipeptidyl peptidase III [Rattus norvegicus]			peptidase	264681, 33657023, 264629
1453	86130434 (2905, 2906)	Novel Protein sim. GBank gl 728831(isp P39188)ALU1_HUMAN - III ALU SUBFAMILY J WARNING ENTRY III			kinase	264510, 264768
1454	11204688 (2907, 2908)					
1455	87787888 (2909, 2910)				UNCLASSIFIED	264556 29331822, 66714117, 29331825, 264805, 29331830, 265008, 265008, 265009, 285011, 265019, 18108351, 21908768, 33657109, 18108376, 264632, 56182323, 87168518
1456	86320218 (2911, 2912)	Novel Protein sim. GBank gl 726230(isp P41004)CUT3_SCHPO - CHROMOSOME SEGREGATION PROTEIN CUT3			transport	22278995, 22278996, 22278997, 22278998, 22278999, 29331827, 264107, 265017, 21906785, 21908768, 21908767, 21906769, 29148629, 18108370, 22278000
1457	80076800 (2913, 2914)				UNCLASSIFIED	264107, 264566
1458	87800460 (2915, 2916)	Novel Protein sim. GBank gl 2246532 (U93872) - ORF 73. contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]			transport	56182575, 22278999, 60432049, 264259, 29331826, 29331827, 29331828, 264102, 264107, 264110, 285009, 80432229, 265019, 265020, 263972, 263976, 264635, 22279002, 264566
1459	95360820 (2917, 2918)	Novel Protein sim. GBank gl 5524667(gb AAD4333.1)AF15935 - (AF159356) Munc13-4 protein [Rattus norvegicus]		Contains protein domain (PF00168) - C2 domain	kinase	22278997, 264259, 29331824, 29331826, 29331827, 29331828, 265017, 265018, 264760, 264682, 264448, 264288, 264766, 265021, 264692, 33657023, 33657109, 35695855, 264566
1460	95354602 (2919, 2920)				UNCLASSIFIED	29331822, 264591, 55811857, 264691, 264693, 65274620
1461	94741513 (2921, 2922)	Novel Protein sim. GBank gl 1707274 (U80931) - strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases [Caenorhabditis elegans]		Contains protein domain (PF00202) - gaba Aminotransferases class-III pyridoxal phosphate		22278997, 29331822, 35696052, 265009, 264768, 265017, 265018, 265019, 264760, 264369, 264687, 21908765, 21906768, 265022, 33657109, 27488281, 264555, 83373044
1462	87732018 (2923, 2924)				UNCLASSIFIED	264555, 264556
1463	80080605 (2925, 2926)	Novel Protein sim. GBank gl 1770466(emb CAA66912) - (X98259) M-phase phosphoprotein 8 [Homo sapiens]		Contains protein domain (PF00385) - 'chromo' (CHR)romatin Organization MOfficer domain	struct	60432049, 264259, 29146499, 264905, 264907, 264512, 265017, 264763, 264766, 18108370, 18108374, 264636, 18108365, 18108388

1464	87620482 (2927, 2928)	Novel Protein sim. GBank gl 3874447 emb CAB02772 - (ZBL1039) predicted using GeneFinder; cDNA EST EMBL:TO1209 comes from this gene; cDNA EST yk278a11.3 comes from this gene; cDNA EST yk308a9.3 comes from this gene; cDNA EST yk308a9.5 com...		UNCLASSIFIED	264569, 22278995, 22278996, 22278997, 22278998, 29331822, 29331824, 29331825, 3596052, 20281100, 264905, 29331830, 264909, 265007, 33657402, 21908754, 265017, 265018, 264682, 264684, 264369, 264288, 264766, 21906765, 21906766, 21908767, 21906769, 35694917, 264691, 33657023, 264692, 35696423, 35695855, 264630, 264631, 264639, 264595
1465	87425192 (2928, 2930)	Novel Protein sim. GBank gl 4589598 db BAA76821.1 - (AB023194) KIAA0977 protein [Homo sapiens]		glucoamylase	264488, 22278994, 56994075, 60432049, 264258, 56182181, 60432289, 29331827, 52844045, 264511, 265007, 265008, 264596, 55812038, 55811366, 264600, 264602, 265017, 265018, 264604, 265019, 18108351, 18108354, 56181562, 21906769, 265021, 33657023, 33657182, 55811576, 264557, 18108382, 60432113
1466	87608227 (2931, 2932)			UNCLASSIFIED	264512, 265017, 264689, 264558
1467	87614328 (2933, 2934)	Novel Protein sim. GBank gl 2248532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	264683, 264636
1468	95342862 (2935, 2936)	Novel Protein sim. GBank gl 4507241 ref NP_003137.1 pSSRP - structure specific recognition protein 1			22278998, 264758, 265018, 265019, 21908789, 265020, 33657109, 22279002
1469	79236174 (2937, 2938)	Novel Protein sim. GBank gl 1906586 (U81788) - kinesin-73 [Drosophila melanogaster]		struct	18108394, 18108397, 18108398, 35696052, 29146499, 265007, 265008, 265009, 265010, 265011, 18108354, 18108365, 18108388, 18108374, 18108381, 18108382, 18108384, 18108388
1470	94890482 (2939, 2940)	Novel Protein sim. GBank gl 5649170 gb AAD43131.2 AF15909 - (AF159092) syld708613 protein [Homo sapiens]		UNCLASSIFIED	18108394, 18108398, 56182375, 264259, 29331822, 29331824, 29331825, 60432289, 264907, 264909, 265007, 264910, 265009, 264591, 60432229, 60433356, 264595, 60433438, 264758, 33109954, 265010, 265011, 265018, 264760, 264448, 264764, 264288, 264368, 18108357, 264769, 18108358, 21906767, 21906769, 55811957, 265021, 18108361, 264691, 18108362, 18108365, 18108368, 264628, 18108379, 264637, 264557, 18108381, 56182323, 18108382, 83373044, 18108384, 18108388, 87188518, 60432113, 264404, 22279002, 264482, 264587, 264487
1471	87826842 (2941, 2942)	Novel Protein sim. GBank gl 3876146 emb CAB01750 - (Z78542) similar to Mitochondrial carrier proteins; cDNA EST EMBL:TO1651 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	transport	29331822, 29331824, 29331825, 264828, 264603, 264689, 264693, 18108374, 55811576

1472	87756616 (2943, 2944)	Novel Protein sim. GBank gi 4680707 gb AAD27743.1 AF132986 - (AF132988) CGI-34 protein [Homo sapiens]		UNCLASSIFIED	284905, 18108351, 21906765, 264486
1473	87791609 (2945, 2946)	Novel Protein sim. GBank gi 3688780 (AF042180) - testis-specific Y-encoded-like protein [Mus musculus]	Contains protein domain (PF00956) - Nucleosome assembly protein (NAP)	MHC	18108394, 22278995, 56394075, 22278999, 29331822, 29331824, 68714117, 29331825, 29331826, 35696052, 264908, 264807, 56182435, 265007, 264758, 265018, 265019, 264760, 264764, 264288, 264685, 264686, 264788, 21908769, 55811957, 285021, 264691, 264693, 264629, 55811578, 264634, 264636, 56182323, 22279002, 264566, 264486
1474	85800989 (2947, 2948)	Novel Protein sim. GBank gi 2494890 sp Q92176 CORO_BOVIN - CORONIN-LIKE PROTEIN P57	Contains protein domain (PF00400) - struct WD domain, G-beta repeat		264486, 35695917, 35696286, 264692, 33657023, 264693, 33657109, 35696052, 264508, 264905, 264908, 264907, 264629, 264908, 264909, 35696423, 35695855, 264511, 264910, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264639, 264758, 60432113, 264804, 264605, 264565, 264586, 264764, 264488, 264685, 264766, 264681, 264682, 264288, 264566
1475	86871935 (2949, 2950)		Contains protein domain (PF00041) - Fibronectin type III domain	UNCLASSIFIED	
1476	87548855 (2951, 2952)	Novel Protein sim. GBank gi 4757752 ref NP_004684.1 pANGP - angiotensinogen 3	Contains protein domain (PF00147) - Fibrinogen beta and gamma chains, C-terminal globular domain	glycoprotein	60424179, 56181886, 29331824, 60424269, 29331826, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264512, 265007, 265008, 265009, 264910, 33657402, 264595, 264596, 55812038, 265011, 264601, 264762, 18108351, 264288, 264369, 264685, 264766, 264689, 55811957, 264691, 264692, 264693, 18108370, 60431528, 18108374, 35696423, 264634, 264635, 264636, 60431850, 264555, 264638, 264557, 264639, 18108382, 18108388, 60432113, 22279002, 264289, 264107, 264905, 265008, 265010, 265011, 264682, 264288, 265020, 265021, 263974
1477	87774278 (2953, 2954)	Novel Protein sim. GBank gi 2498308 sp Q60870 DPI_MOUSE - POLYPOSIS LOCUS PROTEIN 1 HOMOLOG (T82 PROTEIN HOMOLOG) (GP108)		UNCLASSIFIED	
1478	11754412 (2955, 2956)				264686

1479	91840140 (2857, 2858)	Novel Protein sim. GBank gi 5489741 gb AAD43978.1 AF15286 - (AF152861) chromatin-specific transcription elongation factor FACT 140 kDa subunit [Homo sapiens]		peptidase	56182575, 22278995, 22278996, 22278998, 22278999, 29331822, 29331824, 86714117, 264906, 264907, 56182435, 285006, 80170831, 33657402, 264758, 33108954, 21908754, 265017, 265018, 264448, 264288, 264767, 264687, 52644229, 21906764, 264689, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 264691, 33657023, 33657109, 33657182, 27486281, 27486282, 33657349, 18108370, 60431528, 263978, 55811576, 264556, 264557, 60170394, 87168518, 264404, 22279000, 22279002, 264563, 264482
1480	94312412 (2859, 2860)	Novel Protein sim. GBank gi 3550456 emb CAA06328.1 - (AJ005073) A1ix [Mus musculus]		UNCLASSIFIED	18108394, 65274572, 56182575, 22278995, 35698286, 56994075, 22278998, 22278997, 22278998, 22278999, 264091, 264259, 35696052, 28146499, 264103, 264105, 264108, 264807, 52644045, 264112, 265007, 265008, 265009, 60433356, 80433438, 264588, 33108954, 33657084, 52644256, 87168474, 265010, 87168559, 265017, 265018, 265019, 264448, 264682, 264683, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657109, 33657182, 263972, 35695855, 264557, 263981, 83373044, 18108385, 87168518, 264566, 264089, 264486
1481	87021442 (2861, 2862)	Novel Protein sim. GBank gi 4838807 gb AAD30566.1 AF14878 - (AF148793) PFT27 [Mus musculus]		MHC	265008, 265007, 265010, 18108374
1482	85320442 (2863, 2864)	Novel Protein sim. GBank gi 4585372 gb AAD25403.1 AF12292 - (AF122923) Wnt inhibitory factor-1 [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264908, 264910, 264758
1483	94115503 (2865, 2866)	Novel Protein sim. GBank gi 535428 (U13736) - calmodulin- like protein [Plum salivum]	Contains protein domain (PF00036) - struct EF hand		264259, 29331822, 52645080, 29331825, 29331826, 33656970, 29331830, 265007, 55812038, 33108954, 285017, 264288, 21908768, 21908769, 264636, 18108380, 87168518, 22279000
1484	94131544 (2867, 2868)	Novel Protein sim. GBank gi 1911774 gb J180090 - (S83384) putative Rab5-interacting protein (clone L1-57) [human, HeLa cells, Peptide Parliai, 122 aa] [Homo sapiens]		UNCLASSIFIED	264489, 35696286, 264259, 264107, 264909, 265008, 60433356, 33657402, 60433438, 264288, 21906765, 21906766, 29148827, 33657023, 27486282, 18108374, 35698423, 83373044, 60432113
1485	80184441 (2869, 2870)	Novel Protein sim. GBank gi 5360129 gb AAD2883.1 AF155117 NY-REN 62 antigen [Homo sapiens]	Contains protein domain (PF00225) - struct Kinesin motor domain		264369, 265020, 18108374

1486	94125066 (2971, 2972)	Novel Protein sim. GBank gi 4589516 dbj BAA76780.1 - (AB023153) KIAA0936 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	Kinase	56182575, 22278999, 264806, 264907, 21908754, 87168474, 265017, 265019, 18108351, 264288, 265020, 264566, 21908754, 264486
1487	88452711 (2973, 2974)	Novel Protein sim. GBank gi 5019275 emb CAB4443.1 - (AJ132751) xenobiotic/medium-chain fatty acid:CoA ligase form XL-III [Bos taurus]		synthase	
1488	87732028 (2975, 2976)	Novel Protein sim. GBank gi 5712131 gb AAD47378.1 AF12049 - (AF120499) DEM1 protein [Homo sapiens]	Contains protein domain (PF01443) - Viral (Superfamily 1) RNA helicase	fgf	264686, 264769, 264689, 264692, 264693, 264509, 264906, 264907, 18108370, 264908, 264629, 264909, 264510, 265008, 264512, 265007, 265008, 265009, 264555, 264556, 264557, 264558, 264782, 264564, 264682
1489	95104277 (2977, 2978)	Novel Protein sim. GBank gi 2497303 gb O62786 FPRP - RAT - PROSTAGLANDIN F2-ALPHA RECEPTOR REGULATORY PROTEIN PRECURSOR (PROSTAGLANDIN F2-ALPHA RECEPTOR ASSOCIATED PROTEIN)	Contains protein domain (PF00047) - Immunoglobulin domain	prostaglandin	21908767, 22278999, 265022, 264259, 264693, 29331824, 29331825, 29331826, 29331827, 29331828, 264103, 263972, 66712502, 35896423, 35895855, 265007, 265008, 265009, 83373044, 21906754, 56526486, 265017, 264563, 18108351, 264564, 264566, 264369, 264288
1490	87380127 (2979, 2980)			UNCLASSIFIED	56182575, 264259, 29331822, 29331824, 66714117, 29331827, 29331828, 264508, 264905, 66712502, 265007, 265008, 264594, 33657402, 55812038, 87168474, 265018, 18108351, 264369, 264288, 264769, 264689, 21908767, 21906768, 55811957, 60170619, 33657109, 35895855, 264635, 60170394, 56526486, 22279002, 264563
1491	83594305 (2981, 2982)	Novel Protein sim. GBank gi 295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependent RNA polymerase I and III (Saccharomyces cerevisiae)		UNCLASSIFIED	265007, 264448, 18108372, 264558, 56182323
1492	85805383 (2983, 2984)	Novel Protein sim. GBank gi 1656005 (U71205) - nt [Mus musculus]	Contains protein domain (PF00071) - Ras family	oncogene	22278997, 22278998, 29331822, 264907, 66712502

1493	91677215 (2985, 2988)	Novel Protein sim. GBank gi 5689515 dbj BAAB3041.1 - (AB029012) KIAA1089 protein [Homo sapiens]	UNCLASSIFIED	264488, 52846365, 65274572, 56182575, 22278994, 35696286, 56994075, 22278999, 60432049, 29331824, 29331828, 35696052, 264508, 264905, 264906, 52844045, 264909, 56182435, 265006, 265008, 265009, 60170831, 33657402, 55812038, 265010, 265011, 265017, 265018, 265019, 55811150, 264448, 264882, 264885, 264886, 52844228, 21906765, 21906766, 21906768, 21906769, 265020, 265021, 60170615, 52644150, 33657023, 18108384, 18108385, 33657109, 33657182, 27486261, 27486262, 27486264, 33657349, 27486265, 35695763, 18108370, 264829, 18108374, 52844332, 56182323, 87188518, 22279002, 264564, 264566, 264567
1494	87605265 (2987, 2988)	Novel Protein sim. GBank gi 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	Contains protein domain (PF01352) - Kinase KRAB box	264907, 265009, 264789, 18108370, 55811576, 264639, 264565, 264488
1495	87605267 (2989, 2990)	Novel Protein sim. GBank gi 4568568 dbj BAA76816.1 - (AB023189) KIAA0972 protein [Homo sapiens]	Contains protein domain (PF01352) - Transcription factor KRAB box	22278997, 264259, 264806, 264907, 265008, 264594, 33657084, 265017, 264760, 264448, 33657109, 264630, 264634, 56526486, 264563, 264565, 264566, 264486, 264567
1496	87764322 (2991, 2992)	Novel Protein sim. GBank gi 5420387 emb CA846678.1 - (AJ243458) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	35696286, 264906, 265019, 264693
1497	81695428 (2993, 2994)	Novel Protein sim. GBank gi 3874825 emb CAA92591 - (Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase (SW:KRAA_MOUSE); cDNA EST EMBL:D27610 comes from this gene; cDNA EST EMBL:TO1018 comes from this gene; cDNA EST EMBL:D33258 comes from this gene...	Contains protein domain (PF00069) - Kinase Eukaryotic protein kinase domain	264910, 264758, 265011, 264784, 264288, 264690, 264634, 264635, 56526486
1498	90834838 (2995, 2996)	Novel Protein sim. GBank gi 728836 sp P39193 ALU8_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII	oncogene	264488, 65274572, 29331822, 265017, 265018, 21905765, 29148627, 29148629, 18108374, 264637, 264638, 264567
1499	86451589 (2997, 2998)	Novel Protein sim. GBank gi 2570198 (U54556) - microfilament sheath protein SHP3 [Litomosoides sigmodontis]	glucosylase	263978, 264568
1500	80499388 (2999, 3000)	Novel Protein sim. GBank gi 2078483 (U43200) - anifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	22278999, 264769, 18108379
1501	85795297 (3001, 3002)	Novel Protein sim. GBank gi 2078483 (U43200) - anifreeze glycoprotein precursor [Boreogadus saida]	UNCLASSIFIED	264569
1502	80206141 (3003, 3004)	Novel Protein sim. GBank gi 3900855 (AC004874) - similar to N-acetylgalactosaminyltransferase; similar to Q07537 (PID:gi171989) [Homo sapiens]	transferase Glycosyl transferases	264508, 264112, 264604, 264684, 52644150, 55811576, 264632, 264556, 264638, 56182323, 264563, 264486, 29331822, 265007, 264369

1504	78640051 (3007, 3008)		Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	264693
1505	86102872 (3009, 3010)	Novel Protein sim. GBank gll475375(emb)CAB41970.1] - (AJ132545) protein kinase [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	29331826, 35686052, 264509, 264908, 264907, 264908, 264909, 264511, 264810, 55812038, 264759, 264763, 264764, 264689, 35685917, 265022, 33657109, 18108374, 264631, 264635, 264638, 264568
1506	94143219 (3011, 3012)	Novel Protein sim. GBank gll1304201dbjBAA08170] - (D29786) alternatively spliced product [Rattus norvegicus]	Contains protein domain (PF00018) - SH3 domain	glycoprotein	65274572, 56182575, 56994075, 22278997, 22278998, 22278999, 264091, 264082, 60432049, 264259, 52845080, 29331822, 29331827, 264106, 29331830, 264908, 56182435, 264110, 264511, 264512, 55812038, 21908754, 87168559, 264600, 265017, 265018, 264681, 18108354, 264389, 264687, 264689, 21908765, 29148627, 21906768, 21906769, 29148628, 52644150, 33657023, 18108376, 65274791, 56182323, 264558, 264559, 18108385, 87168518, 60432113, 22279000, 264565
1507	83736250 (3013, 3014)	Novel Protein sim. GBank gll5689513dbjBAA83040.1] - (AB029011) KIAA1088 protein [Homo sapiens]		helicase	264639
1508	11618758 (3015, 3016)	Novel Protein sim. GBank			264593
1509	87318451 (3017, 3018)	gll5031975(ef)NP_005875.1pPAK4 - protein kinase related to S. cerevisiae STE20, effector for Cdc42Hs	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331822, 29331824, 29331828, 264591, 33109954, 264563
1510	95362843 (3019, 3020)	Novel Protein sim. GBank		UNCLASSIFIED	264259, 29331822, 265007, 18108374, 264556
1511	88318073 (3021, 3022)	gll113161(esp)P28614JACOR_ALCEU - ACETOIN CATABOLISM REGULATORY PROTEIN		UNCLASSIFIED	264259, 29331822, 29331824, 29331827, 264509, 264907, 264510, 264511, 265007, 264512, 265008, 87168559, 264288, 265022, 33657023, 35695855, 264637, 264638, 264563
1512	95345380 (3023, 3024)	Novel Protein sim. GBank	Contains protein domain (PF01163) - RIO1/ZK632.3/MJ0444 family		52645156, 18108386, 56994075, 60432289, 265008, 60433356, 60433438, 21908754, 87168474, 87168559, 265018, 264782, 264783, 264887, 21906765, 21906769, 27486262, 35695763, 18108374, 35696423, 264555, 18108385, 18108387, 18108388, 87168518, 264482
1513	87436228 (3025, 3026)	Novel Protein sim. GBank gll1330394 (U58761) - C01F1.6 gene product [Caenorhabditis elegans]			35696052, 264905, 264908, 264907, 264908, 264909, 264910, 264591, 264766, 264689, 264692, 264629, 264636

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1526	95105344 (3051, 3052)	Novel Protein sim. GBank gi 728850 sp P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		glycoprotein	35696286, 56182181, 60431735, 264595, 55812038, 264605, 264683, 21906785, 55811957, 265020, 65274791, 264555, 264556, 264557, 264558, 264559, 83373044
1527	88262512 (3053, 3054)	Novel Protein sim. GBank gi 2792498 (AF041107) - tulip 2 [Rattus norvegicus]			56182575, 264259, 60432049, 29331822, 60432289, 264908, 66712502, 60433438, 87168559, 265017, 264288, 21906786, 21906789, 263977, 55811576, 56182323, 18108381
1528	94130918 (3055, 3056)			UNCLASSIFIED	22278995, 22278997, 264259, 66712502, 264596, 265017, 265019, 264682, 264448, 264683, 264764, 264685, 264686, 21906785, 21906786, 21906787, 21906788, 21906789, 265022, 264683, 83373044, 18108385 264488, 263984, 56182575, 22278995,
1529	94120783 (3057, 3058)	Novel Protein sim. GBank gi 4408663 gb AAD20053 - (AF131826) Unknown [Homo sapiens]		UNCLASSIFIED	35696286, 22278997, 264259, 29331822, 60432289, 29331827, 35698052, 264509, 264906, 264907, 264908, 264909, 52644045, 56182435, 264511, 265009, 264910, 80433356, 60433438, 265017, 265018, 264760, 264448, 264764, 264369, 264288, 264786, 18108357, 264788, 52644229, 21906765, 21906766, 21906767, 21906768, 265021, 265022, 52644150, 33657109, 264629, 35695855, 80432113, 22278002, 264583, 264584, 264486, 264567 264488, 264489, 35696286, 29331825,
1530	95012785 (3059, 3060)	Novel Protein sim. GBank gi 2828710 (AF043642) - malrin cyclophilin [Rattus norvegicus]			35696052, 264508, 264905, 264906, 264907, 264909, 264510, 264511, 264512, 264910, 264592, 264595, 18108351, 264764, 264683, 264684, 264766, 264768, 18108357, 264769, 35695917, 264628, 264629, 18108374, 35695855, 264630, 264631, 264634, 264555, 264636, 264637, 264404, 264563, 264566, 264486
1531	95419351 (3061, 3062)	Novel Protein sim. GBank gi 1905874 (U90878) - carboxyl terminal LIM domain protein [Homo sapiens]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	kinase	56182575, 35696286, 264097, 264259, 29331822, 29331825, 29331826, 29331827, 35696052, 264509, 56182435, 264510, 264511, 265007, 60433356, 55811388, 264681, 264369, 264288, 264766, 264687, 55811957, 35695917, 33657023, 35695763, 55810764, 35696423, 55811576, 263981, 60170394, 56182323, 83373044, 60432113, 264568

1532	85718224 (3063, 3064)	Novel Protein sim. GBank gl 3874716 emb CAA81265 - (Z68494) cDNA EST EMBL:D65271 comes from this gene; cDNA EST EMBL:D64845 comes from this gene; cDNA EST EMBL:D64449 comes from this gene; cDNA EST EMBL:D67438 comes from this gene; cDNA EST EMBL:D68087 comes from this gene; cDN...		UNCLASSIFIED	264889
1533	94239830 (3065, 3068)	Novel Protein sim. GBank gl 1490324 emb CAB01543 - (Z78141) unknown [Mus musculus]	struct		29331824, 29146499, 264907, 264112, 265008, 265011, 265017, 265018, 264762, 18108351, 263987, 20281149, 18108374, 263981, 264568
1534	95343841 (3067, 3068)	Novel Protein sim. GBank gl 81286 pir S22697 - extensin - Volvox carter (fragment)		UNCLASSIFIED	264905, 264907, 264766, 264637
1535	90938732 (3069, 3070)				65274572, 22278997, 264259, 60432049, 29331822, 60432289, 29331827, 29146499, 265008, 265008, 60170831, 60433438, 33109954, 87168559, 265018, 18108357, 21808768, 29148829, 265021, 265022, 18108377, 58182323, 60432113, 22279000, 22278002
1536	87602856 (3071, 3072)	Novel Protein sim. GBank gl 108024 pir B32891 - finger protein 2, placental - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	264886, 18108357, 18108394, 21906767, 21908768, 29148829, 35696286, 265020, 265021, 52844150, 264693, 68714117, 29331825, 29331826, 264508, 264905, 20281149, 264909, 18108374, 35696423, 35895855, 265009, 264634, 264636, 264638, 18108385, 58526486, 265017, 265018, 264563, 264762, 18108351, 264448, 264369, 264766
1537	96354558 (3073, 3074)	Novel Protein sim. GBank gl 3876332 emb CAB02096 - (Z79764) cDNA EST EMBL:T01054 comes from this gene; cDNA EST EMBL:D73600 comes from this gene; cDNA EST yk428f12.5 comes from this gene; cDNA EST yk342f10.5 comes from this gene; cDNA EST yk475c5.5 comes from this gene; cDNA ES...			65274572, 58182575, 60432049, 264259, 29331826, 265008, 265007, 60433356, 60433438, 264601, 18108351, 264448, 264369, 264288, 33657023, 65274620, 33657109, 60432113
1538	85724628 (3075, 3076)	Novel Protein sim. GBank gl 403440 (M81787) - [Gallus domesticus skeletal muscle mRNA, partial cds], gene product [Gallus gallus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	18108394, 18108397, 264909, 265008, 265009, 265010, 18108351, 264638, 18108382, 18108385, 18108388

1539	95337628 (3077, 3078)	Novel Protein sim. GBank gl 321841 emb CAA19575.1 - endonuclease ga mna subunit, len:284aa, similar eg. to YAR008W, YAH8_YEAST, P38707, YAR008W, IRNA splicing endonuclease gamma subunit, (275aa), fastia scores, opt:269, E(1):6.4e-2...		nuclease	22278994, 22278996, 35696286, 56994075, 22278997, 22278998, 22278999, 60432049, 284258, 29331822, 29331824, 60424269, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 33656970, 56182435, 265009, 33657402, 60433356, 60433438, 55812038, 21906754, 87168559, 285017, 265018, 265019, 18108351, 264288, 52644228, 18108359, 21906764, 21906767, 21906768, 35695917, 265020, 265021, 52644150, 33657023, 33657109, 27486261, 18108370, 18108376, 35696423, 55811576, 65274791, 264558, 56182323, 60170394, 83373044, 87168518, 60432113, 22278000, 22279002, 264568
1540	95352858 (3079, 3080)	Novel Protein sim. GBank gl 5052634 gb AAD38647.1 AF14567 - (AF145672) BcDNA.GH12174 [Drosophila melanogaster]		UNCLASSIFIED	264369, 264691, 263978
1541	95317948 (3081, 3082)	Novel Protein sim. GBank gl 5052349 gb AAD38515.1 AF13501 - (AF135016) protein phosphatase 2A 48 kDa regulatory subunit [Homo sapiens]		phosphatase	264488, 264489, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264907, 264908, 264511, 264512, 264910, 264592, 264761, 264762, 264448, 264764, 264288, 264687, 21906769, 35611957, 35695917, 265020, 264691, 33657023, 264692, 33657109, 264628, 18108374, 264632, 264634, 264635, 264639, 18108385, 264583, 264584, 264565, 264566, 264486
1542	90937549 (3083, 3084)	Novel Protein sim. GBank gl 505702 gb AAD41779.1 AF12686 - (AF126867) calpain-like protease [Mus musculus]		cathepsin	18108392, 18108394, 55274572, 29331822, 264508, 265007, 265008, 285009, 265011, 264882, 18108354, 18108355, 52644150, 18108368, 264636, 18108381, 18108382, 264106, 33109954, 265019, 264883, 35695917, 264690, 264692, 33657109
1543	84348768 (3085, 3086)	Novel Protein sim. GBank gl 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		nuclease	
1544	87757295 (3087, 3088)	Novel Protein sim. GBank gl 3493162 (AF084259) - bromodomain-containing protein BP75 [Mus musculus]	Contains protein domain (PF00439) - Bromodomain	nuc. recpt	35696286, 56994075, 22278999, 35696052, 60433356, 60433438, 265011, 264883, 33657109, 35696423, 264631, 87168518, 22279000
1545	85757973 (3089, 3090)	Novel Protein sim. GBank gl 1086591 (U41007) - similar to S. cerevisiae nuclear protein SNF2 (SP-P22082) in a region of gly-arg repeats [Caenorhabditis elegans]		UNCLASSIFIED	264112, 264692, 264693, 55811576
1546	79476589 (3091, 3092)			UNCLASSIFIED	264905, 264686
1547	86995984 (3093, 3094)	Novel Protein sim. GBank gl 2661132 (AF035683) - p21 [Mus musculus]		UNCLASSIFIED	55811386, 265010, 264600, 265017, 265019, 264288, 264768, 265020, 265022, 55811576, 18108380, 264563

1548	94233065 (3085, 3086)	Novel Protein sim. GBank glij3043682[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	29331824, 60431528, 264639, 56182323
1549	95330048 (3097, 3098)	Novel Protein sim. GBank glij5689519[dbj BAA83043.1] - (AB028014) KIAA1091 protein [Homo sapiens]		eph	60424178, 22278995, 35696286, 22278998, 22278999, 264092, 264094, 29331822, 56182181, 29331824, 35696052, 264905, 264908, 264908, 264909, 265006, 264511, 265008, 60431735, 60433356, 21906754, 55811386, 87168559, 265017, 265018, 265019, 55811150, 264682, 264288, 264369, 56181562, 264769, 21906765, 21906788, 21906789, 55811957, 265020, 264691, 33657109, 60431528, 35696423, 35695855, 56526486, 60432113, 22279002, 264563, 264566
1550	95201907 (3099, 3100)	Novel Protein sim. GBank glij544463[sp P35350 GUSB_BOVIN - POSSIBLE GUSTATORY RECEPTOR TYPE B (PPR1 PROTEIN)]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	tm7	65274572, 60432289, 265008, 264910, 265011, 265017, 265018, 264768, 56182323
1551	88077111 (3101, 3102)	Novel Protein sim. GBank glij4758568[ref NP_004798.1 pHS6S - heparan-sulfate 6-sulfotransferase]		UNCLASSIFIED	22278999, 29331822, 264508, 264509, 264906, 264907, 264909, 265007, 264512, 264910, 21906754, 265018, 265019, 264681, 264764, 264766, 264688, 264769, 21906769, 264692, 35695763, 264635, 264555, 264556, 264557, 264638, 264558, 264563
1552	87617114 (3103, 3104)			UNCLASSIFIED	264259, 28331828, 66712502, 264764, 264288, 264688, 33657109, 264556
1553	94725512 (3105, 3106)	Novel Protein sim. GBank glij4589570[dbj BAA76807.1] - (AB023180) KIAA0963 protein [Homo sapiens]	Contains protein domain (PF00304) - Gamma-thionins family	- dehydrogenase	56182575, 35696286, 29148499, 264509, 264907, 264908, 264909, 56182435, 265006, 265008, 265009, 264910, 264757, 264758, 265017, 55811150, 18108351, 264764, 56181562, 35695917, 264693, 33657109, 18108374, 35696423, 65274791, 35695855, 264635, 264555, 56182323, 18108382, 83373044, 22279000
1554	94233088 (3107, 3108)	Novel Protein sim. GBank glij3043682[dbj BAA25510] - (AB011156) KIAA0584 protein [Homo sapiens]	Contains protein domain (PF00446) - Gonadotropin-releasing hormones	- transferase	35696286, 22278997, 264259, 28331822, 29331824, 29331825, 29331828, 265007, 265009, 60432229, 33657402, 55812036, 265011, 265019, 264681, 264369, 264686, 264767, 264768, 21906765, 21906769, 35695917, 264693, 18108370, 60431528, 55811576, 264631, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002

1555	87332970 (3109, 3110)	Novel Protein sim. GBank gl 2257485 dbj BAA21392 - (AB004534) p 015 [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	264259, 29331828, 35696052, 264508, 264905, 264908, 264907, 264908, 52644045, 264909, 264910, 60432229, 60433356, 55812038, 264758, 264759, 33657084, 265011, 87186559, 264601, 265018, 265019, 264763, 264764, 264288, 264766, 264768, 21908765, 35695917, 265022, 264691, 33657023, 35696423, 35695855, 264635, 264555, 264636, 264638, 264639, 18108385, 56528486
1556	91229288 (3111, 3112)			UNCLASSIFIED	83373044, 264758, 265022, 264600, 35696052, 264630, 35696423, 265018, 264632, 264682, 29331822, 265020, 265011
1557	87840809 (3113, 3114)	Novel Protein sim. GBank gl 3329611 (AF078783) - contains similarity to C3HC4-type zinc fingers (Pfam; z C3HC4.hmm, score: 34.08; most similar to drosophila goliath protein (SV: Q06003) [Caenorhabditis elegans])	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	60432289, 264509, 264906, 264907, 264908, 264909, 264910, 264758, 55811386, 264761, 264762, 264766, 264769, 264690, 263978, 264634, 264635, 264639, 264584, 264486
1558	84840376 (3115, 3116)	Novel Protein sim. GBank gl 5360105 gb AAD42871.1 AF155105 - (AF155105) putative zinc finger protein NY-REN-34 antigen [Homo sapiens]			22278984, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331824, 29331825, 29331826, 29331827, 264908, 264909, 60433356, 21908754, 265017, 265018, 264448, 21908787, 265021, 265022, 33657023, 33657109, 18108370, 55811578, 83373044, 87186518, 22278000, 22279002, 264259, 29331822, 60432289, 35696052, 264107, 264110, 21906754, 33109954, 87188559, 264760, 264763, 21908784, 21908785, 21908789, 265021, 264680, 35695855
1559	88224865 (3117, 3118)	Novel Protein sim. GBank gl 112908 sp P02750 A2GL_HUMAN - LEUCINE-RICH ALPHA-2-GLYCOPROTEIN (LRG)	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264259, 29331822, 60432289, 35696052, 264107, 264110, 21906754, 33109954, 87188559, 264760, 264763, 21908784, 21908785, 21908789, 265021, 264680, 35695855
1560	84580675 (3119, 3120)	Novel Protein sim. GBank gl 3880146 emb CAA92704 - (Z68319) Similarity to Human hnRNP F protein (PIR Acc. No. S43484); cDNA EST EMBL:D34218 comes from this gene; cDNA EST EMBL:D37248 comes from this gene; cDNA EST EMBL:D71817 comes from this gene; cDNA EST EMBL:D74531 comes from...		UNCLASSIFIED	264908, 264603, 264638
1561	86609159 (3121, 3122)				264510, 264594
1562	83359682 (3123, 3124)			UNCLASSIFIED	263987
1563	85508694 (3125, 3126)			UNCLASSIFIED	264910, 264764, 264766
1564	87786371 (3127, 3128)	Novel Protein sim. GBank gl 168287 sp P45953 ACOV_RAT - ACYL-COA DEHYDROGENASE, VERY-LONG-CHAIN SPECIFIC PRECURSOR (VLCD)	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	UNCLASSIFIED	18108394, 35696286, 264259, 29331822, 60432289, 35696052, 29331828, 264508, 66712502, 264908, 56182435, 265007, 264910, 60170831, 21908754, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 264686, 21906765, 21906768, 265021, 80170815, 264692, 35696423, 35695855, 264557, 56182323, 60432113, 22279002, 264482

1565	87783381 (3129, 3130)	Novel Protein sim. GBank gij129728jip[P05307(PDI_BOVIN - PROTEIN DISULFIDE ISOMERASE PRECURSOR (PDI) (PROLYL 4-HYDROXYLASE BETA SUBUNIT) (CELLULAR THYROID HORMONE BINDING PROTEIN) (P55)		isomerase	264488, 264689, 18108398, 55811957, 264534, 264259, 264508, 264905, 264509, 264908, 18108372, 264510, 264511, 264512, 265008, 264630, 265009, 264910, 264635, 264636, 264591, 264555, 264592, 264637, 264593, 264594, 264595, 264596, 265011, 264603, 22279002, 18108351, 264762, 264585, 284567
1566	87424749 (3131, 3132)	Novel Protein sim. GBank gij3880445[embjCAA20328] - (AL031268) VM108R.1 [Caenorhabditis elegans]		inf	22278996, 22278999, 264259, 29331822, 29331824, 80432289, 29331827, 66712502, 264908, 265008, 18108351, 52644229, 21908765, 21908767, 21908768, 21908769, 33657109, 264555, 264639, 264482, 56182575, 21908769, 264692
1567	84999008 (3133, 3134)	Novel Protein sim. GBank gij4929699[gbjAAD34110.1]AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		UNCLASSIFIED	
1568	87648761 (3135, 3136)	Novel Protein sim. GBank gij4827083[refjNP_005072.1]pZNF1 - zinc finger protein 142 (clone pHZ-49)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	29331827, 29331830, 264511, 265009, 264758, 21908767, 21908768, 264691, 264693, 22279000, 22279002
1569	80936668 (3137, 3138)	Novel Protein sim. GBank gij5689451[dbjBAA83009.1] - (AB028880) KIAA1057 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	65274572, 29331822, 29331824, 29331828, 264905, 56182435, 265007, 265018, 264784, 21908765, 21908769, 55811957, 60170615, 52844150, 264692, 33657023, 33657109, 18108377, 264583, 264567
1570	86943981 (3139, 3140)	Novel Protein sim. GBank gij1255430 (U53155) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	264595, 264682, 265021
1571	91210340 (3141, 3142)	Novel Protein sim. GBank gij4507731[refjNP_001061.1]pTUBG - tubulin, gamma polypeptide	Contains protein domain (PF00091) - TubulinFtsZ family	tubulin	22278996, 35696286, 22278997, 264091, 264259, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 56182435, 264510, 265007, 264758, 265011, 18108351, 264448, 264288, 264369, 21908765, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 33657023, 264693, 18108370, 18108377, 35696423, 35695855, 264634, 264555, 264558, 18108384, 35696052, 264905, 264906, 264908, 264910, 264758, 264768, 35695917, 264637
1572	81201864 (3143, 3144)			UNCLASSIFIED	
1573	80207068 (3145, 3146)			UNCLASSIFIED	263972

1574	84216142 (3147, 3148)	Novel Protein sim. GBank gij4758334[ref]NP_004258.1[pFADS - delta-6 fatty acid desaturase	Contains protein domain (PF00173) - Heme-binding domain in cytochrome b5 and oxidoreductases	cytochrome	18108394, 264887, 18108397, 18108398, 22278996, 22278997, 22278998, 264259, 29331825, 29331827, 29146498, 29146499, 264107, 264907, 264909, 52644045, 264511, 265008, 264910, 265009, 264591, 21906754, 265011, 265019, 18108351, 264682, 264763, 264764, 18108354, 264389, 264288, 264685, 264766, 264686, 264768, 264688, 21906765, 21906766, 21906767, 21906768, 21906769, 29146629, 264690, 264691, 264693, 20281089, 18108370, 18108374, 18108379, 35695855, 264634, 18108384, 18108385, 22279002, 264563, 264568
1575	95340019 (3149, 3150)	Novel Protein sim. GBank gij3881810[emb]CAA94856[(Z70783) similar to EF-hand calcium binding protein; cDNA EST EMBL:C08700 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00036) - EF hand	phosphatase	56994075, 264259, 29331822, 29331824, 29331825, 60432288, 29331828, 264909, 265006, 265008, 265009, 285010, 87168559, 55811150, 264448, 18108354, 264369, 264288, 18108357, 55811857, 265020, 265021, 60170615, 264691, 33657023, 33657109, 60431528, 65274791, 35695855, 18108385, 60432113, 22279002, 264482
1576	85314019 (3151, 3152)	Novel Protein sim. GBank gij2773195 (AF039711) - contains similarity to Physcomitrella patens glyceraldehyde 3-phosphate dehydrogenase (GB:X72381) [Caenorhabditis elegans]		UNCLASSIFIED	264569, 264092, 264094, 264095, 264259, 264508, 264905, 264509, 264907, 264909, 264510, 264511, 285006, 264910, 21906754, 265010, 265011, 87168559, 264761, 264762, 264288, 264766, 264769, 264691, 264693, 35695855, 264632, 264634, 264635, 264636, 83373044, 264486
1577	87613800 (3153, 3154)	Novel Protein sim. GBank gij2489130[ep]P70315[WASP_MOUSE - WISKOTT - ALDRICH SYNDROME PROTEIN HOMOLOG (WASP)]		UNCLASSIFIED	264511, 265011, 264681, 264369, 264686, 264689, 264629, 264555, 264558, 264559
1578	87123138 (3155, 3156)				264259, 29331826, 265017, 264689, 264693, 60432113
1579	88085141 (3157, 3158)	Novel Protein sim. GBank gij2978255[db]BAA25180[- (AB007407) myeloid zinc finger protein-2 [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	35698288, 264908, 264909, 60433438, 55811386, 264369, 264685, 33657023, 264555, 264556, 264557, 87168518
1580	87255702 (3159, 3160)	Novel Protein sim. GBank gij4324682[gb]AAD16986[- (AF109674) late gestation lung protein 1 [Rattus norvegicus]	Contains protein domain (PF00188) - SCP-like extracellular protein	glycoprotein	22278999, 35696052, 29331830, 52644045, 55812038, 87168474, 265018, 264448, 265022, 264638, 56526486, 22279000
1581	95087431 (3161, 3162)	Novel Protein sim. GBank gij2088838 (AF003386) - F59E12.4 gene product [Caenorhabditis elegans]			22278995, 29331822, 29331824, 29331826, 56182435, 264595, 55812038, 87168559, 265017, 264288, 21906784, 55811957, 35695917, 264692, 55811578, 264637, 55182323, 264559, 83373044, 60432113

1582	95358052 (3163, 3164)	Novel Protein sim. GBank gl 5420387 emb CAB46878.1 - (A243459) proleophosphoglycan [Leishmania major]		phosphatase	264259, 60432288, 29331827, 264509, 264905, 264906, 264907, 264909, 264910, 264762, 264288, 264768, 264769, 264632, 264555, 264639, 56526486, 22279000, 60170831, 33657402, 264682, 21906766, 35695555, 264563
1583	87622715 (3165, 3166)	Novel Protein sim. GBank gl 5578958 emb CAB51351.1 - (AL050308) dJ47587.2 (novel protein) [Homo sapiens]		UNCLASSIFIED	
1584	95337722 (3167, 3168)	Novel Protein sim. GBank gl 5531815 gb AAD44482.1 - (AF078850) steroid dehydrogenase homolog [Homo sapiens]	Contains protein domain (PF00108) - short chain dehydrogenase	dehydrogenase	60424179, 52648842, 65274572, 56182575, 22278995, 35696286, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 60424269, 60432288, 29331827, 29331828, 35696052, 29146498, 66712502, 29331830, 52844045, 56182435, 284510, 264512, 265008, 60433356, 33657402, 60433438, 55812038, 21906754, 55811388, 52644296, 87188474, 87188559, 265018, 265019, 264448, 264369, 264288, 18108358, 21906765, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 265022, 52844150, 33657023, 33657109, 18108374, 55810764, 55811576, 35696423, 65274791, 35695855, 56182323, 83373044, 18108387, 87188518, 60432113, 22278002
1585	87626117 (3169, 3170)	Novel Protein sim. GBank gl 4240132 db BAA74846.1 - (AB020630) KIAA0823 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	phosphatase	35696286, 22278998, 264259, 29331822, 29331824, 29331825, 264905, 285008, 265007, 265008, 60433356, 33109954, 87188474, 265011, 265017, 264604, 264369, 264288, 264885, 264769, 18108359, 21906765, 18108364, 18108370, 264629, 263972, 18108383, 18108386, 264482, 264564
1586	88067081 (3171, 3172)	Novel Protein sim. GBank gl 3786494 (AF098993) - No definition line found [Caenorhabditis elegans]			285017, 265018, 264689, 33657023, 263978, 264636, 264563
1587	87617126 (3173, 3174)	Novel Protein sim. GBank gl 3253159 (AF005355) - translation initiation factor eIF2C [Oryctolagus cuniculus]		UNCLASSIFIED	284907, 264908, 264511, 264910, 264591, 264594, 264629, 264631, 264563, 264483, 284567
1588	87802538 (3175, 3176)	Novel Protein sim. GBank gl 1077573 pir J552680 - probable ribosomal protein L34, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00468) - Ribosomal protein L34	UNCLASSIFIED	264259, 29331828, 264905, 265006, 264758, 21906754, 264761, 264762, 21906765, 21906769, 60170815, 52644150, 33657109, 35695855, 56182323, 18108385
1589	90980653 (3177, 3178)	Novel Protein sim. GBank gl 2137756 pir K48746 - senaphorin C - mouse (fragment)		UNCLASSIFIED	65274572, 264490, 29331822, 66714117, 29331827, 29331828, 56182435, 265008, 60170831, 264595, 264758, 264596, 265011, 264686, 21906766, 21906768, 55811957, 27488265, 264639, 18108385, 56526486, 60432113

1590	95318825 (3178, 3180)			UNCLASSIFIED	264489, 22276996, 264259, 29331824, 29331825, 29331826, 29331827, 265006, 80433356, 21906754, 265017, 265018, 265019, 264448, 264785, 264288, 52844229, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 27486285, 35695763, 96528488, 60432113, 22278000, 22278002, 264564
1591	86877160 (3181, 3182)	Novel Protein sim. GBank gi 4557749 ref NP_000237.1 pMHC2 - MHC class II transactivator		MHC	264259, 264905, 29331830, 264595, 265017, 264448, 264288, 264690, 264629, 67168518
1592	87882533 (3183, 3184)			UNCLASSIFIED	65274572, 60432048, 264509, 60433356, 21906754, 21906767, 21906768, 18108370, 35698423, 22279000, 264595, 264567
1593	84991661 (3185, 3186)			UNCLASSIFIED	264488, 29331827, 264605, 264906, 264807, 264908, 264909, 264910, 264592, 264593, 264757, 264802, 264604, 264760, 264681, 264288, 264768, 264768, 29148629, 35695917, 264692, 264628, 264629, 264630, 264632, 264634, 264635, 264636, 264639, 264563, 264564, 264568
1594	87773752 (3187, 3188)	Novel Protein sim. GBank gi 3677072 emb CAA87060 - (Z46937) similarity with ribosomal protein L21 [Caenorhabditis elegans]		UNCLASSIFIED	29331826, 264908, 55811957
1595	78819425 (3189, 3190)	Novel Protein sim. GBank gi 3152703 (AF065389) - tetraspan NET-4 [Homo sapiens]	Contains protein domain (PF00335) - 4 transmembrane segments Integral membrane proteins	UNCLASSIFIED	
1596	78933928 (3191, 3192)			UNCLASSIFIED	28146498, 264758, 263967
1597	86871857 (3193, 3194)	Novel Protein sim. GBank gi 5257114 gb AAD41244.1 AF094480 - (AF094480) cholesterol 24-hydroxylase [Homo sapiens]	Contains protein domain (PF00067) - Cytochrome P450	cyto450	264092, 29331824, 264508, 264682, 264369, 264688, 264630, 264563
1598	87882939 (3195, 3196)				264259, 264634
1599	87849829 (3197, 3198)	Novel Protein sim. GBank gi 4508797 ref NP_000324.1 pSCA7 - spinocerebellar ataxia 7 (olivopontocerebellar atrophy with retinal degeneration)	Contains protein domain (PF01581) - FMRFamide related peptide family	UNCLASSIFIED	52645080, 29331824, 29331826, 264511, 265009, 265011, 264605, 264448, 264764, 265020, 264692, 264693, 18108370, 264635, 18108385
1600	80056002 (3199, 3200)				29331826, 264603, 264691, 264563
1601	15023248 (3201, 3202)				264635
1602	86926987 (3203, 3204)	Novel Protein sim. GBank gi 5305704 gb AAD41780.1 AF12853 - (AF128535) cytoplasmic phosphoprotein PACSIN2 [Mus musculus]	Contains protein domain (PF00018) - SH3 domain	struct	29146499, 264112, 264782, 18108351, 28146827, 263974
1603	80502072 (3205, 3206)	Novel Protein sim. GBank gi 283920 pir S27939 - tensin - chicken		collagen	264490, 29331824, 264907, 264909, 264511, 265008, 264592, 265010, 265011, 264782, 264764, 264388, 264288, 264687, 264769, 264693, 264628, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 18108385
1604	80221813 (3207, 3208)	Novel Protein sim. GBank gi 4788831 gb AAD29633.1 AF116827 - (AF116827) unknown [Homo sapiens]	ATPase associated	ATPase associated	263977

1605	91221129 (3209, 3210)			struct	264905, 264509, 264906, 264907, 264908, 264909, 264504, 264768, 264768, 264692, 264693, 33657109, 264629, 35695855, 264635, 264636, 264637
1606	94312703 (3211, 3212)	Novel Protein sim. GBank gl 4505313 ref NP_003794.1 pMYOM - UNKNOWN	Contains protein domain (PF00047) - Immunoglobulin domain	struct	22278996, 22278999, 264259, 33657402, 265017, 18108351, 264448, 21906767, 21906769, 52644150, 264691, 87168518, 264689
1607	10871805 (3213, 3214)	Novel Protein sim. GBank gl 5174473 ref NP_005888.1 pPPI - Intracisternal A particle-promoted polypeptide		transcript/factor	
1608	80428900 (3215, 3216)	Novel Protein sim. GBank gl 2224629 db BAA20802 - (AB002342) KIAA0344 [Homo sapiens]		UNCLASSIFIED	264094, 264906, 264907, 264909, 264910, 264691, 264603, 264768, 264693, 264634, 264635, 264637, 264639
1609	94311572 (3217, 3218)	Novel Protein sim. GBank gl 4884073 emb CAB43213.1 - (AL048934) hypothetical protein [Homo sapiens]			52644507, 52645156, 52646365, 52646842, 56102575, 22278994, 56994075, 35696288, 22278997, 22278998, 22278999, 264259, 52645080, 29147620, 29331828, 35696052, 33656970, 264508, 264509, 264807, 52644045, 56182435, 264510, 264511, 264512, 33657402, 21908754, 52646317, 33109954, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264448, 264288, 264769, 52644229, 21906765, 21906766, 21906767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 33657109, 52645129, 27486291, 27486262, 35695763, 264628, 18108370, 18108376, 35698423, 264638, 52644332, 18108387, 87168518, 22279000, 264563, 264486
1610	65468200 (3219, 3220)	Novel Protein sim. GBank gl 263920 p ref S27639 - lensin - chicken		UNCLASSIFIED	264593, 264757, 55812038, 265018, 265020, 264691, 264692, 264693, 264631, 264634, 264635, 264555, 22279000, 264564
1611	94122843 (3221, 3222)	Novel Protein sim. GBank gl 107284 p ref A35415 - peroxidase (EC 1.11.1.7), thyroid (Grave's disease) - human (fragment)	Contains protein domain (PF00008) - EGF-like domain	peroxidase	35696286, 21906765, 264691, 35696423
1612	85746031 (3223, 3224)	Novel Protein sim. GBank gl 3874846 emb CAA94337 - (Z70307) Similarly to B. subtilis tetracycline resistance protein (SW:TCR2_BACSU); cDNA EST EMBL-C09951 comes from this gene; cDNA EST EMBL-C08265 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264508, 18108370, 18108387, 264486
1613	82247354 (3225, 3226)			UNCLASSIFIED	264759

1614	81228634 (3227, 3228)	Novel Protein sim. GBank gi 4680873 gb AAD27726.1 AF13295 - (AF132951) CGI-17 protein [Homo sapiens]	Contains protein domain (PF01605) - ERF1-like proteins	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 264908, 264512, 265009, 265011, 265017, 265018, 265019, 18108351, 264683, 264288, 264766, 21908787, 21908788, 21906789, 35695917, 265021, 265022, 35696423, 35695855, 60170394, 56182323, 83373044, 264568 22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1615	86121809 (3228, 3230)	Novel Protein sim. GBank gi 5689485 db BAA83026.1 - (AB028987) KIAA1074 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	homeobox	22278996, 35696286, 22278997, 29331822, 35696052, 29331828, 264508, 264908, 264909, 56182435, 264511, 265017, 265019, 264766, 264767, 264768, 265020, 264691, 264628, 264632, 264635, 264555, 264556, 56182323, 264558, 22279002
1616	94311819 (3231, 3232)	Novel Protein sim. GBank gi 3578260 emb CAB01696 - (Z78416) cDNA EST EMBL:D71020 comes from this gene; cDNA EST EMBL:D73593 comes from this gene; cDNA EST EMBL:C07649 comes from this gene; cDNA EST EMBL:C09081 comes from this gene; cDNA EST yk399f2.3 comes from this gene; cDNA ...		UNCLASSIFIED	264488, 52644507, 52645156, 52646365, 52646842, 22278994, 22278995, 35696286, 22278996, 22278997, 22278999, 52645080, 29331822, 29331824, 29331825, 29331827, 29331828, 35696052, 35696970, 264905, 264909, 264594, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 265019, 264681, 264448, 264684, 52644228, 21906764, 264689, 21908785, 21906786, 21906789, 35695917, 265020, 265021, 52644150, 33657023, 52645129, 33657109, 33657182, 27486281, 27486282, 33657349, 27486265, 35695783, 18108376, 35696423, 35695855, 264557, 52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264768, 264769, 264689, 264693, 18108374, 264635, 264636, 264638
1617	88090742 (3233, 3234)	Novel Protein sim. GBank gi 468053 sp P34879 YO41_CAEL - HYPOTHETICAL 88.7 KD PROTEIN ZK757.1 IN CHROMOSOME III	Contains protein domain (PF01529) - DHHC zinc finger domain	peptidase	52644332, 264558, 18108385, 87168518 35696052, 264905, 264509, 264907, 264908, 264510, 264511, 264764, 264768, 264769, 264689, 264693, 18108374, 264635, 264636, 264638
1618	86272860 (3235, 3236)	Novel Protein sim. GBank gi 4240231 db BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		struct	35696286, 22278999, 264092, 29331824, 29331825, 35696052, 33657084, 21906765, 27486284
1619	95354580 (3237, 3238)	Novel Protein sim. GBank gi 5031763 ref NP_005515.1 pHRY - hairy (Drosophila)- homolog	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcription factor	52646842, 65274572, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 56182435, 265007, 265008, 264910, 60170831, 60432229, 60433356, 60433438, 265019, 264448, 264288, 264686, 21906788, 265021, 60170815, 33657023, 65274620, 33657109, 18108374, 18108376, 35696423, 35695855, 56182323, 56526486 264684
1620	87344655 (3239, 3240)	Novel Protein sim. GBank gi 1351047 sp P45843 SCRT_DROME - SCARLET PROTEIN		UNCLASSIFIED	56182323, 56526486 264684

1821	87078708 (3241, 3242)				UNCLASSIFIED	264910	18108382, 65274572, 18108388, 22278996, 22278997, 22278999, 28146498, 28148499, 284905, 264808, 284909, 284928, 52844045, 284592, 60433356, 21906754, 284602, 285017, 284389, 21908768, 55811957, 285021, 60170615, 284635, 284557, 60170394, 83373044, 18108385, 22279000, 22279002, 284568
1822	94741738 (3243, 3244)	Novel Protein sim. GBank gi 3822553 (AF098788) - nuclear calmodulin-binding protein [Gallus gallus]	Contains protein domain (PF00622) - SPRY domain		UNCLASSIFIED		18108398, 284239, 284909, 56182435, 87168474, 284448, 21908768, 35695917, 284691, 87168518, 284583
1823	87778108 (3245, 3246)	Novel Protein sim. GBank gi 731086 sp P40389 UV22_SCHPO - UV-INDUCED PROTEIN UV122			ribosomalpro		66714117, 28331825, 284909, 265008, 264758
1824	87338178 (3247, 3248)	Novel Protein sim. GBank gi 387566 emb CAB05478 - (Z83104) cDNA EST EMBL.T00015 comes from this gene; cDNA EST EMBL.D33665 comes from this gene; cDNA EST EMBL.D36540 comes from this gene; cDNA EST yk24018.3 comes from this gene; cDNA ES... comes from this gene; cDNA ES...			UNCLASSIFIED		
1825	95354748 (3249, 3250)	Novel Protein sim. GBank gi 458622 db BAA76833.1 - (AB023208) KIAA0989 protein [Homo sapiens]			Kinase		264489, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264259, 29331824, 29331825, 29331827, 29331828, 264102, 284106, 284508, 33657084, 265017, 265018, 18108351, 284683, 284389, 284288, 21908765, 21908766, 21908767, 21908769, 35695917, 265021, 264691, 65274820, 18108368, 283972, 18108376, 35696423, 284631, 264634, 22279000, 22279002
1826	94734369 (3251, 3252)	Novel Protein sim. GBank gi 587907 gb AA046844.1 AF160904 - BcDNA.HL05938 [Drosophila melanogaster]					52844507, 52845156, 52846365, 52846842, 22278994, 56994075, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 66714117, 29331826, 60432289, 29331827, 29331828, 35696052, 284906, 66712502, 284909, 285008, 285009, 60432229, 60433356, 60433438, 21908754, 52846317, 52844298, 285011, 87168559, 284804, 265018, 284448, 284389, 284288, 264768, 52844229, 284689, 21908765, 21908768, 35695917, 265021, 285022, 52844150, 33657023, 65274620, 27486261, 27486262, 27486285, 35695763, 263972, 52844332, 80170394, 87168518, 60432113, 284587
1827	83368773 (3253, 3254)				UNCLASSIFIED		284288
1828	85708459 (3255, 3256)	Novel Protein sim. GBank gi 3686087 (AC004667) - hypothetical protein [Arabidopsis thaliana]			eph		284288, 284686, 264767, 22279002

1629	84993841 (3257, 3258)	Novel Protein sim. GBank gij4240175[dbj BAA74866.1] - (AB020850) KIAA0843 protein [Homo sapiens]		struct	284555
1630	87779027 (3259, 3260)			UNCLASSIFIED	29331822, 29331827, 265010, 284693, 284634, 22279002
1631	87756454 (3261, 3262)	Novel Protein sim. GBank gij1915892[emb CAA69995] - (Y06740) tom-1A protein [Gallus gallus]		UNCLASSIFIED	55811857, 284259, 33657023, 284693, 29331822, 29331824, 29331827, 29331828, 284908, 284908, 55811576, 284910, 284634, 284638, 284637, 56182323, 284559, 284758, 18108385, 284583, 284764, 284766
1632	87871692 (3263, 3264)	Novel Protein sim. GBank gij2558501[dbj BAA22896] - (D63850) hepatoma-derived growth factor [Mus musculus]		UNCLASSIFIED	284687, 284768, 284691, 284692, 29148489, 284509, 284905, 284907, 284511, 284512, 284482, 284681, 284763, 284682, 284683
1633	87773683 (3265, 3266)				284488, 284259, 284907, 284908, 284909, 284628, 284629, 284631
1634	85892817 (3267, 3268)	Novel Protein sim. GBank gij4887229[gb AAD32244.1 AF150755] microtubule-actin crosslinking factor [Mus musculus]	Contains protein domain (PF00435) - spectrin repeat	struct	265007, 284637, 22279002
1635	94232800 (3269, 3270)			UNCLASSIFIED	85274572, 22278998, 35696052, 52844045, 284511, 265008, 265009, 265010, 265011, 285018, 265019, 284448, 284369, 21908785, 21908788, 265021, 284690, 284482
1636	80413227 (3271, 3272)	Novel Protein sim. GBank gij453781[fr JNP_001339.1 pDAPK - death-associated protein kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED - kinase	22278995, 284594, 284763, 285020
1637	80070435 (3273, 3274)				284558
1638	87101854 (3275, 3276)	Novel Protein sim. GBank gij3420051 (AC004680) - unknown protein [Arabidopsis thaliana]			21908785, 21908767, 22278998, 35696286, 22278999, 284259, 284692, 284693, 29331824, 33657109, 284508, 284908, 18108370, 284628, 265007, 33657402, 21908784, 284602, 284604, 284764, 284683, 284586, 284288
1639	94322194 (3277, 3278)	Novel Protein sim. GBank gij5420389[emb CAB46680.1] - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	284488, 18108394, 65274572, 56182575, 35696286, 29331824, 29331826, 29331827, 35696052, 284908, 56182435, 284112, 265008, 265008, 284757, 284758, 55811386, 284603, 284760, 18108351, 284764, 284288, 284766, 284768, 21908767, 55811957, 284691, 33657023, 65274620, 18108370, 55810784, 55811576, 284558, 284639, 83373044, 18108385, 87168518

1640	94143185 (3278, 3280)	Novel Protein sim. GBank gll2842469[emb]CAA18847.1 - (AL021747) hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 56994075, 35686286, 60432049, 60432289, 29331827, 35698052, 52644045, 56182435, 284510, 265006, 265007, 265008, 264910, 265009, 33657402, 55812038, 265010, 265011, 265017, 265018, 264288, 52644229, 21908785, 21908786, 21908788, 35695917, 265021, 60170815, 52644150, 33657023, 33657109, 33657349, 18108374, 35698423, 65274781, 35695855, 264632, 264555, 58182323, 22279000
1641	87825160 (3281, 3282)			UNCLASSIFIED	28148489, 265006, 265007, 265008, 265009, 55812038, 265010, 265011, 264555, 264556, 264558, 18108383
1642	94312557 (3283, 3284)	Novel Protein sim. GBank gll1575333 (U90416) - myr 6 myosin heavy chain [Rattus norvegicus]	Contains protein domain (PF01843) - struct DIL domain		22278899, 28147620, 29331826, 29331828, 33658970, 55812038, 265010, 265018, 265019, 18108351, 264689, 265020, 265022, 264690, 33657023, 65274620, 35695763, 52644332, 18108381, 60170394, 56182323, 18108388, 87168518, 22279002, 264564, 29331825, 29331827, 29331828, 21906754, 265019, 264288, 264693, 33657349, 18108370, 18108376, 264555, 83373044, 22278002, 264482
1643	94131768 (3285, 3286)				264505, 264907, 264908, 264910, 265009, 264757, 264758, 264761, 264762, 264763, 264766, 264768, 264769, 264628, 264629, 264630, 264631, 264632, 264563, 264564, 264565, 264566, 264567
1644	88085125 (3287, 3288)			UNCLASSIFIED	264885, 264893
1645	95013858 (3289, 3290)	Novel Protein sim. GBank gll1076802[pir]S49915 - extensin like protein - maize		UNCLASSIFIED	22278894, 56994075, 35686286, 264259, 29331824, 29331825, 29331826, 60432289, 264508, 60433356, 60433438, 87168559, 265018, 264687, 35695917, 264692, 33657023, 33657182, 27486261, 27486265, 33657349, 60432113, 264563, 264564
1647	94278428 (3293, 3294)	Novel Protein sim. GBank gll5002573[emb]CAB44338.1 - (Y17466) alpha-N-acetylgalactosamine alpha-2,6-sialyltransferase [Fugu rubripes]		UNCLASSIFIED	29331822, 264906, 264908, 264359, 21908788, 60170815, 264639, 22278000
1648	87842098 (3295, 3296)		Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	265009, 264686, 55811957, 35695917, 55810764, 264556, 56182323, 264558, 18108385

1648	95347628 (3297, 3298)	Novel Protein sim. GBank gij654085[emb]CAA58337[-] (X83413) U88 [Human herpesvirus 8]		cadherin	264488, 22278995, 35696286, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264905, 264907, 66712502, 264908, 52844045, 264909, 56182435, 264511, 265007, 265008, 265009, 264591, 264593, 60433438, 264596, 55812038, 21906754, 265011, 264601, 264602, 265017, 265018, 265019, 264682, 264448, 264764, 264683, 264288, 264766, 264685, 264687, 264768, 264688, 264769, 52844229, 264689, 21906765, 21906768, 21906767, 21906768, 55811937, 35695917, 265021, 265022, 52844150, 264692, 33657023, 33657109, 20281149, 18108370, 264628, 18108374, 18108376, 35696423, 35695655, 264632, 264634, 264635, 264636, 18108380, 264639, 264558, 18108382, 18108384, 18108385, 18108387, 264080, 264404, 60432113, 22278000, 22279002, 264482, 264565, 264566, 264487 265011, 264602, 21906767, 18108374, 18108377, 18108385
1650	87418538 (3298, 3300)	Novel Protein sim. GBank gij3647335[emb]CAA21059[-] (AL031644) possible zinc-finger protein [Schizosaccharomyces pombe]			
1651	81639773 (3301, 3302)	Novel Protein sim. GBank gij4884278[emb]CAB43247.1[-] (AL050037) hypothetical protein [Homo sapiens]		synthase	264488, 52645156, 18108397, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264508, 264908, 29331830, 264910, 60432229, 21906754, 265010, 265011, 265017, 265019, 264448, 18108354, 264288, 264688, 21906765, 21906768, 21906768, 21906769, 265022, 264692, 264693, 264629, 35695955, 264558, 264637, 264557, 264559, 83373044, 56526486, 22279000, 22279002, 264564 22278997, 29148498, 56182435, 21906754, 264369, 21906765, 21906768, 21906769, 265020, 52644150, 33657109, 22279000, 22279002
1652	86596622 (3303, 3304)	Novel Protein sim. GBank gij1657837 (U73200) - p116Rip [Mus musculus]	Contains protein domain (PF00169) - PH domain		
1653	84256983 (3305, 3306)	Novel Protein sim. GBank gij3776054[emb]CAA06273[-] (AJ004999) Tapasin [Gallus gallus]	Contains protein domain (PF00047) - immunoglobulin domain	glycoprotein	18108398, 22278995, 22278998, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331830, 264909, 265006, 265009, 60432229, 60433356, 60433438, 21906754, 265017, 265019, 264448, 264683, 264288, 265021, 265022, 264692, 18108364, 65274791, 18108384, 60432113, 264567 33657109, 264565
1654	78756471 (3307, 3308)			UNCLASSIFIED	

1655	86889346 (3309, 3310)	Novel Protein sim. GBank gl 3355717 emb CAA73486 - (Y13053) seryl-tRNA synthetase [Zea mays]		synthase	52644507, 35686286, 22278998, 22278999, 29331824, 29331825, 29331826, 33856970, 264908, 52644045, 264511, 264910, 52646317, 264288, 52644229, 33657023, 33657109, 52644332, 264557, 56182323, 56526486, 50432113
1656	79962287 (3311, 3312)	Novel Protein sim. GBank gl 1890141 dbj BAA16847 - (D83208) P24 protein [Mus musculus]		UNCLASSIFIED	29331822, 29331824, 29331825, 264563
1657	87771994 (3313, 3314)	Novel Protein sim. GBank gl 4557845 ref NP_001524.1 p NRP - heterogeneous nuclear ribonucleoprotein L	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331827, 265009, 21906766, 21906767, 265020, 265022, 33857109, 264638, 56526486, 264482
1658	87773778 (3315, 3316)	Novel Protein sim. GBank gl 3877072 emb CAA67060 - (Z48937) similarity with ribosomal protein L21 [Caenorhabditis elegans]	Contains protein domain (PF00829) - Ribosomal protkaryotic L21 protein	UNCLASSIFIED	22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 29146498, 264905, 264908, 52644045, 265006, 60433356, 264757, 60433438, 21906754, 265011, 18108351, 264448, 264389, 264288, 264766, 264768, 21906765, 21906767, 21906768, 21906769, 29148628, 265021, 265022, 18108362, 263969, 263971, 18108374, 35698423, 18108383, 22279000, 264482
1659	88230701 (3317, 3318)	Novel Protein sim. GBank gl 538218 pir J38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	52646317, 21906766, 21906767, 21906768, 87188518, 22278996, 265020, 22278999, 87188559, 264603, 265017, 264631, 265018, 265019, 22279002, 264482, 264835, 264565
1660	94315313 (3319, 3320)	Novel Protein sim. GBank gl 2487012 sp Q10010 YSV4_CAEEL - HYPOTHETICAL 26.8 KD PROTEIN T19C3.4 IN CHROMOSOME III		UNCLASSIFIED	264488, 35696286, 264259, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 265007, 264512, 265009, 264910, 264592, 264596, 265010, 264600, 264602, 265017, 265018, 264605, 264760, 264764, 264288, 264766, 264688, 264768, 264769, 264689, 21906768, 35695917, 264690, 33657023, 264893, 33657109, 264628, 35698423, 35695855, 264634, 264835, 264555, 264636, 264637, 264556, 264638, 264639, 264559, 18108365, 18108388, 264563, 264483, 264564, 264565, 264566, 264486, 264567

1661	94234071 (3321, 3322)	Novel Protein sim. GBank gi 4759100 ref NP_004759.1 pSFRS - splicing factor, arginine/serine-rich 11	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	264488, 22278998, 264259, 29331824, 29331828, 29331827, 29331828, 264509, 86712502, 29331830, 264908, 52644045, 265007, 264512, 60433356, 60433438, 55812038, 21906754, 265018, 264448, 264766, 264768, 264769, 21906788, 21906769, 265020, 33657023, 33657109, 65274791, 87168518, 264482, 264563, 264564, 264565, 264567
1662	94135172 (3323, 3324)	Novel Protein sim. GBank gi 1730302 sp P52875 PF27_MOUSE - TRANSMEMBRANE PROTEIN PFT27			18108392, 29331822, 29331828, 20281100, 264106, 265008, 265007, 265008, 18108348, 21906766, 18108365, 18108366, 18108374, 83373044, 18108365
1663	94217148 (3325, 3326)	Novel Protein sim. GBank gi 4884136 emb CA843275.1 - (AL050107) hypothetical protein [Homo sapiens]	Contains protein domain (PF00397) - WW domain	kinase	52645156, 56182575, 22278994, 22278995, 35698286, 22278998, 56994075, 22278997, 22278998, 22278999, 264259, 29331822, 29331826, 29331827, 29331828, 33656970, 29331830, 264908, 56182435, 264511, 60433356, 33657402, 33109954, 87168474, 87168559, 265017, 265018, 264605, 18108351, 264764, 264288, 264766, 264768, 21906765, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 264691, 33657023, 264693, 263967, 33657109, 264630, 52644332, 83373044, 87168518, 60432113, 22278900
1664	94234078 (3327, 3328)	Novel Protein sim. GBank gi 3043692 dbj BA25510 - (AB011156) KIAA0584 protein [Homo sapiens]		UNCLASSIFIED	264488, 263994, 35698288, 29331824, 35698052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 60170831, 264591, 264592, 264595, 87168474, 265011, 264600, 264601, 264604, 264605, 264760, 264762, 18108351, 264681, 264682, 264763, 264683, 264764, 264288, 264684, 264768, 264687, 264768, 264769, 21906764, 21906765, 21906767, 35695917, 265021, 264534, 80170615, 264690, 264691, 264692, 33657109, 33657182, 264628, 18108370, 264629, 35698423, 35695855, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264553, 264566, 264488

1665	91226952 (3329, 3330)	Novel Protein sim. GBank gji1083506 pirij S50085 - eloadhesin - mouse	Contains protein domain (PF00047) - Immunoglobulin domain	immunoglob	284488, 29331826, 29331828, 284509, 284906, 284907, 284909, 284510, 284511, 284910, 284592, 284593, 284595, 284758, 284596, 284600, 284760, 284762, 284764, 284766, 284768, 284629, 284630, 284634, 284638, 83373044, 284564, 284566, 284567, 284488
1666	95358160 (3331, 3332)	Novel Protein sim. GBank gji3913431 spj042843 DDX8_SCHPO - PUTATIVE PRE-MRNA SPLICING FACTOR ATP-DEPENDENT RNA HELICASE SPAC10F6.02C	Contains protein domain (PF00575) - S1 RNA binding domain	helicase	56994075, 22278998, 284259, 29331824, 29331826, 29331827, 29140498, 285009, 33108954, 87188559, 285019, 284288, 284688, 21808767, 21808769, 284691, 33857182, 18108370, 18108374, 18108385, 22278002
1667	91226855 (3333, 3334)	Novel Protein sim. GBank gji5689535 dbj BAA83051.1 - (AB029022) KIAA1089 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	transport	284259, 29331822, 29331826, 284905, 284906, 284908, 284510, 285009, 284595, 284758, 285011, 87188559, 285017, 285018, 285019, 284448, 284766, 284688, 21808765, 21808767, 21808769, 285020, 285021, 60170815, 284890, 284692, 284693, 18108368, 18108370, 283972, 55810764, 284555, 83373044, 60432113, 22278000, 22278002
1668	88095135 (3335, 3336)	Novel Protein sim. GBank gji2078894 gbj AAB53983.1 - (AF002197) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind), Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]		kinase	66714117, 284508, 284509, 284906, 284907, 284908, 284511, 284910, 284784, 284687, 284689, 33857109, 35698423, 35695855, 284632
1669	91227846 (3337, 3338)	Novel Protein sim. GBank gji3875371 embj CAA85414.1 - (Z38948) contains a valine and arginine rich domain, possesses weak similarity with the RNA binding domains from RNA splicing factor U2AF 65 KD subunit; cDNA EST EMBL:D84658 comes from this gene; cDNA EST EMBL:D66829 comes fr...		UNCLASSIFIED	29331825, 33108954, 284368, 284767, 284689, 33857109, 83373044
1670	87628009 (3339, 3340)			UNCLASSIFIED	284259, 29331824, 28331827, 60433438, 285022, 284638
1671	87346372 (3341, 3342)	Novel Protein sim. GBank gji462451 spjP34244 KKK1_YEAST - PROBABLE SERINE/THREONINE-PROTEIN KINASE YKL101W	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	35698286, 22278997, 29331825, 284909, 21808754, 285017, 285018, 285019, 284682, 284683, 284768, 284688, 21808766, 21808767, 21808768, 21808769, 284691, 284555, 284558, 22279000, 284566, 284906, 284909, 284632, 18108381
1672	86281834 (3343, 3344)	Novel Protein sim. GBank gji1814270 (U74586) - double-stranded RNA specific adenosine deaminase [Rattus norvegicus]		deaminase	

1673	88095137 (3345, 3346)	Novel Protein sim. GBank gl 2076894 gb AAB53883.1 - (AF002187) short region of weak similarity to protein kinase C; contains similarity to Pfam domain PF00130 (DAG_PE-bind). Score=10.0, E-value=0.0034, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00130) - Phorbol esters/diacylglycerol binding domain (C1 domain)	Kinase	264488, 264569, 18108394, 56994075, 22278998, 284259, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60170831, 264592, 264594, 264595, 264758, 264601, 264760, 264762, 264683, 264764, 264288, 264766, 264686, 264768, 264687, 264769, 264689, 264690, 33857023, 264692, 264693, 33857109, 264628, 264629, 18108374, 35698423, 35695855, 264631, 264632, 264634, 264635, 264637, 264556, 264638, 264639, 264563, 264482, 264564, 264565, 264568, 264567, 264489
1674	88258028 (3347, 3348)	Novel Protein sim. GBank gl 5262467 emb CAB45683.1 - (AL080062) hypothetical protein [Homo sapiens]		kinase	26433358, 87188559, 264448, 264288, 264688, 264691
1675	87606468 (3349, 3350)	Novel Protein sim. GBank gl 3128366 (AF010496) - 50S ribosomal protein l9 [Rhodobacter capsulatus]		UNCLASSIFIED	56181686, 35696286, 22278997, 22278998, 264259, 29331824, 29331827, 35696052, 68712502, 264764, 264288, 264686, 264687, 35695917, 265020, 264690, 264693, 35695763, 18108370, 35698423, 35695855, 264637, 264639, 18108385, 264564
1676	85358086 (3351, 3352)	Novel Protein sim. GBank gl 4184065 gb AAD05327 - (AF111081) latrophilin 3 splice variant bbar [Bos taurus]		UNCLASSIFIED	264259, 29331827, 29331828, 264106, 264907, 265009, 264600, 265019, 264288, 21908765, 265020, 265022, 35695855, 83373044, 18108385
1677	87408587 (3353, 3354)	Novel Protein sim. GBank gl 3327046 db BAA31591 - (AB014516) KIAA0816 protein [Homo sapiens]		UNCLASSIFIED	264808
1678	86868828 (3355, 3356)	Novel Protein sim. GBank gl 550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]	Contains protein domain (PF00289) - Carbamoyl-phosphate synthase (CPSase)	UNCLASSIFIED	29331824, 264102
1679	91214108 (3357, 3358)	Novel Protein sim. GBank gl 550452 (U08469) - 3-methylcrotonyl-CoA carboxylase, biotin-carrier domain [Glycine max]		carboxylase	264488, 18108392, 18108394, 52648842, 18108397, 18108398, 35696286, 29331824, 265008, 265007, 265008, 265009, 18108348, 265011, 18108351, 264683, 18108354, 18108358, 18108359, 21908765, 29146627, 29148629, 264690, 18108361, 18108362, 18108384, 18108365, 18108368, 264628, 18108379, 35696423, 35695855, 264635, 18108381, 18108382, 18108383, 18108384, 18108385, 18108388
1680	81005372 (3359, 3360)	Novel Protein sim. GBank gl 2394478 (AF024500) - No definition line found [Caenorhabditis elegans]		transport	63274572, 22278994, 22278999, 68714117, 29331827, 56182435, 21908754, 265018, 264288, 21908759
1681	94324150 (3361, 3362)	Novel Protein sim. GBank gl 5689537 db BAA83052.1 - (AB029023) KIAA1100 protein [Homo sapiens]		UNCLASSIFIED	22278998, 29331822, 264908, 264593, 264804, 265019, 264683, 55811957, 264690, 33857023, 35696423, 83373044, 264563
1682	86042710 (3363, 3364)			UNCLASSIFIED	264909, 265017, 264605

1683	94316213 (3365, 3366)	Novel Protein sim. GBank gi 5031717 ref NP_005704.1 pGPBP - goodpasture antigen- binding protein	Contains protein domain (PF01852) - UNCLASSIFIED START domain	263994, 35696286, 35696052, 264508, 284509, 264905, 264906, 264907, 264908, 264909, 264511, 265006, 265007, 265009, 264910, 264593, 264758, 265010, 265011, 264780, 264761, 264762, 264763, 264764, 264389, 264766, 264768, 35695917, 264692, 33657109, 35698423, 35695855, 264634, 264635, 264636, 264638, 264639, 83373044, 284488
1684	80083408 (3367, 3368)		UNCLASSIFIED	264563, 264566
1685	94323182 (3369, 3370)	Novel Protein sim. GBank gi 1255371 (U53147) - coded for by C. elegans cDNA yk34a9.6; coded for by C. elegans cDNA yk34a9.3; Similar to guanylate kinase. [Caenorhabditis elegans]	Contains protein domain (PF00825) - Guanylate kinase	60424178, 52846842, 22278994, 35698286, 22278998, 264259, 52845080, 29331824, 29331826, 265007, 33657084, 265018, 284681, 284448, 264683, 264369, 264689, 21906765, 21906767, 21906768, 21906769, 265021, 264692, 65274620, 33657109, 27488262, 284635, 52844332, 56182323, 22279000
1686	87820710 (3371, 3372)	Novel Protein sim. GBank gi 2244707 dbj BAA21115.1 - (AB005287) thrombospondin 1 [Bos taurus]	UNCLASSIFIED	56182575, 264259, 264508, 264905, 264509, 264907, 264908, 264510, 264511, 265006, 284512, 265009, 264910, 264758, 285010, 285011, 264605, 18108351, 264764, 264766, 18108357, 264768, 18108362, 264628, 284630, 284631, 284634, 264635, 264637, 264638, 264639, 284585, 264486, 284587, 35695917, 284806, 284907, 264908, 284510, 265006, 265007, 264910, 264558, 18108381, 18108383, 285011
1687	94719400 (3373, 3374)	Novel Protein sim. GBank gi 4680879 gb AAD27729.1 AF13295 - (AF132954) CG-20 protein [Homo sapiens]	UNCLASSIFIED	264905, 284910, 264760, 264629, 264555 UNCLASSIFIED
1688	82158442 (3375, 3376)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1 - (AB020659) KIAA0852 protein [Homo sapiens]	UNCLASSIFIED	264569, 35696286, 22278999, 264508, 284908, 264909, 56182435, 33657402, 60433438, 55812038, 265017, 265018, 284448, 264784, 264288, 264686, 29148629, 35695917, 265020, 265021, 263972, 18108374, 65274781, 83373044, 264089
1689	94325049 (3377, 3378)	Novel Protein sim. GBank gi 4240193 dbj BAA74875.1 - (AB020659) KIAA0852 protein [Homo sapiens]	UNCLASSIFIED	264369, 21908766, 264682, 264639, 87188518
1690	83255346 (3379, 3380)	Novel Protein sim. GBank gi 3800736 (AF031572) - seven- pass transmembrane receptor precursor [Mus musculus]	Contains protein domain (PF00029) - Cadherin domain	264768, 33657109, 29331827, 29148629, 264510, 264108, 264910, 284109, 264508, 60170831, 264563, 264905, 264564, 284691, 264637, 264628, 264907, 284908, 33657023, 264567, 264768, 263974
1691	88095223 (3381, 3382)	Novel Protein sim. GBank gi 2773208 (AF039713) - No definition line found [Caenorhabditis elegans]		264768, 33657109, 29331827, 29148629, 264510, 264108, 264910, 284109, 264508, 60170831, 264563, 264905, 264564, 284691, 264637, 264628, 264907, 284908, 33657023, 264567, 264768, 263974
1692	86106709 (3383, 3384)			264768, 33657109, 29331827, 29148629, 264510, 264108, 264910, 284109, 264508, 60170831, 264563, 264905, 264564, 284691, 264637, 264628, 264907, 284908, 33657023, 264567, 264768, 263974
1693	87012775 (3385, 3386)	Novel Protein sim. GBank gi 121271 sp P02207 GLB_LAMFL - GLOBIN	Contains protein domain (PF00042) - Globin	28331826, 264508, 264905, 264907, 264595, 265010, 265011, 21908768, 33657023, 284629, 263978, 264558

1694	94208168 (3387, 3388)	Novel Protein sim. GBank gi 5453932 ref NP_008225.1 pPOLR - polymerase (RNA) II (DNA directed) polypeptide J (13.3kD)	Contains protein domain (PF01193) - RNA polymerases L / 13 to 16 kDa subunit	inapolymerase	35696286, 22278998, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331828, 35696052, 29148499, 264905, 284808, 52644045, 264511, 285008, 265007, 265009, 264592, 60433356, 21908754, 265010, 265011, 18108351, 264763, 264682, 284448, 284683, 284288, 264788, 264689, 21908768, 60170815, 264691, 284692, 264693, 18108370, 18108374, 263978, 35696423, 35695855, 264556, 18108381, 18108385, 87168518, 264482, 264486, 264634
1695	94719325 (3389, 3390)	Novel Protein sim. GBank gi 4680878 gb AAD27729.1 AF13295 - (AF132954) CGI-20 protein [Homo sapiens]		UNCLASSIFIED	
1696	87824038 (3391, 3392)	Novel Protein sim. GBank gi 4220517 emb CAA22980 - (AL035356) hypothetical protein [Arabidopsis thaliana]			22278997, 264259, 265010, 18108351, 264764, 21908766, 18108370
1697	85740863 (3393, 3394)	Novel Protein sim. GBank gi 505652 (U10382) - GP36b glycoprotein [Homo sapiens]		glycoprotein	264682
1698	87445285 (3395, 3396)	Novel Protein sim. GBank gi 5052031 gb AAD38411.1 AF15573 - (AF155739) axotrophin [Mus musculus]			58994075, 22278998, 22278999, 264509, 33857402, 264758, 87168474, 87168558, 265017, 265018, 264448, 264687, 29148627, 21908789, 29148629, 265020, 265022, 33657023, 264558, 87168518, 22279002
1699	87424783 (3397, 3398)	Novel Protein sim. GBank gi 543344 pir IS41647 - zinc finger 5 protein - mouse	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED nuc_recpt	35696286, 264635 29331824, 52644045, 265008, 265009, 263989, 263971
1701	86570488 (3401, 3402)	Novel Protein sim. GBank gi 3877439 emb CAA86652 - (Z72510) similarity to yeast UTR3 protein [Swiss Prot accession number P21374]; cDNA EST EMBL:D72822 comes from this gene; cDNA EST EMBL:D75763 comes from this gene; cDNA EST yk274e3.3 comes from this gene; cDNA EST yk274e3.5 c...		UNCLASSIFIED MHC	22278995, 22278997, 264092, 29148498, 29148499, 264107, 264508, 264907, 284110, 284112, 265009, 60170831, 21908754, 265011, 265017, 264782, 18108351, 264288, 21908765, 35695917, 265021, 60170615, 263987, 33857109, 18108370, 263972, 263974, 18108374, 263976, 35695855, 264555, 263981, 60170394, 18108385, 58529486, 87168518, 60432113
1702	87785082 (3403, 3404)	Novel Protein sim. GBank gi 451544 (U04267) - proline-rich cell wall protein [Gossypium barbadense]		UNCLASSIFIED	264909, 265017, 264628, 264629, 264638
1703	78568651 (3405, 3406)	Novel Protein sim. GBank gi 1263289 (U47856) - fibron-4 [Araneus diadematus]		UNCLASSIFIED	264368
1704	86622878 (3407, 3408)	Novel Protein sim. GBank gi 4518621 dbj BAA75670.1 - (AB017614) OASIS protein [Mus musculus]		UNCLASSIFIED	264569, 35696288, 264907, 265010, 264687, 264768, 264692, 264693, 264636, 264566, 22278996, 22278998, 264259, 264509, 265018, 264764, 264685, 284686, 21908768, 21908769, 265022, 264691, 264558, 22279000
1705	87795175 (3409, 3410)	Novel Protein sim. GBank gi 3123034 sp Q15011 Y025_HUMAN - HYPOTHETICAL PROTEIN KIAA0025			
1706	87790987 (3411, 3412)				

1707	88041230 (3413, 3414)	Novel Protein sim. GBank gll4321684[gb]AAD15797] - (AF055470) ZNF258 [Homo sapiens]	UNCLASSIFIED	18108398, 22278997, 264259, 29147820, 29331826, 29146498, 284905, 264906, 265008, 264593, 264595, 264758, 264596, 265016, 284760, 18108351, 284764, 264766, 264889, 264693, 18108370, 35698423, 55811576, 264558, 87168518, 60432113, 264567
1708	91220519 (3415, 3416)	Novel Protein sim. GBank gll5174591[re]NP_005947.1[p]MTHF - 5,10-methylenetetrahydrofolate dehydrogenase, 5,10-methylenetetrahydrofolate cyclohydrolase, 10-formyltetrahydrofolate synthetase	Contains protein domain (PF01268) - synthase Formate-tetrahydrofolate ligase	56182575, 22278996, 56994075, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 29146498, 29146499, 29331830, 285009, 80170831, 33857402, 33109954, 87168559, 265019, 18108351, 264448, 21908765, 21908767, 21908768, 29148627, 29148628, 29148784, 60170615, 52644150, 33657023, 33657109, 18108374, 55811576, 264559, 18108385, 22279000, 264563, 264107, 55811957, 263974, 263976, 263977, 263981
1709	80222583 (3417, 3418)		UNCLASSIFIED	263981
1710	20754572 (3419, 3420)	Novel Protein sim. GBank gll5031735[re]NP_005760.1[p]HEC - N-acetylglucosamine B-O-sulfotransferase	UNCLASSIFIED	264556
1711	91013729 (3421, 3422)		sulfotransferase	85274572, 29331824, 29331826, 264768, 80431528, 35698423, 60432113, 264563
1712	95330184 (3423, 3424)	Novel Protein sim. GBank gll5454168[re]NP_006453.1[p]XAP4 - HBV associated factor	Contains protein domain (PF00641) - Zn-finger in Ran binding protein and others.	56984075, 264053, 264259, 29331822, 264089, 29331824, 29331827, 264107, 284110, 264511, 264592, 265011, 265018, 264883, 264886, 264889, 265020, 33657023, 263967, 33657109, 263974, 35698423, 35698555, 264630, 264636, 264558, 264569, 22278995, 264508, 264758, 18108351, 18108370, 263974, 18108374, 264634, 56182323, 83373044, 60432113
1713	84143453 (3425, 3426)	Novel Protein sim. GBank gll160409 (M69183) - mature-parasite-infected erythrocyte surface antigen [Plasmodium falciparum]	Contains protein domain (PF00643) - B-box zinc finger.	UNCLASSIFIED
1714	87420048 (3427, 3428)			22278997, 264757, 21906765, 265020, 285021, 264892, 56528486
1715	94260257 (3429, 3430)	Novel Protein sim. GBank gll5689537[db]BAA83052.1] - (AB028023) KIAA1100 protein [Homo sapiens]	UNCLASSIFIED	264509, 264905, 264906, 264907, 264908, 264909, 264910, 264591, 285011, 264786, 264788, 264769, 264691, 264692, 264632, 264634, 264635, 264636, 264637, 264556, 264639, 264564
1716	87400449 (3431, 3432)	Novel Protein sim. GBank gll4589469[db]BAA78761.1] - (AB012808) mBOCT [Mus musculus]	transport	56182575, 29331824, 60432289, 264109, 264909, 265007, 264600, 265019, 264886, 285020, 264693, 55811576, 264558, 60432113, 22279002

1717	87583223 (3433, 3434)	Novel Protein sim. GBank gl 2765411 emb CAA74749 - (Y14391) GTP-binding protein [Homo sapiens]		UNCLASSIFIED	264569, 264259, 29331825, 29331826, 29331828, 35696052, 264509, 264905, 264907, 264908, 264909, 264512, 265009, 264910, 264592, 264595, 264758, 264759, 265017, 264681, 264764, 264766, 264686, 18108357, 35695917, 264690, 264692, 264683, 264628, 264629, 35698423, 264630, 264631, 264635, 264636, 18108380, 264638, 264639, 18108398, 18108391
1718	87032828 (3435, 3436)	Novel Protein sim. GBank gl 2833262 sp Q14899 Y076_HUMAN - HYPOTHETICAL PROTEIN KIAA0076 (HA0936)		UNCLASSIFIED	265011, 264681, 264682, 264684, 264686, 264689, 21906765, 265021, 264691, 33657023, 264683, 18108370, 35695855, 264632, 264634, 264636, 18108398, 22279002
1719	94315258 (3437, 3438)	Novel Protein sim. GBank gl 4505197 ref NP_003473.1 pMLL2 - myeloid/lymphoid or mixed-lineage leukemia 2		UNCLASSIFIED	18108396, 65274572, 35696286, 22278997, 60432049, 58182181, 68714117, 60432289, 29331826, 35696052, 29331828, 264906, 29331830, 58182435, 264592, 60431735, 60433438, 5812038, 264759, 265010, 264600, 264601, 265017, 264448, 264764, 264288, 264769, 21906766, 21906769, 55811957, 265020, 265021, 52644150, 33657023, 33657109, 33657182, 27486262, 33657349, 35695763, 18108370, 60431528, 18108374, 35698423, 55811576, 35695855, 264631, 58182323, 264559, 264564, 264486
1720	84853063 (3439, 3440)	Novel Protein sim. GBank gl 2129478 pir J S51939 - chitinase (EC 3.2.1.14) precursor - beet		UNCLASSIFIED	58182575, 22278999, 264259, 29331824, 60432289, 29331827, 35696052, 264508, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 264758, 21906754, 265011, 264601, 264760, 264762, 264288, 264766, 264686, 18108357, 264689, 21906765, 55811957, 264693, 20281149, 264629, 18108374, 55811576, 65274791, 264630, 20281071, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 56182323, 87188518
1721	91722288 (3441, 3442)	Novel Protein sim. GBank gl 4886461 emb CAB43381.1 - (AL050280) hypothetical protein [Homo sapiens]		UNCLASSIFIED	22278994, 22278999, 29331822, 265008, 265007, 265008, 55812038, 21906754, 60174639, 265011, 87168559, 18108351, 18108354, 21906765, 21906766, 21906768, 21906769, 265020, 33657109, 18108370, 18108374, 264556, 60170394, 83373044, 18108385, 264486
1722	84134549 (3443, 3444)	Novel Protein sim. GBank gl 5688375 db BAA02868.1 - (AB030844) tudor repeat associator with PCTAIRE 2 [Rattus norvegicus]	Contains protein domain (PF00567) - kinase Tudor domain		56994075, 29331824, 29331828, 265009, 18108351, 21906768, 265020, 33657023, 18108374, 83373044

1723	95358181 (3445, 3448)	Novel Protein sim. GBank gij4428982(gbjAAD20633) - (AF126082) Art-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264488, 264687, 264768, 21906767, 21908768, 56182375, 55811857, 22278997, 22278998, 265020, 264258, 264692, 33657023, 29331822, 29331824, 29331825, 60433289, 33657182, 33656970, 33657349, 28146489, 264508, 264907, 18108370, 264628, 264908, 264909, 18108374, 55811576, 264510, 265008, 264511, 265007, 264910, 264632, 264591, 60432228, 264592, 60433356, 264594, 60433438, 264595, 83373044, 55812038, 33108954, 33657084, 87168518, 87168474, 265010, 265011, 87168559, 264600, 60432113, 264604, 265019, 264563, 264448, 264682, 264566, 264764, 264288, 264587, 264488, 264369, 264768
1724	87713808 (3447, 3448)	Novel Protein sim. GBank gij2340162 (AF005083) - dsRBP-ZFa [Xenopus laevis]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264905, 18108359, 264693, 264628, 264631, 264638, 264555, 264558, 264558, 264559, 35696286, 264259, 29331822, 35696052,
1725	85655191 (3449, 3450)	Novel Protein sim. GBank gij3152662 (AF064604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - homeobox Ank repeat		264508, 264509, 264905, 264905, 264907, 264908, 264909, 264910, 265009, 264591, 264601, 264760, 18108351, 264681, 264764, 264288, 264768, 264768, 21906769, 35695917, 264628, 35696423, 264630, 264631, 264632, 264635, 264636, 264638, 87168518, 264566
1726	85754255 (3451, 3452)			UNCLASSIFIED	28146498, 264683, 264689
1727	85286362 (3453, 3454)	Novel Protein sim. GBank gij4689348(gbjAAD27861.1)AF13256 - (AF132562) BcDNA.LD14270 [Drosophila melanogaster]		UNCLASSIFIED	264805, 265011, 264689, 21906768

1728	95348515 (3455, 3456)	Novel Protein sim. GBank gl 4406549 gb AAD20027 - (AF131738) Unknown [Homo sapiens]		UNCLASSIFIED	60424179, 18108397, 56182575, 22278995, 56994075, 35696286, 22278997, 22278998, 22278998, 264094, 60432049, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331826, 29331827, 35696052, 264905, 264906, 264907, 29331830, 56712502, 264908, 56182435, 264511, 265008, 265009, 60432229, 60433356, 33657402, 60433438, 264759, 21906754, 87168474, 265010, 265011, 87168559, 265017, 265018, 265019, 55811150, 264681, 264446, 264682, 264763, 264683, 264288, 264684, 264368, 264685, 264766, 264687, 264769, 21906764, 264686, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 265021, 265022, 264535, 264691, 264692, 33657023, 264693, 33657109, 18108370, 264628, 263972, 264629, 18108374, 18108376, 55810764, 65274791, 35695855, 264631, 264634, 264635, 60431850, 264636, 264638, 60170394, 264639, 83373044, 56526486, 87168518, 60432113, 22279000, 22279002, 264564, 264566
1729	91227948 (3457, 3458)	Novel Protein sim. GBank gl 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 8]		UNCLASSIFIED	264906, 264907, 264908, 264511, 264555, 83373044, 264596, 264566
1730	85483474 (3459, 3460)			UNCLASSIFIED	29331822, 29331825, 29331828, 264907, 264908, 264909, 265011, 264764, 264629
1731	88266088 (3461, 3462)	Novel Protein sim. GBank gl 831600 pir S47094 - hypothetical protein - rabbit		UNCLASSIFIED	52646842, 264907, 264909, 56182435, 55811386, 87168559, 265018, 265019, 264760, 52644229, 55811576
1732	91218878 (3463, 3464)	Novel Protein sim. GBank gl 4240231 dbj BAA74894.1 - (AB020678) KIAA0871 protein [Homo sapiens]		struct	56182575, 29331822, 29331824, 29331827, 66712502, 264591, 33657402, 60433356, 265019, 21906768, 21906769, 35695917, 265020, 265021, 264636, 56182323
1733	87617178 (3465, 3466)	Novel Protein sim. GBank gl 1575756 U70674 - m-Numb [Mus musculus]	Contains protein domain (PF00640) - Phosphotyrosine interaction domain (PTB/PID).	- synthase	264907, 264910, 33657402, 265010, 264681, 264683, 264684, 264686, 264769, 264691, 264692, 264693, 264628, 264636, 264556
1734	87785261 (3467, 3468)				264693

1735	88318638 (3469, 3470)	Novel Protein sim. GBank gi4836807 gb AAD30566.1 AF14678 - (AF146793) PFT27 [Mus musculus]	Contains protein domain (PF01169) - Uncharacterized protein family UPF0016	264488, 18108394, 18108398, 22278988, 80432049, 264259, 29331822, 264908, 265008, 265007, 265008, 265009, 264591, 33857402, 265010, 265011, 87168559, 265017, 18108351, 264682, 18108354, 264769, 264689, 21908765, 21908768, 21908769, 29148829, 29148784, 265021, 265022, 52844150, 18108364, 18108365, 33857109, 18108370, 18108374, 18108380, 18108385, 87168518, 264563, 18108390
1738	95362884 (3471, 3472)	Novel Protein sim. GBank gi4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	UNCLASSIFIED	264490, 264259, 60714117, 66712502, 56182435, 265006, 265008, 264910, 60433358, 87168559, 265017, 265019, 18108351, 265020, 265022, 33857023, 33657109, 264555, 60431650, 264637, 60170394, 264558, 264639, 264564
1737	88165549 (3473, 3474)	Novel Protein sim. GBank gi4885647 ref NP_005472.1 pTRAP - thyroid hormone receptor-associated protein complex component	kinase	265018, 265019, 22279002
1738	85788811 (3475, 3476)	Novel Protein sim. GBank gi2225941 emb CAA687141 - (Y08460) Mdes protein [Mus musculus]	UNCLASSIFIED	264908, 264909, 265008, 264910, 264566
1739	87328576 (3477, 3478)	Novel Protein sim. GBank gi2143607 pir S68695 - B/K protein - rat	Contains protein domain (PF00168) - C2 domain	28331822, 29331830, 264591, 265011,
1740	83592839 (3479, 3480)	Novel Protein sim. GBank gi4809 emb CAA443091 - (X62452) YCR601 [Saccharomyces cerevisiae]	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	35696052, 264603, 264557
1741	95010100 (3481, 3482)	Novel Protein sim. GBank gi4883898 gb AAD31695.1 AF13042 - (AF130420) serine protease-like protein isoform [Homo sapiens]	traffic	264604, 21906764, 18108384, 264629, 35695855, 264638
1742	85788814 (3483, 3484)	Novel Protein sim. GBank gi4505193 ref NP_003667.1 pMLD1 - membrane fatty acid (lipid) desaturase	UNCLASSIFIED	60432289, 29331827, 264509, 265009, 60432229, 264759, 265017, 264767, 264688, 264689, 21908769, 265020, 33857109
1743	86966475 (3485, 3486)	Novel Protein sim. GBank gi728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	264908, 264910, 264758, 265011, 264631, 264638, 264568
1744	91224003 (3487, 3488)	Novel Protein sim. GBank gi728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	UNCLASSIFIED	265017, 265020, 264692
1745	20280075 (3489, 3490)	Novel Protein sim. GBank gi731756 sp P38873 YHY8_YEAST - HYPOTHETICAL 175.8 KO PROTEIN IN GND1-K11 INTERGENIC REGION	UNCLASSIFIED	22278998, 264508, 264907
1746	94326110 (3491, 3492)	Novel Protein sim. GBank gi731756 sp P38873 YHY8_YEAST - HYPOTHETICAL 175.8 KO PROTEIN IN GND1-K11 INTERGENIC REGION	UNCLASSIFIED	
1747	94324333 (3493, 3494)	Novel Protein sim. GBank gi1658503 (U75467) - Alu [Drosophila melanogaster]	transcript factor	264558 65274791, 264639, 264559

1748	88003580 (3495, 3498)	Novel Protein sim. GBank gi 4504511 ref NP_001530.1 pHSJ2 - heat shock protein, DNAJ-like 2	Contains protein domain (PF00584) - DnaJ central domain (4 repeats)	eph	264489, 5618257, 29331824, 56182435, 284112, 265007, 265019, 264764, 21906768, 265020, 264691, 55811578, 264635, 264555, 264556, 264557, 264559 264106
1749	83363091 (3497, 3498)	Novel Protein sim. GBank gi 5650780 gb AA045948.1 AF151968 - (AF151968) RGS protein RGS-17 [Gallus gallus]	Contains protein domain (PF00615) - Regulator of G protein signaling domain	oncogene	
1750	84321684 (3499, 3500)	Novel Protein sim. GBank gi 4996894 gb AAC28444.2 - (AF065184) hyperpolarization-activated, cyclic nucleotide- gated channel 2 [Homo sapiens]			
1751	83373058 (3501, 3502)	Novel Protein sim. GBank gi 2760161 dbj BA021841 - (AB010054) outer arm dynein light chain 2 [Anthodidaris crassispina]	Contains protein domain (PF00560) - Leucine Rich Repeat	ATPase_associated	33657402, 264288, 52644150, 263974, 83373044
1752	86456530 (3503, 3504)	Novel Protein sim. GBank gi 3919482 sp P74346 YG29_SYNY3 - HYPOTHETICAL 38.0 KO PROTEIN SLR1829	Contains protein domain (PF00849) - RNA pseudouridylylate synthase	deaminase	264510, 264593, 264682, 21906765, 18108370
1753	84235159 (3505, 3506)	Novel Protein sim. GBank gi 2852636 (AF007155) - unknown [Homo sapiens]	Contains protein domain (PF01553) - Acyltransferase	phosphatase	56994075, 22278996, 264908, 60170831, 264682, 264764, 264369, 264288, 264685, 264687, 21906768, 264692, 264693, 65274820, 65274791, 35695855, 264637, 264564
1754	88095323 (3507, 3508)	Novel Protein sim. GBank gi 731421 sp P39981 YE44_YEAST - HYPOTHETICAL 53.3 KD PROTEIN IN HXT8-CANT INTERGENIC REGION		transport	264488, 35696286, 264509, 264908, 264907, 264908, 264909, 264511, 264910, 264591, 33657402, 264594, 264757, 264758, 264600, 264804, 264762, 264763, 264685, 264766, 264691, 264628, 35696423, 264632, 264634, 264637, 264638, 263981, 264558, 264639, 264563, 264564, 264565, 264566, 264567, 264688
1755	78470282 (3509, 3510)	Novel Protein sim. GBank gi 1178422 (U43194) - rhophilin [Mus musculus]		UNCLASSIFIED	
1756	82962614 (3511, 3512)	Novel Protein sim. GBank gi 4432860 gb AAD20708 - (AC006300) putative glucose-induced repressor protein [Arabidopsis thaliana]			52646842, 22278994, 22278995, 56994075, 22278996, 22278997, 264259, 28331822, 60432289, 28331827, 33656970, 265006, 265009, 60432229, 60433356, 60433438, 33109954, 21906754, 265017, 265018, 265019, 264448, 264369, 264288, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 265022, 264692, 27486262, 27486264, 18108376, 20281152, 264558, 18108388, 87168518, 60432113, 22279000, 22279002, 264482
1757	95357380 (3513, 3514)	Novel Protein sim. GBank gi 5441615 jemb CA846856.1 - (AJ388557) zinc finger protein [Canis familiaris]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	22278997, 264259, 60432289, 29331827, 264908, 52644045, 265008, 264593, 265019, 264766, 21908768, 65274620, 18108385, 60432113, 264566, 264487

1758	87612871 (3515, 3516)	Novel Protein sim. GBank gl 3881040 emb CAA184031 - (AL021497) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	22278994, 22278999, 29331822, 29331824, 29331825, 33658970, 284508, 285008, 285007, 265009, 284591, 33657402, 33109854, 87168474, 264600, 265017, 285018, 21906769, 265020, 265021, 33857023, 33857109, 264629, 18108374, 35895855, 284632, 52844332, 22278002, 264563
1759	36994372 (3517, 3518)			UNCLASSIFIED	264759
1760	87329716 (3519, 3520)	Novel Protein sim. GBank gl 5262748 emb CAB45688.1 - (AJ133120) Proline rich synapse associated protein 2 [Rattus norvegicus]		UNCLASSIFIED	56182575, 60432048, 35896052, 284905, 284906, 284907, 264908, 284909, 285006, 285009, 284910, 60432229, 284592, 284595, 55812038, 284758, 264762, 18108351, 264764, 264766, 264768, 264769, 21906765, 55811857, 35895917, 284690, 284692, 284628, 284629, 55811576, 35898423, 284632, 284634, 284636, 284557, 284639, 60432113, 284585, 284486
1761	87409588 (3521, 3522)	Novel Protein sim. GBank gl 127749 sp P10569 MYSC_ACACA - MYOSIN IC HEAVY CHAIN	Contains protein domain (PF00618) - Guanine nucleotide exchange factor for Ras-like GTPases; N-terminal motif	UNCLASSIFIED	29331822, 284910, 284685, 284686
1762	95318887 (3523, 3524)	Novel Protein sim. GBank gl 3169158 (AC004770) - BC289730_2 [Homo sapiens]	Contains protein domain (PF00173) - desaturase Heme-binding domain in cytochrome b5 and oxidoreductases		22278999, 284259, 264905, 264907, 60170831, 285010, 265011, 285017, 264448, 21906765, 21906766, 21906767, 21906768, 265021, 284690, 33857109, 18108374, 284558, 60170394
1763	91224013 (3525, 3526)	Novel Protein sim. GBank gl 4809028 gb AAD30062.1 - (AF132856) suppressor of G2 allele of skp1 homolog [Homo sapiens]			56181888, 29331825, 35896052, 284905, 284906, 284909, 264763, 284682, 284769, 35895917, 265022, 33857023, 18108374, 35898423, 284634
1764	87757697 (3527, 3528)	Novel Protein sim. GBank gl 1360689 pir CGHU1V - collagen alpha 1(V) chain precursor - human	Contains protein domain (PF01410) - collagen Fibrillar collagen C-terminal domain		22278998, 284259, 35896052, 29331828, 56182435, 285008, 285017, 265018, 284448, 284288, 21906766, 21906767, 29148627, 35895917, 284691, 33857023, 60432113, 22279002
1765	91230091 (3529, 3530)	Novel Protein sim. GBank gl 466806 pir IS35503 - finger protein neutralized - fruit fly (Drosophila melanogaster)		UNCLASSIFIED	264488, 18108394, 22278995, 22278997, 22278999, 284259, 284104, 264508, 284905, 264807, 284511, 265007, 265008, 264910, 285009, 21906754, 265010, 265017, 284603, 265018, 265019, 18108351, 284682, 284448, 264369, 264288, 264766, 18108358, 21906766, 21906767, 29148627, 29148628, 35895917, 265020, 265021, 284692, 284628, 264629, 18108374, 283976, 284636, 83373044, 22279000, 22279002

1766	95081201 (3531, 3532)	Novel Protein sim. GBank gi 249087 sp Q09332 UGGG, DROME - UDP- GLUCOSE:GLYCOPROTEIN GLUCOSYLTRANSFERASE PRECURSOR (DUGT)		glycoprotein	52645156, 87168559, 60170615, 33657023, 284683, 33657109, 27486261, 264555, 83373044
1767	87755998 (3533, 3534)	Novel Protein sim. GBank gi 4176443 emb CAA18263.1 - (AL022238) dJ1042K10.4 (novel protein) [Homo sapiens]		UNCLASSIFIED	265017, 265019, 264686, 264768, 265020, 264692
1768	80253216 (3535, 3536)			UNCLASSIFIED	29331824, 29331825, 264581, 56182323
1769	87388988 (3537, 3538)			UNCLASSIFIED	264563
1770	85413144 (3539, 3540)	Novel Protein sim. GBank gi 116204 sp P00736 C1R, HUMAN - COMPLEMENT C1R COMPONENT PRECURSOR	Contains protein domain (PF00089) - Trypsin	complement	264488, 264768, 264769, 56182575, 55811957, 264890, 264691, 35696052, 264905, 264509, 264906, 264907, 264628, 264908, 264909, 264910, 264634, 264635, 264636, 264556, 264757, 264758, 55812038, 65274444, 264760, 264563, 264762, 264764, 264694, 264766
1771	94233542 (3541, 3542)	Novel Protein sim. GBank gi 3914181 sp P56558 OGT1_RAT - UDP-N- ACETYLGLUCOSAMINE-PEPTIDE N- ACETYLGLUCOSAMINYLTRANSFERASE 110 KD SUBUNIT (O-GLCNAC TRANSFERASE P110 SUBUNIT)	Contains protein domain (PF00515) - TPR Domain	transferase	264758, 264600, 264369, 55811957, 265020, 83373044, 22278000
1772	87643510 (3543, 3544)	Novel Protein sim. GBank gi 4959442 gb AA034351.1 AF12136 - (AF121360) DNZDHH/CNEW1 zinc finger protein 11 [Drosophila melanogaster]	Contains protein domain (PF01529) - DHH zinc finger domain		22278998, 29331828, 33109954, 265018, 265019, 264784, 21906765, 265020, 265021, 264556
1773	94116824 (3545, 3546)	Novel Protein sim. GBank gi 3978464 (AF085693) - G protein-coupled receptor kinase-associated ADP ribosylation factor GTPase-activating protein [Rattus norvegicus]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	potassium_channel	65274572, 56182575, 22278996, 35696286, 22278999, 264259, 29331824, 60424259, 29331825, 60432289, 35696052, 264106, 264509, 264906, 264907, 29331830, 264908, 52644045, 264511, 265008, 265007, 265008, 60170831, 60433438, 264758, 55811388, 87168559, 265017, 264604, 265019, 55811150, 264288, 56181562, 264689, 21906768, 21906767, 21906768, 21906769, 55811957, 265020, 265022, 52644150, 264691, 33657023, 264692, 264693, 60431528, 35696423, 35695855, 264636, 56182323, 18108387, 56526486, 22279000, 22279002, 264563, 264564, 264565, 264566, 264567
1774	94232573 (3547, 3548)	Novel Protein sim. GBank gi 2495698 sp Q15034 Y032_HUMAN - HYPOTHETICAL PROTEIN KIAA0032	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	UNCLASSIFIED	65274572, 56182575, 35696052, 55812038, 33109954, 21906754, 265017, 21906767, 21906768, 21906769, 265020, 264691, 264636, 56182323, 22278002

1775	95359330 (3549, 3550)	Novel Protein sim. GBank gl 1469199 dbj BAA09487 - (D50928) The KIAA0138 gene product is novel. [Homo sapiens]		UNCLASSIFIED	65274572, 56182575, 56994075, 35696286, 22278987, 29331822, 29331828, 60432289, 29331828, 35696052, 29331830, 68712502, 264828, 56182435, 264511, 265007, 265009, 60170831, 60432229, 80433438, 55812038, 21906754, 85658542, 87168559, 264601, 265017, 265018, 265019, 264762, 284448, 264288, 264689, 21906765, 21906768, 21906767, 21906768, 265020, 265021, 285022, 264691, 33857023, 264892, 33657109, 27486261, 33657349, 18108370, 18108377, 35696423, 55811576, 35695855, 264632, 264634, 264636, 264639, 56182323, 83373044, 56326486, 87168518, 60432113, 22279000, 22279002, 264482, 264486, 264910
1776	94133756 (3551, 3552)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]			
1777	87447171 (3553, 3554)	Novel Protein sim. GBank gl 3218938 sp P87115 YDK9 SCHPO - HYPOTHETICAL 118.5 KD PROTEIN C20G8.08C IN CHROMOSOME 1		nucl_rept	56994075, 29331828, 265008, 87168474, 265017, 265018, 264761, 55811150, 264764, 56181562, 264689, 21906765, 21906768, 21906769, 35695917, 264690, 33657023, 35695763, 60431528, 35696423, 55811576, 35695855, 22279000, 22279002, 264564, 29331828, 29331827, 35696052, 264512, 265007, 265009, 265017, 265019, 264762, 18108351, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264691, 264693, 18108370, 264556, 83373044
1778	94851624 (3555, 3556)	Novel Protein sim. GBank gl 3875648 emb CAA91454.1 - (Z68561) Similarity to Human rab13 protein (PIR Acc. No. A49647). Contains the ATP/GTP-binding site motif (PROSITE PS00017); cDNA EST EMBL:M89412 comes from this gene; cDNA EST yk212g9.3 comes from this gene; cDNA EST yk212g9.		UNCLASSIFIED	
1779	94133758 (3557, 3558)	Novel Protein sim. GBank gl 4589676 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]		UNCLASSIFIED	29148627, 35696286, 29147620, 265008, 265007, 265008, 18108385, 65274727, 264482, 264369, 264768
1780	87023497 (3559, 3560)		Contains protein domain (PF00807) - Apidaecin	UNCLASSIFIED	264107, 33657109, 56526486
1781	84047477 (3561, 3562)			UNCLASSIFIED	264508, 264905, 264639
1782	88094607 (3563, 3564)	Novel Protein sim. GBank gl 729225 sp P4123 CTXN_RAT - CORTEXIN			264259, 29331822, 264508, 264905, 264906, 264907, 264908, 265007, 265009, 264910, 264591, 264758, 264764, 264288, 264768, 264769, 264635, 264636, 264637, 264639, 264563
1783	85717905 (3565, 3566)	Novel Protein sim. GBank gl 2257543 dbj BAA21436 - (AB004538) protein arginine N-methyltransferase [Schizosaccharomyces pombe]		interferon	264768

1784	95197093 (3567, 3568)	Novel Protein sim. GBank gi 1755049 (U55042) - myosin X [Bos taurus]	Contains protein domain (PF00169) - struct PH domain	35696286, 284259, 35696052, 284508, 284805, 284908, 284907, 68712502, 284908, 284909, 285007, 285008, 285009, 284910, 284591, 284594, 284757, 284758, 284759, 285010, 285011, 284601, 284602, 284604, 284605, 18108351, 284762, 284763, 284784, 284369, 284766, 284887, 284788, 284688, 21908768, 35695917, 284690, 284691, 284692, 284693, 284628, 18108374, 35696423, 284631, 284632, 284635, 284637, 284638, 284639, 18108385, 22279000, 22279002, 284565, 284568, 284488
1785	95357475 (3569, 3570)	Novel Protein sim. GBank gi 4589552[db][BAA76798.1] - (AB023171) KIAA0954 protein [Homo sapiens]	UNCLASSIFIED	65274572, 284259, 29331822, 29331824, 29331825, 29331827, 29331828, 284905, 284908, 284908, 66712502, 56182435, 284511, 285007, 60433356, 55811150, 284683, 284369, 284687, 52844229, 21908767, 52844150, 33857023, 65274620, 33857182, 65274791, 35695855, 284555, 65274727, 22279002
1786	85298485 (3571, 3572)	Novel Protein sim. GBank gi 117788[sp]P28770(CYA4_RAT ADENYLATE CYCLASE, TYPE IV(ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)	UNCLASSIFIED	284808, 35698423, 284636
1787	87434784 (3573, 3574)	Novel Protein sim. GBank gi 3877175[emb]CAA90338.1 - (Z50028) cDNA EST yk32'h8.5 comes from this gene; cDNA EST EMBL:D88896 comes from this gene; cDNA EST yk395f9.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	284488, 284905, 284908, 284909, 284595, 284784, 284786, 284692, 60431528, 284629, 284636, 284564, 284566
1788	91228779 (3575, 3576)		UNCLASSIFIED	284488, 83373044
1789	88084529 (3577, 3578)	Novel Protein sim. GBank gi 2088669 (AF003130) - F55A12.9 gene product [Caenorhabditis elegans]	UNCLASSIFIED	284488, 29331828, 284909, 18108351, 284288, 285021, 284555, 284638
1790	82489734 (3579, 3580)			35696052, 284905, 284908, 284907, 284908, 284909, 285008, 284910, 284758, 285011, 285018, 284784, 284786, 284769, 284628, 284635

1791	95197259 (3581, 3582)	Novel Protein sim. GBank gll2114321[ob]BAA20037] - (D88733) membrane glycoprotein [Equine herpesvirus 1]	Contains protein domain (PF00047) - Immunoglobulin domain	glycoprotein	264488, 264686, 264687, 264768, 18108394, 264769, 18108397, 264259, 264691, 264692, 33857023, 264693, 264509, 264905, 264906, 264628, 264907, 264629, 264908, 264909, 264510, 265008, 264511, 265008, 264630, 265009, 264631, 264910, 264632, 264634, 264635, 264555, 264636, 264592, 264637, 264593, 264638, 18108381, 264639, 264758, 265010, 265011, 264602, 22279000, 264604, 264760, 264564, 264681, 264762, 264565, 264763, 264683, 264588, 264764, 264288, 264684, 264567, 18108354, 18108391, 264685, 264766
1792	87782690 (3583, 3584)	Novel Protein sim. GBank gll4337106[gb]AAD18082] - (AF129758) BAT4 [Homo sapiens]	Contains protein domain (PF01585) - G-patch domain	UNCLASSIFIED	22278997, 264259, 264508, 265007, 33857402, 87188559, 264369, 33857023, 35895855, 20281071, 264559, 18108367, 87188518
1793	95337877 (3585, 3586)	Novel Protein sim. GBank gll5578331[gb]AAD45504.1[AF14573] - (AF145732) endoplasmic reticulum alpha-mannosidase I [Homo sapiens]	Contains protein domain (PF01532) - ATPase-associated Glycosyl hydrolase family 47	-ATPase_associated	85274572, 22278995, 22278998, 22278997, 22278999, 264093, 264259, 29331824, 86714117, 60432289, 29331827, 29331828, 264103, 264105, 29331830, 265007, 264910, 265009, 60170831, 60433356, 21908754, 265010, 265017, 265019, 264681, 264682, 264288, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 265022, 60170815, 52644150, 33857023, 33857109, 18108370, 18108374, 85274791, 20281071, 60432113, 22279000, 264482, 264564
1794	87759806 (3587, 3588)	Novel Protein sim. GBank gll4814604[emb]CAB43877.1] - (AL050388) hypothetical protein [Homo sapiens]	Contains protein domain (PF01788) - Putative snRNA binding domain	UNCLASSIFIED	18108394, 22278995, 22278999, 264259, 29331822, 29331824, 29331825, 29146498, 29146499, 264508, 264905, 52644045, 264112, 265006, 265008, 264910, 60433356, 264757, 55812038, 87188474, 265011, 265017, 18108351, 264783, 264448, 264683, 264369, 21908765, 21908766, 21908767, 21908769, 29148784, 35895917, 60170815, 33857023, 264629, 18108374, 18108378, 35896423, 35895855, 264556, 264557, 264638, 264558, 18108385, 264564
1795	78747856 (3589, 3590)			UNCLASSIFIED	264632, 264635, 264636, 264595, 264596, 264907, 264566, 264909
1796	88568486 (3591, 3592)	Novel Protein sim. GBank gll585084[sp]Q07803[EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)]		glycoprotein	264488, 264907, 264909, 264594, 264595, 264768, 264687, 21908765, 21908767, 264628, 264630, 264559

1787	91223219 (3593, 3594)	Novel Protein sim. GBank gl 1842111 (U87586) - decoy [Arabidopsis thaliana]		ribosomalprot	22278996, 22278997, 22278998, 22278999, 29331822, 264910, 60170831, 21906754, 52644229, 21906765, 21906766, 21906769, 35695917, 265022, 52644150, 264691, 33657023, 263967, 33657109, 22279000
1788	91221276 (3595, 3596)	Novel Protein sim. GBank gl 2832906[dbj BAA24608.1] - (D89340) dipeptidyl peptidase III [Rattus norvegicus]		peptidase	22278994, 56994075, 22278997, 22278998, 22278999, 264259, 29331826, 60432289, 29331828, 33656970, 265008, 60432229, 264757, 80433438, 21906754, 33657084, 87168559, 265017, 18108351, 264682, 264446, 264288, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 33657023, 33657182, 27486261, 27486265, 33657349, 263973, 18108374, 55811576, 35695855, 18108365, 87168518, 22279000, 264486
1789	86321713 (3597, 3598)	Novel Protein sim. GBank gl 5689541[dbj BAA83054.1] - (AB029025) KIAA1102 protein [Homo sapiens]		eph	264908, 21906754, 21906767, 21906769, 265020, 33657023, 264692, 264693, 264404, 22279000
1800	87080116 (3599, 3600)	Novel Protein sim. GBank		UNCLASSIFIED	264691, 264556, 264566
1801	95060723 (3601, 3602)	gl 4680879[gb AAD27729.1] (AF132954) CGI-20 protein [Homo sapiens]			52644045, 265007, 264632
1802	87771012 (3603, 3604)	Novel Protein sim. GBank gl 134920[sp P21997/SSGP_VOLCA - SULFATED SURFACE GLYCOPROTEIN 185 (SSG 185)]			35696288, 66714117, 264508, 264509, 58182435, 264512, 18108351, 264688, 55811957, 264692, 55811576, 35695855, 264486
1803	95060725 (3605, 3606)	Novel Protein sim. GBank gl 4680879[gb AAD27729.1] (AF132954) CGI-20 protein [Homo sapiens]			264686, 264488, 264687, 264489, 264768, 264789, 264689, 21906769, 35696288, 35695917, 264259, 264691, 264692, 264693, 20281098, 18108364, 35696052, 264508, 264509, 264905, 264906, 18108370, 264628, 264907, 68712502, 264908, 264909, 18108374, 18108376, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264631, 264632, 264634, 264635, 264591, 264636, 264637, 264592, 264638, 264593, 264639, 264594, 83373044, 264758, 264596, 18108385, 18108387, 265011, 264760, 264563, 18108351, 264762, 264564, 264448, 264565, 264763, 264583, 264764, 264586, 264288, 264486, 264567, 264765, 264766

1804	87770203 (3607, 3608)	Novel Protein sim. GBank gl 3878914 emb CAA8538.1 - (Z74043) predicted using GeneFinder: cDNA EST EMBL:C13850 comes from this gene; cDNA EST EMBL:C11575 comes from this gene; cDNA EST yk34314.5 comes from this gene [Caenorhabditis elegans]			52646365, 22278997, 22278999, 264905, 264908, 264909, 264910, 21908754, 264766, 21908765, 21908768, 35695917, 265020, 265022, 264691, 264637, 264639, 22279000, 264564, 264566
1805	95330375 (3609, 3610)	Novel Protein sim. GBank gl 5453644 ref NP_006461.1 pEBBP - estrogen-responsive B box protein			29331824, 29331825, 29331826, 29331827, 29331828, 87168559, 264288, 264687, 52644229, 35696423, 264636, 60432113
1806	94133762 (3611, 3612)	Novel Protein sim. GBank gl 4589576 dbj BAA76857.1 - (AB023230) KIAA1013 protein [Homo sapiens]	struct		264094, 264105, 264908, 35696423, 265006, 265007, 265008, 264555, 264592, 265011, 265018, 264369
1807	86943032 (3613, 3614)				29331824, 264908, 264910, 33657023, 263978
1808	87642711 (3615, 3616)	Novel Protein sim. GBank gl 4884079 emb CAB43235.1 - (AL050008) hypothetical protein [Homo sapiens]	UNCLASSIFIED		264468, 35696286, 66714117, 35696052, 66712502, 264592, 60433436, 52644296, 265010, 264683, 264369, 264689, 55811957, 35695917, 33657109, 35695763, 55810764, 18108379, 35696423, 35695855, 56182323, 264363, 264584, 264487
1809	95321468 (3617, 3618)	Novel Protein sim. GBank gl 1918927 (U87965) - putative G protein [Mus musculus]	UNCLASSIFIED		264594, 55811150, 264686, 29146629, 29148784, 264690, 264629, 18108374, 264556, 264557, 264558
1810	88086316 (3619, 3620)	Novel Protein sim. GBank gl 1352944 sp P47179 YJBP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DAL5 INTERGENIC REGION PRECURSOR	UNCLASSIFIED		264468, 35696052, 264905, 264906, 264907, 264908, 264909, 264511, 265009, 264910, 264592, 264593, 264594, 33657402, 264757, 264595, 264758, 264596, 264759, 264600, 264601, 264762, 264683, 264764, 264288, 264684, 264766, 264767, 264688, 264768, 264687, 264769, 264689, 265021, 264690, 264691, 264693, 264628, 264629, 18108374, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264563, 264566, 264486, 264567
1811	88086272 (3621, 3622)	Novel Protein sim. GBank gl 2134984 pir j137275 - death-associated protein kinase (EC 2.7.1.-) - human	kinase Ank repeat	Contains protein domain (PF00023)	264488, 264259, 264508, 264509, 264905, 264906, 264907, 56182435, 264511, 264512, 264910, 264758, 265011, 264600, 264604, 18108354, 264768, 264686, 264769, 264534, 60170615, 33657023, 264629, 264631, 264639, 264563, 264482, 264483
1812	79245772 (3623, 3624)				29331822, 29331824, 265018, 18108351, 21908769

1813	88080972 (3625, 3628)	Novel Protein sim. GBank gi 5031636 gb AAD36326.1 AF07372 - (AF07372) EH domain-binding mitotic phosphoprotein [Homo sapiens]	Contains protein domain (PF01417) - ENTH domain	glucoamylase	56182575, 284259, 29331824, 66714117, 29331828, 35696052, 284509, 284905, 284908, 264907, 284908, 6671502, 284909, 265007, 284910, 284591, 284593, 55812038, 265011, 265018, 264760, 264682, 284764, 284683, 284369, 284768, 284788, 284769, 21906768, 21906768, 284691, 284693, 18108374, 35695855, 284634, 284635, 284637, 284639, 284559, 22279000, 22279002, 284568
1814	88178047 (3627, 3628)	Novel Protein sim. GBank gi 3643608 (AC005395) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	284488, 35696286, 22278998, 284092, 284094, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 284105, 264107, 52644045, 56182435, 285009, 60432229, 60433356, 87168474, 87168559, 284369, 284288, 21906765, 35895917, 265021, 265022, 33657023, 33657109, 18108374, 35696423, 284638, 56528486, 264482
1815	85296473 (3628, 3630)	Novel Protein sim. GBank gi 117788 sp P26770 CYA4_RAT ADENYLATE CYCLASE, TYPE IV (ATP PYROPHOSPHATE-LYASE) (ADENYL CYCLASE)		struct	22278998, 284508, 284509, 284907, 284908, 284910, 265011, 284760, 284766, 284834, 284636
1816	83738845 (3631, 3632)	Novel Protein sim. GBank gi 1176823 sp P41846 Y096_CAEEL - HYPOTHETICAL 93.9 KD PROTEIN T20812.6 IN CHROMOSOME III		UNCLASSIFIED	18108394, 18108397, 284509, 284907, 284908, 284909, 285008, 284591, 265011, 265017, 284687, 284688, 285022, 284691, 18108362, 18108368, 18108370, 18108374, 18108378, 284635, 284557, 284564, 284567, 284488, 22278997, 22278999, 60432049, 29331822, 29331824, 60432289, 52644045, 60170831, 265017, 265018, 265019, 18108351, 264682, 52644229, 21906765, 21906767, 21906768, 52644150, 33657023, 33657109, 27486282, 18108370, 18108374, 60170394, 56182323, 22279002
1817	86095288 (3633, 3634)	Novel Protein sim. GBank gi 3766377 emb CAA21428 - (AL031907) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	-histone	35866286, 60433356, 284758, 284369, 284686, 21906768, 284693, 284632
1818	85806775 (3635, 3636)	Novel Protein sim. GBank gi 3879121 emb CAA84370 - (Z70310) predicted using GeneFinder; Similarity to Mouse ankyrin (PIR Acc. No. S3771); cDNA EST EMBL.T01923 comes from this gene; cDNA EST EMBL.D32335 comes from this gene; cDNA EST EMBL.D32723 comes from this gene; cDNA EST E...	Contains protein domain (PF00023) - Ank repeat	transcript factor	22278995, 22278997, 22278999, 284259, 29331826, 284908, 265007, 265008, 285009, 60432229, 265017, 265018, 265019, 284448, 284286, 21906768, 21906768, 265020, 18108381, 18108384, 22279000, 22279002, 284567
1819	87759572 (3637, 3638)	Novel Protein sim. GBank gi 5031865 ref NP_005771.1 pLHFP - lipoma HM/GIC fusion partner		UNCLASSIFIED	

1820	87769455 (3839, 3840)				284905, 284807, 284594
1821	80431510 (3841, 3842)				284807, 284788, 283978
1822	91221523 (3843, 3844)	Novel Protein sim. GBank gi 4884130 emb CAB43272.1 - (AL050101) hypothetical protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 284259, 29331824, 29331825, 29331828, 35688052, 29331828, 284908, 29331830, 60170831, 284591, 284593, 60433356, 284598, 285017, 285019, 18108351, 284783, 284683, 21906765, 21906787, 21906788, 21906789, 35695917, 285020, 285021, 33857023, 18108364, 18108370, 35695855, 22279000, 22279002, 284488, 284259, 284511, 284288, 284768, 284693, 35696423, 284634, 18108385, 284486
1823	85522330 (3845, 3846)			UNCLASSIFIED	284807, 284908, 284909, 284511, 284631, 284634, 284635, 284637, 284638, 284639, 284758, 284588
1824	86612025 (3847, 3848)	Novel Protein sim. GBank gi 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00047) - Immunoglobulin domain	UNCLASSIFIED	60432049, 284910, 284487
1825	87430125 (3849, 3850)	Novel Protein sim. GBank gi 3036803 emb CAA18493 - (AL022373) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	
1826	91723612 (3851, 3852)	Novel Protein sim. GBank gi 4680885 gb AAD27732.1 AF13295 - (AF132957) CGI-23 protein [Homo sapiens]	ATPase associated		52844507, 52845156, 52846842, 22278994, 22278996, 56994075, 284259, 60432049, 52845080, 35688052, 66712502, 52844045, 285008, 285009, 60432229, 60433356, 60433438, 52846317, 52844298, 285011, 87188558, 284448, 284288, 284369, 284688, 52644229, 284689, 21906765, 21906788, 285020, 60170815, 52844150, 33657023, 27488262, 27488264, 27486265, 35695763, 35696423, 35695855, 83373044, 87168518, 284404, 22279002
1827	81647212 (3853, 3854)				284758

1828	95074017 (3655, 3656)	Novel Protein sim. GBank g k4503571 ref NP_001419.1 pENO1 - enolase 1, (alpha)	Contains protein domain (PF00113) - Enolase	oncogene	264488, 52646842, 56182576, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 264105, 264508, 264907, 66712502, 52844045, 56182435, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 60432229, 264593, 60433356, 60433438, 264758, 33108954, 21908754, 87168474, 265010, 265011, 87168559, 265017, 265019, 264761, 264762, 264448, 264764, 264683, 264288, 264369, 18108355, 264768, 18108357, 18108358, 264688, 264769, 264689, 21906768, 21906769, 35695917, 285021, 60170615, 33657023, 33657349, 263972, 55811576, 35695855, 264635, 264555, 264556, 264638, 264557, 87168518, 22279000, 22279002, 264563, 264482, 264555, 264484, 264567
1829	80197720 (3657, 3658)				264508, 264634, 264509, 264482, 28331827, 264908, 265009, 264910
1830	94312842 (3659, 3660)	Novel Protein sim. GBank g 2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		nuclease	52645156, 22278994, 22278995, 35696286, 22278998, 22278997, 22278998, 22278999, 29331822, 29331825, 35696052, 52646317, 52644298, 87168559, 265019, 21908765, 21908766, 21908767, 21906768, 21908769, 35695917, 265021, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 35695783, 283974, 35696423, 35695855, 52844332
1831	94138063 (3661, 3662)			UNCLASSIFIED	29331824, 35696052, 29331830, 264595, 264758, 265010, 265019, 265022, 264693, 65274791 264602
1832	94521863 (3663, 3664)	Novel Protein sim. GBank g 1330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk48e8.5; coded for by C. elegans cDNA yk48d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk48e8....			

1833	85314184 (3665, 3668)	Novel Protein sim. GBank gi 5174413 ref NP_006028.1 pCDC4 - CDC42-binding protein kinase beta (DMPK-like)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	22278994, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 35696052, 29146499, 264508, 264509, 264908, 264907, 68712502, 264908, 5284045, 264909, 264512, 265008, 264591, 264593, 60433358, 21908754, 33857084, 265011, 265017, 264604, 265018, 265019, 264681, 18108351, 264683, 264288, 264685, 264766, 264687, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 265020, 265021, 264690, 264692, 33657023, 65274620, 33657182, 27486284, 33657349, 65274791, 264634, 264635, 264556, 264557, 264558, 264559, 18108385, 56528486, 87168518, 60432113, 22279000, 22279002, 264563
1834	80562790 (3667, 3668)			264259, 264807, 264689, 22279000, 22279002
1835	84135718 (3669, 3670)		UNCLASSIFIED	22278998, 29331822, 29331826, 87168474, 264603, 21908768, 263976, 35695855, 83373044
1836	87348450 (3671, 3672)	Novel Protein sim. GBank gi 4759288 ref NP_004268.1 UCP4 - uncoupling protein 4	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	29331825, 264908, 265019, 264764, 264686, 21908765, 264635
1837	84234297 (3673, 3674)	Novel Protein sim. GBank gi 3334400 sp Q24574 UBPE_DROME - UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 64E (UBIQUITIN THIOLESTERASE 64E) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 64E) (DEUBIQUITINATING ENZYME 64E)	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	22278995, 29146499, 265006, 265008, 265009, 265010, 264683, 21906765, 29148627, 29148629, 265020, 265021, 265022, 65274620, 18108370, 18108374, 264556, 18108385
1838	84324369 (3675, 3676)	Novel Protein sim. GBank gi 1362599 pir JAS6154 - Abl substrate ena (enabled) - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00568) - WH1 domain	29331822, 265017, 264760, 265020, 83373044
1839	87456508 (3677, 3678)	Novel Protein sim. GBank gi 2117310 emb CAC09116.1 - (Z95620) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	60433438, 264601, 21908765, 21906766, 265021, 33657109, 264556
1840	87391708 (3678, 3680)	Novel Protein sim. GBank gi 127560 sp P23249 MOV10 - MOUSE - PROTEIN MOV-10	UNCLASSIFIED	264693
1841	85818445 (3681, 3682)	Novel Protein sim. GBank gi 4572484 gb AA023834.1 AF12365 - (AF12365) FEZ1 [Homo asplena]		56182575, 29331824, 29331826, 60433356, 264764, 264288, 33657023, 263967, 18108370, 18108374, 264631, 264555, 264556, 264639

1842	90982645 (3683, 3684)	Novel Protein sim. GBank gji1326268 (U58728) - C54H2.1 gene product [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 29331822, 29331824, 29331825, 66714117, 29331826, 29331827, 264907, 264909, 52644045, 56182435, 264510, 265006, 265007, 265009, 264910, 60433356, 264757, 60433438, 55812038, 265017, 18108354, 264686, 264769, 33657023, 264693, 18108384, 33657109, 18108368, 264628, 55810764, 56182323, 18108384, 264593, 264584
1843	95292692 (3685, 3686)			UNCLASSIFIED	264488, 56182435, 264769, 29331826, 29331828, 264511, 265006, 265007, 264910, 264631, 264509, 264690, 264636, 264564, 264691, 60432229, 60432049, 264259, 264629, 33657023, 264486, 264909, 264567, 264595, 264766
1844	87444784 (3687, 3688)	Novel Protein sim. GBank gji2496887/spiQ09232/yQ22_CAEEL - HYPOTHETICAL 32.0 KD PROTEIN C09F5.2 IN CHROMOSOME III		UNCLASSIFIED	264908, 265022, 33657023, 87168518, 22279002
1845	95096673 (3689, 3690)	Novel Protein sim. GBank gji1175494/spiQ09819/YAC5 SCHPO - HYPOTHETICAL 45.0 KD PROTEIN C16C9.05 IN CHROMOSOME I	Contains protein domain (PF00628) - PHD-finger	transcriptfactor	264259, 29331824, 264907, 264908, 66712502, 264510, 265007, 265008, 55812038, 265018, 21908765, 52644150, 33657109, 264555, 264566, 264557, 56182323, 18108382, 83373044, 18108385, 264584
1846	84287872 (3691, 3692)	Novel Protein sim. GBank gji3881080/embjCAA217391 - (AL032657) similar to EGF-like domain; cDNA EST yk299a12.3 comes from this gene; cDNA EST EMBL:D35398 comes from this gene; cDNA EST yk331h8.5 comes from this gene; cDNA EST yk299a12.5 comes from this gene; cDNA EST yk487g8.5 c...	Contains protein domain (PF00008) - EGF-like domain	UNCLASSIFIED	264905, 264908
1847	87621487 (3693, 3694)	Novel Protein sim. GBank gji5059323/jgbjAAD38667.1JAF15152 - (AF151522) hairy and enhancer of split related-1 [Homo sapiens]	Contains protein domain (PF00010) - Helix-loop-helix DNA-binding domain	transcriptfactor	22276997, 264259, 29331824, 264909, 18108351, 263974, 22279002
1848	86789360 (3695, 3696)	Novel Protein sim. GBank gji5701854/embjCAB52191.1 - (AJ245417) Gsb protein [Homo sapiens]		lm7	29331825, 29331826, 29331827, 265017, 264683, 264288, 264766, 264768, 21906767, 21906788, 264692, 22279002
1849	84287874 (3697, 3698)	Novel Protein sim. GBank gji4503665/jrefjNP_001988.1jpfBLN - fibulin 2 precursor	Contains protein domain (PF00008) - ATPase-associated EGF-like domain	ATPase-associated	56182575, 265018
1850	86689650 (3699, 3700)	Novel Protein sim. GBank gji4599582/jgbjBAA76813.1 - (AB023186) KIAA0369 protein [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	60432049, 264908
1851	95419789 (3701, 3702)	Novel Protein sim. GBank gji220637/jgbjBAA01477 - (D10827) zinc finger protein [Mus musculus]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_ma_bind	29331824, 35696052, 264910, 60433438, 264688, 35695917, 265020, 52644150, 65274620, 52644332

1852	95413170 (3703, 3704)	Novel Protein sim. GBank gi 5174829 ref NP_006090.1 pPIAS - protein inhibitor of activated STAT3		UNCLASSIFIED	56182575, 35686286, 22278996, 22278997, 22278999, 264490, 60432049, 264259, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 35696052, 52644045, 265007, 264910, 60432229, 60433356, 60433438, 55812038, 65274444, 265018, 265019, 18108351, 264448, 264686, 264687, 21908765, 21908767, 21908769, 265021, 265022, 52644150, 264693, 33657109, 18108370, 18108374, 55811576, 35695855, 56182323, 60432113, 22278002, 264563 264887, 264768, 52644507, 264769, 21908765, 21908767, 21908768, 22278995, 56994075, 22278999, 52644150, 264259, 264892, 29331822, 29331824, 52645128, 29331827, 33656970, 33657349, 35695763, 264508, 264806, 264628, 264907, 264629, 264909, 35696423, 35695855, 264510, 265008, 264511, 264512, 264630, 265009, 264631, 264910, 264634, 264635, 264637, 264593, 264638, 264639, 33657402, 18108385, 52646317, 52644298, 87188518, 87188559, 264602, 265017, 22279000, 265018, 264760, 264762, 264682, 264448, 264764, 264684, 264587, 264288, 264369, 264768 264582
1853	91222287 (3705, 3706)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	
1854	88038152 (3707, 3708)	Novel Protein sim. GBank gi 2072864 (U83569) - putative p150 [Homo sapiens]		nuclease	
1855	91221459 (3709, 3710)	Novel Protein sim. GBank gi 4539520 emb CAB39994.1 - (AL035424) dA22D12.1 (novel protein similar to Drosophila Kelch (Ring Canal protein, KEL) and a heterogeneous set of other types of proteins) [Homo sapiens]	Contains protein domain (PF01344) - Kelch motif	nucl_recl	18108392, 52646365, 65274572, 56182575, 22278994, 56994075, 22278996, 35696286, 22278999, 264259, 60432049, 264908, 264510, 265007, 265008, 265009, 264595, 21908754, 87188474, 265011, 87188559, 264681, 264288, 264768, 18108359, 21908764, 21908768, 29148627, 265020, 265021, 265022, 52644150, 33657023, 33657109, 18108372, 18108374, 18108376, 35696423, 264631, 264638, 18108381, 264482
1856	94231871 (3711, 3712)	Novel Protein sim. GBank gi 3954978 emb CAA06945 - (AJ008278) acetylglucosaminyltransferase-like protein (Mus musculus)		UNCLASSIFIED	56994075, 264259, 29331828, 264511, 264910, 264758, 264693, 264637, 18108381, 83373044
1857	94324455 (3713, 3714)	Novel Protein sim. GBank gi 4322670 gb AAD16120 - (AF094508) dentin phosphoryn [Homo sapiens]		ATPase_associated	22278999, 264259, 264906, 60170831, 264448, 264686, 265020, 265022, 33657109, 60170394, 83373044

1858	87628311 (3715, 3716)	Novel Protein sim. GBank gi 4881903 gb AAD36415.1 AE001788 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - ribosomal prot	264757
1859	84407484 (3717, 3718)	Novel Protein sim. GBank gi 4240317 dbj BAA74837.1 - (AB020721) KIAA0914 protein [Homo sapiens]	Ribosomal protein S15	22278998, 28331824, 285007, 33109954, 285019, 284369, 21908768, 29148784, 27486261, 52844332, 22279002 285019
1860	17929308 (3719, 3720)	Novel Protein sim. GBank gi 4009522 (AF099731) - connexin 31.1 [Homo sapiens]		
1861	88086370 (3721, 3722)	Novel Protein sim. GBank gi 2143637 pir j 84503 - calcium- dependent actin-binding protein - rat	Contains protein domain (PF00285) - Citrate synthase	264887, 284259, 28331822, 28331824, 29331825, 285007, 285009, 284591, 33109954, 285010, 285019, 284369, 284288, 284886, 284691, 284693, 27486264, 18108370, 18108374, 263977, 55811576, 58182323, 264639, 22279000, 22279002, 264482
1862	87372823 (3723, 3724)	Novel Protein sim. GBank gi 125493 sp P07313 KMLC_RABIT - MYOSIN LIGHT CHAIN KINASE, SKELETAL MUSCLE (MLCK)	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	35698286, 264259, 87168474, 264369, 21908768, 284558, 284563
1863	85775037 (3725, 3726)	Novel Protein sim. GBank gi 3820909 emb CAA09299 - (AJ010842) Dof protein [Drosophila melanogaster]	UNCLASSIFIED	284601, 284766, 29148627, 29148629, 264692, 284629, 284635
1864	85547832 (3727, 3728)	Novel Protein sim. GBank gi 4322263 gb AAD15985 - (AF077738) metalloproteinase CPX-1 [Mus musculus]	Contains protein domain (PF00754) - F5/6 type C domain	22278999, 284259, 284807, 285018, 18108370, 284634, 284635, 284555, 284556, 284638, 18108387
1865	87740827 (3729, 3730)	Novel Protein sim. GBank gi 2485727 sp Q93073 Y258_HUMAN - HYPOTHETICAL PROTEIN KIAA0256		22278999, 284490, 28331822, 66714117, 68712502, 285006, 285007, 285008, 285009, 284591, 60433438, 285010, 285019, 284760, 284448, 284768, 29148627, 29148629, 285020, 285022, 18108385, 60432113
1866	87266816 (3731, 3732)	Novel Protein sim. GBank gi 5282617 emb CAB45748.1 - (AL080157) hypothetical protein [Homo sapiens]	kinase	18108374, 284769, 18108377, 21908765, 21908766, 35696423, 58182575, 21908769, 29148629, 35696286, 35695917, 285021, 284510, 284511, 284512, 284534, 284535, 60170831, 52844150, 284555, 284691, 284259, 284556, 284692, 284557, 33657023, 80433358, 28331822, 284559, 284595, 28331824, 18108385, 21908754, 33657182, 29331827, 35696052, 33656970, 87168518, 285017, 60431602, 22279000, 284508, 284509, 18108351, 284907, 284682, 284567, 18108372, 284765, 284486 284094
1867	84579159 (3733, 3734)	Novel Protein sim. GBank gi 3859930 (AF078096) - forkhead/winged helix-like transcription factor 7 [Homo sapiens]	UNCLASSIFIED	

1868	87357459 (3735, 3738)	Novel Protein sim. GBank gi 3881525 emb CA493884 - (Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D3254 comes from this gene; cDNA EST YK224b3.5 comes from this gene; cDNA EST YK357110.5 comes from this gene [Caenorhabditis elegans]			nuclease	284489, 22278997, 22278999, 29331825, 29331826, 265008, 265009, 33857402, 87188474, 18108351, 21906765, 21906768, 21906769, 265020, 265021, 60170815, 27486284, 264628, 18108374, 264631, 18108385, 87168518, 22279000, 22279002, 264566, 264567
1869	86877292 (3737, 3738)	Novel Protein sim. GBank gi 4826772 ref NP_004981.1 pIGFA - insulin-like growth factor binding protein, acid labile subunit		Contains protein domain (PF00560) Leucine Rich Repeat	glycoprotein	284508, 264509, 264906, 264808, 264909, 264810, 264591, 264600, 18108351, 264683, 264766, 264768, 35695855, 264634, 264556, 264639, 18108385, 264583, 264486
1870	95348488 (3739, 3740)	Novel Protein sim. GBank gi 1869859 emb CA806722 - (Z86089) very large tegument protein [human herpesvirus 2]			UNCLASSIFIED	29331824, 60424269, 265007, 265008, 21906754, 265017, 265018, 265019, 264288, 264766, 264686, 264688, 21906768, 21906769, 35695817, 80170815, 264692, 18108368, 35695763, 35696423, 65274791, 264638, 264639, 58528486
1871	80234464 (3741, 3742)				UNCLASSIFIED	284509, 264905, 264595, 264768, 264635, 264636, 264583, 264486
1872	80235355 (3743, 3744)	Novel Protein sim. GBank gi 2460316 (AF022147) - uterus-ovary specific putative transmembrane protein [Rattus norvegicus]			protease	284510, 264594, 264565
1873	80213890 (3745, 3746)					264509, 264512, 265009, 265011, 18108351, 264687, 264691, 18108370, 18108374, 264635
1874	95351136 (3747, 3748)			Contains protein domain (PF00293) - Bacterial muT protein	UNCLASSIFIED	284488, 35695917, 264259, 284905, 264907, 264908, 264909, 263978, 264511, 264635, 264636, 264637, 264638, 33657402, 264558, 18108385, 264600, 264604, 264764, 264567, 264766
1875	87330516 (3749, 3750)	Novel Protein sim. GBank gi 4589520 db BAA76782.1 - (AB023155) KIAA0938 protein [Homo sapiens]			UNCLASSIFIED	35696286, 264828, 264582, 264557, 264558
1876	87112950 (3751, 3752)	Novel Protein sim. GBank gi 263810 bbs I22920 - collagen alpha chain [Riftia pachyptila=lube worms, Peptide, 1027 aa]			UNCLASSIFIED	264259, 29331822, 60432289, 264908, 264909, 264604, 264764, 264288, 264769, 18108376, 264558, 264558, 264559, 18108385
1877	87315208 (3753, 3754)	Novel Protein sim. GBank gi 3983356 gb AAC83924.1 - (AF102545) riboflavin binding protein precursor [Scaphiopus couchii]			UNCLASSIFIED	264767, 264686, 264768, 263978, 264693, 264639, 265010, 264563, 264905, 264906, 264907

1878	95351056 (3755, 3756)	Novel Protein sim. GBank gll4510345[gblAAD21434.1] - (AC008921) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF01428) - AN1-like Zinc finger	ubiquitin	264589, 264486, 35686286, 56994075, 264259, 29331822, 29331824, 29331825, 3569052, 29331828, 29146498, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 33657402, 264594, 264758, 55812038, 265011, 264602, 264760, 18108351, 264762, 264681, 264682, 264764, 264389, 264288, 264766, 264687, 264768, 264769, 21908766, 35695917, 265021, 60170615, 33857023, 264692, 264693, 33657109, 27486265, 264628, 18108370, 264629, 18108374, 35696423, 264634, 264635, 264555, 264638, 264639, 83373044, 18108385, 56526486, 87168518, 264563, 264594, 264566, 264486, 264567
1879	95310883 (3757, 3758)	Novel Protein sim. GBank gll4929643[gblAAD34082.1]AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264905, 264907, 264908, 265007, 264565, 264586
1880	91012978 (3759, 3760)	Novel Protein sim. GBank gll1550785[emb]CAA69283] - (Y08026) Immune associated protein 38 [Mus musculus]		UNCLASSIFIED	264766, 264691, 264692, 83373044
1881	80214948 (3761, 3762)	Novel Protein sim. GBank gll93144[pil]B40505 - hypothetical protein - suid herpesvirus 1 (strain Indiana-Funkhuser or Becker)		UNCLASSIFIED	264509, 264905, 264908, 264909, 264910, 264762, 264687, 33657023, 264632
1882	86582450 (3763, 3764)	Novel Protein sim. GBank gll2384956 (AF022985) - No definition line found [Caenorhabditis elegans]			264908, 21906766, 18108370, 263974, 87168518
1883	94216817 (3765, 3766)	Novel Protein sim. GBank gll1351218[sp]P47226[TES2_MOUSE - TESTIN 2 (TES2)] [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	264908, 264910, 87168559, 21906766, 264636

1884	95310885 (3767, 3768)	Novel Protein sim. GBank gi 4929643 gb AAD34082.1 AF15184 - (AF151845) CGI-87 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108394, 58181688, 22278998, 60432048, 264259, 29331822, 29331824, 29331825, 68714117, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 265007, 264512, 265008, 264910, 264592, 264593, 33657402, 55812038, 264758, 55811388, 265010, 265011, 87188559, 264780, 55811150, 264761, 264882, 264763, 264883, 264764, 264288, 264369, 264766, 264886, 264768, 264769, 29148784, 35695917, 264690, 264691, 33657023, 264692, 264693, 33657109, 18108370, 264628, 60431528, 264629, 263973, 18108374, 55810784, 55811576, 35696423, 35695855, 264631, 264634, 60431850, 264637, 264638, 56182323, 264639, 18108382, 83373044, 18108385, 60432113, 22278002, 264583, 264584, 264585, 264586, 264488, 264587
1885	87644280 (3769, 3770)	Novel Protein sim. GBank gi 2507155 sp P37370 VRP1_YEAST - VERPROLIN		UNCLASSIFIED	58182575, 264259, 264905, 264909, 265008, 264598, 264766, 265020, 264628, 60431528, 264634, 58528488, 264080, 264583 22278998, 22278999, 60432049, 264810, 265018, 264766, 21906768, 29148829, 264690, 264693, 264628, 264555, 264488
1886	86674082 (3771, 3772)	Novel Protein sim. GBank gi 2834158 gb AAC02577.1 - (AF045841) No definition line found [Caenorhabditis elegans]			29331822, 29331824, 29331825, 29331826, 29331827, 264908, 265007, 264681, 264768, 29148827, 264693, 18108384, 35696423, 65274791, 35695855, 264632, 56182323, 264639, 264583 263978
1887	94139139 (3773, 3774)	Novel Protein sim. GBank gi 5174421 ref NP_006023.1 PCPNE - copine VI (neuronal)	Contains protein domain (PF00168) - C2 domain	ATPase-associated	
1888	87822804 (3775, 3776)	Novel Protein sim. GBank gi 3318931 emb CAB10841 - (Z98046) dJ1409.2 (Melanoma-Associated Antigen MAGE LIKE) [Homo sapiens]	Contains protein domain (PF01454) - MAGE family		
1889	91255783 (3777, 3778)	Novel Protein sim. GBank gi 1083308 pir IA56559 - enhancer-trap-locus-1 protein - mouse (fragment)	Contains protein domain (PF00176) - SNF2 and others N-terminal domain	helicase	264906, 55812038, 264758, 265010, 265018, 265019, 18108351, 264288, 21905765, 21906768, 21908769, 265021, 33657023, 33657109, 56182323, 83373044, 18108385, 22279000, 22279002
1890	87626705 (3779, 3780)	Novel Protein sim. GBank gi 4240195 db BAA74876.1 - (AB020680) KIAA0853 protein [Homo sapiens]		UNCLASSIFIED	18108388, 29147620, 264907, 265009, 264800, 265018, 18108351, 264288, 264689, 21908765, 21906768, 21908769, 264691, 264692, 264693, 264628, 18108370, 264636, 264558, 264404

1891	87013895 (3781, 3782)			UNCLASSIFIED	264686, 264768, 264687, 264692, 264693, 29331822, 29331824, 264508, 264905, 264906, 18108370, 264628, 264907, 264908, 264809, 18108378, 265007, 265008, 264910, 264632, 264591, 264639, 264596, 18108384, 265010, 265011, 264601, 264605, 264563, 264369
1892	87642825 (3783, 3784)	Novel Protein sim. GBank gl 5689535 cbj BAA83051.1 - (AB029022) KIAA1089 protein [Homo sapiens]	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	struct	22278995, 264509, 87168559, 18108351, 264448, 264682, 265020, 264693, 18108374, 22279000
1893	88533828 (3785, 3786)			lamihin	264569, 65274572, 22278997, 22278999, 264259, 29331822, 29331824, 86714117, 29331828, 264908, 265008, 265009, 264592, 265016, 264681, 264448, 264683, 18108354, 264369, 264684, 264685, 264766, 264687, 264689, 21908768, 265020, 265022, 60170615, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 264628, 18108374, 35695855, 264630, 264632, 264634, 264557, 264558, 60170394, 18108381, 18108385, 22279000
1894	86989120 (3787, 3788)				264508, 264905, 264906, 264907, 264594, 264684, 264690, 264692, 264630, 264635, 264636, 264639, 264563
1895	87631891 (3789, 3790)	Novel Protein sim. GBank gl 5282574 emb CAB45729.1 - (AL080133) hypothetical protein [Homo sapiens]	Contains protein domain (PF00435) - Spectrin repeat		56182575, 264259, 60432289, 29331826, 264107, 264805, 264908, 264910, 60170831, 264758, 265010, 265018, 264448, 264288, 264768, 33657109, 264628, 55810764
1896	86673555 (3791, 3792)		Contains protein domain (PF00627) - UBA domain	UNCLASSIFIED	18108379, 264634, 56182323, 56526486
1897	80565569 (3793, 3794)	Novel Protein sim. GBank gl 728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		cadherin	264907, 265008, 264692, 264686, 21908768, 264629, 264631, 264634, 264555
1898	87817637 (3795, 3796)	Novel Protein sim. GBank gl 127560 sp P23249 MV10_MOUSE - PROTEIN MOV-10		helicase	264259
1899	86673087 (3797, 3798)	Novel Protein sim. GBank gl 2909819 (AF031548) - erythrocyte membrane glycoprotein RH50 [Homo sapiens]			22278996, 22278998, 22278999, 29331824, 29331825, 60432289, 29331827, 35696052, 29331828, 265008, 265019, 264681, 264682, 264448, 264369, 52644229, 21908765, 21908766, 21908768, 21908769, 60170615, 55810764, 22279000
1900	87841858 (3799, 3800)	Novel Protein sim. GBank gl 4102881 (AF017250) - vitellogenin precursor [Oreochromis aureus]	Contains protein domain (PF00909) - Ammonium Transporter Family	glycoprotein	264259, 264508, 264909, 60432229, 264769, 21908765, 21908769
				UNCLASSIFIED	264683

1801	95196847 (3801, 3802)	Novel Protein sim. GBank gi 565959 sp P38378 S61A_RAT PROTEIN TRANSPORT PROTEIN SEC61 ALPHA SUBUNIT	Contains protein domain (PF00242) - DNA polymerase (viral) N-terminal domain	transport	264488, 52644507, 52845156, 18108398, 52846385, 52846842, 18108397, 56182575, 22278994, 22278995, 56994075, 35896286, 22278997, 22278998, 284490, 60432049, 284259, 28331822, 52645080, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 29331828, 35698032, 33656970, 29148498, 284906, 264907, 29331830, 284908, 52844045, 284909, 284112, 285006, 284512, 285008, 284910, 285009, 60170831, 60432228, 60433356, 33657402, 60433438, 55812038, 284758, 33109954, 21908754, 33657084, 52844298, 87188474, 265010, 285011, 87168559, 285017, 265018, 265019, 18108351, 284448, 284288, 284688, 52844229, 21908765, 21908768, 21908767, 21908769, 55811957, 35695917, 265020, 265021, 52844150, 18108362, 33657023, 264693, 263887, 33657109, 33657182, 27488284, 33657349, 35895763, 18108370, 18108378, 55811576, 35698423, 35695855, 60431850, 284638, 263981, 52844332, 60170384, 83373044, 18108385, 87168518, 80432113, 284584
1902	80202013 (3803, 3804)	Novel Protein sim. GBank gi 426613 gb AAD20451 (AF098788) SLM-1 [Mus musculus]		dna_ma_bind	264107, 263978
1903	87778554 (3805, 3806)	Novel Protein sim. GBank gi 3747107 (AF095741) - unknown [Rattus norvegicus]		UNCLASSIFIED	264259, 28331825, 29331827, 264508, 264907, 285008, 60170831, 60433358, 60433438, 284759, 21908754, 284448, 264288, 265021, 265022, 33657023, 264693, 55811578, 284555, 284556, 22279000
1904	80434213 (3807, 3808)	Novel Protein sim. GBank gi 135291 sp P47147 YJ80_YEAST - HYPOTHETICAL 80.2 KD PROTEIN IN CPA2-NNF1 INTERGENIC REGION		struct	264509, 264805, 264806, 264807, 264908, 265007, 284910, 284888, 284788, 284887, 264769, 264693, 284628, 18108374, 284634, 264638, 284637, 284585
1905	95351140 (3809, 3810)	Novel Protein sim. GBank gi 3043714 gb BAA25521 (AB011167) KIAA0595 protein [Homo sapiens]	Contains protein domain (PF00283) - Bacterial mutT protein		264488, 284768, 284769, 284889, 29148829, 35695917, 35696286, 284259, 284892, 18108362, 33657023, 29331824, 33657109, 29148499, 284508, 264509, 284905, 284906, 264907, 66712502, 284908, 284909, 35898423, 35895855, 284510, 284511, 284512, 284910, 284634, 284635, 284637, 284638, 33657402, 284758, 85858542, 284602, 284760, 284781, 264482, 264563, 284782, 284483, 284784, 284586, 284288, 284789
1908	12763822 (3811, 3812)			UNCLASSIFIED	264637

1907	95351144 (3813, 3814)	Novel Protein sim. GBank gi 4929585 gb AAD34053.1 AF15181 - (AF151816) CGI-58 protein [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	hydrolase	65274572, 22278996, 35696286, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 60424269, 29331828, 35696052, 264593, 60433356, 21908754, 55811386, 85658542, 87168559, 265018, 264681, 264682, 264684, 264288, 21908765, 21908768, 21908768, 265020, 265022, 264690, 52644150, 264692, 33657023, 264693, 33657109, 35695855, 264636, 264638, 60432113
1908	95313841 (3815, 3816)	Novel Protein sim. GBank gi 3986770 (AF109806) - NG22 [Mus musculus]		UNCLASSIFIED	264488, 65274572, 56182575, 56181686, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 60432289, 29331826, 29331827, 29331828, 29146499, 264905, 264908, 264907, 264908, 66712502, 264908, 56182435, 264510, 264511, 265008, 264910, 60170831, 264592, 60433356, 33657402, 264594, 60433438, 264598, 55812038, 33109954, 52646317, 265011, 265017, 264604, 265018, 265019, 264605, 55811150, 264681, 264448, 264288, 264686, 264688, 264789, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 29146629, 35695917, 265020, 265022, 264691, 264692, 18108364, 65274620, 33657109, 33657349, 35695763, 18108374, 263978, 55810764, 55811576, 35696423, 65274791, 264631, 264632, 264556, 264557, 60170394, 56182323, 83373044, 18108385, 60432113, 22279000, 22279002, 264566, 264486 264259, 264508, 264905, 264906, 264907, 264908, 264511, 264910, 264593, 264758, 264764, 264766, 18108370, 264634, 264637, 264486
1909	85514505 (3817, 3818)	Novel Protein sim. GBank gi 2242653 db JBAA20813 - (AB002354) KIAA0356 [Homo sapiens]		UNCLASSIFIED	35696286, 22278996, 22278999, 35696052, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 265007, 264512, 264910, 264758, 265011, 264601, 264602, 264604, 264605, 264761, 264764, 264288, 264766, 264768, 264687, 264769, 35695917, 265021, 52644150, 264692, 264628, 18108370, 264629, 18108372, 18108374, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 18108385, 264565, 264566, 264486
1910	94216821 (3818, 3820)	Novel Protein sim. GBank gi 1351218 sp P47226 TES2_MOUSE - TESTIN 2 (TES2) [CONTAINS: TESTIN 1 (TES1)]	Contains protein domain (PF00412) - LIM domain containing proteins	homeobox	

1911	81725345 (3821, 3822)	Novel Protein sim. GBank gi 4809339 gb AAD30184.1 AC006530 hypothetical protein [Homo sapiens]	Contains protein domain (PF01119) - DNA mismatch repair protein	nuclease	18108394, 56182575, 56182181, 29331826, 29331827, 33658970, 264906, 265007, 264591, 55812038, 87168559, 264448, 264369, 21908765, 21908768, 265022, 264691, 264693, 18108385, 55811576, 264556, 18108385, 18108388
1912	95413518 (3823, 3824)	Novel Protein sim. GBank gi 5689439 dbj BAA63003.1 - (AB028974) KIAA1051 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	18108397, 56182575, 56181686, 22278994, 22278995, 56994075, 22278996, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 66714117, 35696052, 264805, 264906, 264907, 264908, 52844045, 58182435, 265007, 265008, 264910, 265009, 264591, 264596, 65274444, 55811386, 87168474, 265011, 87168559, 265018, 265019, 264760, 18108351, 264681, 264369, 264684, 264288, 264686, 264768, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 265020, 265021, 265022, 60170615, 264692, 33657023, 264693, 18108376, 55811576, 35696423, 85274791, 264637, 56182323, 83373044, 56526486, 22278002, 264583, 264568
1913	95305548 (3825, 3826)	Novel Protein sim. GBank gi 5032245 ref NP_005665.1 pZNF2 - zinc finger protein (C2H2) homologous to mouse MOK-2			56182575, 22278994, 22278995, 56994075, 22278996, 22278998, 22278999, 29331826, 29331827, 265008, 55812038, 265010, 265017, 265018, 265019, 264681, 18108351, 264683, 264764, 264369, 264288, 264685, 264686, 264769, 21908765, 21908768, 21908768, 21908769, 55811957, 265020, 265022, 264691, 55811576, 264634, 264635, 264638, 56182323, 83373044, 18108385
1914	83423982 (3827, 3828)	Novel Protein sim. GBank gi 4589604 dbj BAA76824.1 - (AB023187) KIAA0980 protein [Homo sapiens]	Contains protein domain (PF00036) - EF hand	struct	56182575, 29331824, 35696052, 264906, 264908, 264828, 264909, 264592, 264758, 87168559, 18108351, 18108354, 264684, 264686, 33657023, 264693, 264628, 264631, 264632, 264634, 264635, 264639
1915	95340459 (3829, 3830)	Novel Protein sim. GBank gi 5689415 dbj BAA62891.1 - (AB028962) KIAA1039 protein [Homo sapiens]		UNCLASSIFIED	264259, 29331824, 29331826, 29331827, 264508, 264909, 265009, 265017, 265019, 264768, 264769, 264689, 264628, 264635, 264637, 264639, 83373044, 264565 264683, 264639
1916	78640761 (3831, 3832)				

1917	97821680 (3833, 3834)	Novel Protein sim. GBank gi 568938 dbj BA482879.1 - (AB028950) KIAA1027 protein [Homo sapiens]		struct	264769, 264889, 21906765, 21906768, 22278996, 264259, 264691, 264693, 29331824, 29331825, 29331826, 29331828, 264805, 264906, 264628, 264907, 264608, 264909, 264510, 264630, 264910, 264634, 264635, 264636, 264637, 264638, 263981, 264639, 264758, 18108385, 21906754, 265011, 264604, 264563, 18108351, 264762, 264763, 264568, 264784, 264766
1918	95302785 (3835, 3836)	Novel Protein sim. GBank gi 5281817 gb AAD41524.1 AF15483 - (AF15483) PV-1 [Rattus norvegicus]		struct	264488, 18108392, 18108357, 21906765, 21906767, 21906768, 56182575, 21906769, 22278994, 35696266, 35695917, 22278998, 22278997, 265021, 265022, 264534, 264690, 264691, 264692, 33657023, 264693, 29331824, 29331825, 33657109, 29331826, 52645129, 35696052, 29331828, 27486262, 27486264, 35695763, 264508, 264905, 264509, 264906, 264628, 264907, 18108370, 264908, 264629, 264909, 18108372, 18108374, 263978, 35696423, 35695855, 264510, 264511, 265006, 265007, 264512, 265008, 264631, 265009, 264910, 264634, 264635, 264555, 264636, 264556, 264637, 264557, 264593, 264638, 264594, 60170394, 264595, 264559, 264596, 83373044, 264758, 52646317, 18108385, 52644298, 56526488, 87168518, 265010, 265011, 87168559, 264600, 264601, 264602, 265017, 264603, 264604, 265018, 264605, 264760, 264761, 264482, 264584, 18108351, 264762, 264682, 264585, 264448, 264784, 264566, 264486, 264567, 264369, 264288, 264766, 264487, 264695
1919	94143847 (3837, 3838)	Novel Protein sim. GBank gi 3876584 emb CA801237 - (Z77687) cDNA EST EMBL:CO8125 comes from this gene; cDNA EST EMBL:CO9753 comes from this gene [Caenorhabditis elegans]		oxidase	22278997, 29331822, 265007, 60170831, 60432229, 60433438, 264448, 264682, 264288, 55811957, 33657023, 33657109, 65274791, 56182323, 22279002, 264510, 264511, 264512, 264566
1920	91229953 (3839, 3840)	Novel Protein sim. GBank gi 1808231 AC000115 - coded for by human cDNAs R76043 (NID:g850725), R65857 (NID:g838495) and H12868 (NID:g877688) [Homo sapiens]		UNCLASSIFIED	
1921	79555226 (3841, 3842)	Novel Protein sim. GBank gi 4560897 gb AAD24571.1 AF12108 - (AF12108) cAMP inducible 2 protein [Mus musculus]		UNCLASSIFIED	264693

1922	87641663 (3843, 3844)	Novel Protein sim. GBank gi1138595 sp P02845 VT2_CHICK - VITELLOGENIN II PRECURSOR (MAJOR VITELLOGENIN) [CONTAINS: LIPOVITELLIN I (LV); PHOSVITIN (PV); LIPOVITELLIN II (LVII); YGP40]		UNCLASSIFIED	264686, 264688, 264490, 18108370, 264909, 18108374, 265008, 264557, 264564, 18108351
1923	84323589 (3845, 3846)	Novel Protein sim. GBank gi119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	264488, 264489, 22278895, 264094, 264259, 35886052, 264509, 264905, 264906, 264907, 264908, 66712502, 264909, 264511, 264512, 265007, 264910, 265009, 264591, 264592, 264593, 264594, 264595, 264758, 264596, 264759, 265011, 265017, 265018, 265019, 55811150, 264881, 264762, 264448, 264764, 264288, 264369, 264766, 264767, 264686, 264687, 264768, 264769, 56181562, 264689, 21908766, 264691, 33657023, 264693, 65274620, 33857109, 18108370, 264628, 264634, 264555, 264636, 264637, 264638, 264639, 264558, 83373044, 87168518, 264563, 264564, 264565, 264566, 264567, 29331826, 264906, 264908, 264595, 265017, 265018, 265019, 265021, 264691, 264693, 264637, 18108385, 264565
1924	87338825 (3847, 3848)	Novel Protein sim. GBank gi13877655 emb CAA86657 - (Z72511) possible zinc finger protein; cDNA EST EMBL:IM89115 comes from this gene; cDNA EST EMBL:D71533 comes from this gene; cDNA EST EMBL:D72314 comes from this gene; cDNA EST EMBL:D75164 comes from this gene; cDNA EST EMBL:C1....	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		
1925	87628338 (3849, 3850)	Novel Protein sim. GBank gi4881903 gb AAD36415.1 AE00178 - (AE001788) ribosomal protein S15 [Thermotoga maritima]	Contains protein domain (PF00312) - Ribosomal protein S15	ribosomalprot	22278895, 22278896, 22278897, 264259, 29331824, 66714117, 29146499, 264909, 52644045, 265008, 265009, 264758, 265011, 265017, 264605, 264448, 264288, 264692, 33657109, 18108374, 60170394
1926	86084739 (3851, 3852)	Novel Protein sim. GBank gi12246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma- associated herpesvirus]		struct	264905, 264906, 264907, 264810, 264593, 265018, 264780, 264764, 264288, 264692, 264693, 263978, 264631, 264634, 264637, 264593
1927	85654657 (3853, 3854)	Novel Protein sim. GBank gi13043632 db BAA25480 - (AB011126) KIAA0554 protein [Homo sapiens]			264689, 264631
1928	87798054 (3855, 3856)	Novel Protein sim. GBank gi11665761 db BAA13377 - (D87433) KIAA0246 [Homo sapiens]	Contains protein domain (PF00193) - Extracellular link domain	Inf	264488, 264259, 265017, 265021, 264692
1929	86997238 (3857, 3858)	Novel Protein sim. GBank gi15001993 gb AAD37247.1 AF13432 - (AF134321) chimeric AFGP/hypsinogen-like serine protease precursor [Dissostichus mawsoni]		UNCLASSIFIED	264508, 264591, 33657402, 265017, 264768, 264632, 264556, 264639

1930	87889128 (3859, 3860)	Novel Protein sim. GBank gi 1709230 sp P52963 NBL4_MOUSE - NBL4 PROTEIN		phosphatase	35688286, 29331828, 284905, 284907, 284908, 284909, 264511, 284910, 284758, 284601, 285017, 285019, 284805, 284780, 284784, 284766, 284688, 284769, 285022, 35698423, 284638, 60432113
1931	87787278 (3861, 3862)	Novel Protein sim. GBank gi 404634 (U01840) - serine/threonine kinase [Mus musculus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	284906, 284908, 60432229, 284758, 284764, 284288, 285020, 284892, 284634, 284637, 284884, 284891, 284635
1932	15030972 (3863, 3864)			UNCLASSIFIED	284595
1933	11813688 (3865, 3866)			struct	56182375, 56182435, 284510, 284757, 284758, 55812038, 55811388, 285018, 55811150, 21906765, 284681, 284631, 284635, 284637
1934	84426360 (3867, 3868)	Novel Protein sim. GBank gi 115749 db BAA38494 - (AB022023) nonmuscle myosin heavy chain B [Bos taurus]		UNCLASSIFIED	284686, 285011, 284511, 284905, 18108351, 284584, 284681, 284259, 18108370, 284566, 284764, 284369, 284595
1935	87752511 (3869, 3870)			UNCLASSIFIED	60432289, 285007, 285010, 285011, 285019, 33657109, 18108374
1936	95414338 (3871, 3872)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit			
1937	84847141 (3873, 3874)	Novel Protein sim. GBank gi 543187 pir S37771 - ankyrin, erythrocyte - mouse	Contains protein domain (PF00023) - Ank repeat	kinase	85558542, 21906767, 35689517, 60170815, 284693, 33657109
1938	87403277 (3875, 3876)	Novel Protein sim. GBank gi 4544431 gb AAD22340.1 AC00695 - (AC006955) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00888) - Cullin family	collagen	284488, 29146498, 284905, 284559
1939	81004978 (3877, 3878)	Novel Protein sim. GBank gi 500858 db BAA03210 - (D14168) 50kDa lectin [Bombyx mori]		UNCLASSIFIED	65274572, 22278999, 60432289, 56182435, 60433356, 285017, 21906765, 21906766, 21908788, 55811957, 27486284, 35696423, 80432113, 284584
1940	87348810 (3879, 3880)	Novel Protein sim. GBank gi 1948300 emb CAA73132 - (Y12529) hypothetical protein [Silene latifolia]	Contains protein domain (PF00560) - Leucine Rich Repeat	struct	284488, 29331822, 284448, 284683, 284288, 285020, 33657023, 284831
1941	84147177 (3881, 3882)	Novel Protein sim. GBank gi 4206386 (AF060570) - rig-1 protein [Mus musculus]		UNCLASSIFIED	56994075, 22278998, 284259, 29331824, 29331827, 284805, 285008, 33657084, 285017, 285018, 284288, 284687, 21908765, 21908786, 21908787, 285020, 52844150, 27486284, 83373044, 18108387, 60432113, 22278002, 284585
1942	87841870 (3883, 3884)	Novel Protein sim. GBank gi 4927204 gb AAD33049.1 AF13391 - (AF13391) ARL-6 interacting protein-4 [Mus musculus]		UNCLASSIFIED	284488, 18108388, 29331825, 27486281, 284509, 18108370, 18108374, 284482
1943	84325288 (3885, 3886)	Novel Protein sim. GBank gi 3122852 sp O15736 TIPO_DICD1 - TIPO PROTEIN	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	22278998, 29331822, 29331827, 35696052, 284511, 285008, 284592, 60432229, 285017, 285018, 285019, 284684, 284692, 33657109, 65274791, 284636

1944	94232858 (3887, 3888)	Novel Protein sim. GBank gl 1786570 gb BAA13432 - (D87671) TIP120 [Rattus norvegicus]	UNCLASSIFIED	65274572, 22278994, 22278995, 22278996, 22278998, 22278999, 264259, 52845080, 29331824, 29331826, 29331827, 66712502, 56182435, 264512, 264910, 60170831, 60432228, 60433356, 33657402, 60433438, 264596, 33109954, 21906754, 87168474, 87168559, 265017, 265018, 265019, 18108351, 264369, 264686, 264768, 21908765, 21908768, 21908787, 21908769, 35695917, 265020, 265021, 60170815, 264682, 33657023, 18108370, 18108374, 35696423, 35695855, 264634, 60170394, 264639, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264553
1945	87641872 (3888, 3890)	Novel Protein sim. GBank gl 4927204 gb AAD33048.1 AF13391 - (AF13391) ARL-6 Interacting protein-4 [Mus musculus]	UNCLASSIFIED	264488, 22278996, 264510, 264511, 18108351, 264683, 264488, 264567
1946	87443980 (3891, 3892)	Novel Protein sim. GBank gl 2498104 sp Q27969 AD50_BOVIN - ADRENAL MEDULLA 50 KD PROTEIN	UNCLASSIFIED	60432289, 29331827, 35696052, 265007, 265008, 60433356, 60433438, 264369, 56181562, 21908767, 52844150, 264693, 27488284, 264637, 87168518, 264563
1947	86438662 (3893, 3894)	Novel Protein sim. GBank gl 3914801 sp O54888 RPA2_RAT - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135) (RNA POLYMERASE I 127 KD SUBUNIT)	mapolymerase	22278998, 264905, 264906, 264908, 264909, 264512, 264758, 264762, 264682, 264683, 264784, 264288, 264768, 264688, 21908768, 264693, 18108374, 35695855, 264635, 264637, 264638, 18108385, 22279002
1948	95199174 (3895, 3896)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]	struct	264909, 60170831, 264591, 264594, 235010, 265011, 264784, 264369, 264689, 264631, 264638
1949	7840129 (3897, 3898)	Novel Protein sim. GBank gl 3876766 emb CAA93466.1 - (Z89637) predicted using GeneFinder: Similarity to E.coli hypothetical protein YCAC (SW:YCAC_ECOLI) [Caenorhabditis elegans]	UNCLASSIFIED	264369, 264768, 264688, 264689, 264259, 29331822, 33657109, 29331828, 264103, 264509, 18108370, 35695855, 264510, 265008, 265009, 33657402, 18108385, 265018, 264563, 55811150, 18108351, 264369, 264288, 18108354
1951	86988253 (3901, 3902)	Novel Protein sim. GBank gl 2626753 gb BAA23424 - (AB008782) sulfate transporter [Arabidopsis thaliana]	transport	56182575, 22278997, 52845080, 29331824, 29331825, 29331827, 55812038, 52846317, 265018, 265019, 264369, 21908765, 21908767, 55811957, 265020, 265021, 33657023, 264693, 35695763, 56182323, 22279002
1952	87069775 (3903, 3904)	Novel Protein sim. GBank gl 4929833 gb AAD34077.1 AF15184 - (AF15184) CGI-82 protein [Homo sapiens]	reductase	264591, 264593, 264594, 264595, 264555, 264556, 264557, 264558, 264559

1953	20470371 (3905, 3906)	Novel Protein sim. GBank gij1168715sp P31721 C1QB_RAT - COMPLEMENT C1Q SUBCOMPONENT, B CHAIN, PRECURSOR	Contains protein domain (PF00386) - C1q domain	Complement	264259, 264558
1954	91226025 (3907, 3908)	Novel Protein sim. GBank gij14240271 dbj BAA74914.1 - (AB020698) KIAA0891 protein [Homo sapiens]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	ubiquitin	264488, 263394, 18108394, 35698286, 22278998, 29331822, 66714117, 29331828, 29331827, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 265007, 265008, 264810, 265009, 60170831, 60432228, 265011, 265017, 264603, 264604, 265019, 18108351, 264685, 264786, 264789, 35895917, 265020, 265021, 264691, 33657023, 264692, 33657109, 264628, 18108374, 35696423, 55811576, 35695855, 264630, 264635, 264636, 264555, 264556, 264638, 264557, 264639, 264558, 264559, 83373044, 18108385, 264563, 264584, 264586, 264486, 264567
1955	95308310 (3909, 3910)			UNCLASSIFIED	56182575, 56181686, 22278994, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 35698052, 264508, 29331830, 265008, 265009, 264591, 55812038, 87168474, 265017, 265018, 265019, 264448, 264766, 21906765, 21906766, 21906767, 55811857, 265020, 265021, 52645129, 33657109, 27488264, 33657349, 35695763, 60431528, 18108374, 55811576, 35695855, 264635, 60431850, 264639, 83373044
1956	95092121 (3911, 3912)	Novel Protein sim. GBank gij1665821 dbj BAA134071 - (D87469) Similar to D melanogaster cadherin-related tumor suppressor [Homo sapiens]	Contains protein domain (PF00028) - Cadherin domain	cadherin	264488, 56182575, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35698052, 29331828, 264508, 264906, 264908, 264909, 264511, 265007, 264910, 264591, 55812038, 265010, 265018, 18108351, 264768, 56181562, 264689, 21906768, 21908769, 265022, 264691, 264628, 18108374, 55810764, 55811576, 35695855, 264631, 264632, 264635, 264637, 264639, 60170394, 56182323, 83373044, 18108385, 22279000, 22279002, 264583, 264584

1957	94328510 (3913, 3914)	Novel Protein sim. GBank gi 4589674 dbj BAA78856.1 - (AB023229) KIAA1012 protein [Homo sapiens]		UNCLASSIFIED	52846842, 56182575, 22278997, 22278998, 22278999, 29331824, 68714117, 29331827, 29146498, 284593, 33857402, 33109954, 87168474, 285018, 284448, 284389, 284288, 284788, 21908766, 21908767, 21908768, 21908769, 285020, 265021, 284692, 65274620, 27486264, 33657349, 27486265, 35695855, 22279002, 284482
1958	95313902 (3915, 3916)	Novel Protein sim. GBank gi 4240227 dbj BAA74892.1 - (AB020676) KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	80432049, 29331824, 58182181, 68714117, 284107, 284109, 284909, 284511, 60170831, 60432229, 21906754, 285010, 21908769, 35695817, 285022, 65274620, 263987, 283978, 35696423, 284631, 284632, 284634, 284635, 18108385, 22279000, 22279002, 284593, 265019
1959	85701470 (3917, 3918)	Novel Protein sim. GBank gi 2281983 emb CAB10860 - (Z88056) hypothetical protein [Schizosaccharomyces pombe]		ubiquitin	
1960	80308608 (3919, 3920)	Novel Protein sim. GBank gi 2274851 dbj BAA21515 - (D84159) 3-7 gene product [Homo sapiens]		siucl	284905, 284806, 284907, 284908, 284909, 285006, 265007, 284910, 284595, 265017, 284604, 285018, 18108351, 284784, 284369, 284788, 284788, 21908765, 18108388, 284628, 18108379, 284635, 284636, 284637, 284638, 284488
1961	16292607 (3921, 3922)				284635
1962	91008385 (3923, 3924)				
1963	80936017 (3925, 3926)	Novel Protein sim. GBank gi 3721853 dbj BAA33581 - (AB012933) acyl-CoA synthetase 5 [Rattus norvegicus]		UNCLASSIFIED	65274572, 284592, 284593, 285019, 284691, 65274572, 18108388, 35696286, 28331825, 60432289, 29331827, 284828, 285006, 285009, 80433386, 60433438, 21906754, 285020, 265021, 33657023, 33657109, 27486265, 35695855, 284555
1964	94317605 (3927, 3928)	Novel Protein sim. GBank gi 5262638 emb CAB45757.1 - (AL080169) hypothetical protein [Homo sapiens]		cadherin	284488, 284092, 284259, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 284511, 285007, 285009, 284910, 284592, 284593, 284594, 284595, 284758, 284600, 284803, 284604, 284805, 284760, 284782, 284448, 284764, 284288, 284685, 284768, 284768, 284769, 21908768, 284691, 284692, 284693, 18108370, 284628, 284629, 18108374, 284630, 284631, 284634, 284638, 284637, 284638, 18108382, 83373044, 18108385, 284483, 284584, 284565, 284566, 284486, 284567
1965	94317445 (3929, 3930)	Novel Protein sim. GBank gi 4107017 dbj BAA36294 - (AB001773) PEM-6 [Clona savignyi]	Contains protein domain (PF01428) - ANI-like Zinc finger	ubiquitin	284488, 284510, 284760, 284788, 284486

1966	84192058 (3931, 3932)	Novel Protein sim. GBank gi 4929707 gb AAD34114.1 AF15187 - (AF151877) CGI-119 protein [Homo sapiens]	Contains protein domain (PF01027) - Uncharacterized protein family	glycoprotein	22278999, 264092, 264259, 29331826, 29331828, 29146498, 264595, 265011, 264448, 18108354, 264288, 264684, 264766, 264685, 264686, 265022, 264691, 264692, 18108370, 18108377, 264555, 18108381, 18108385, 264486, 264587
1967	87396123 (3933, 3934)	Novel Protein sim. GBank gi 2957270 (AF044578) - phospholipase C PLC210 [Caenorhabditis elegans]	Contains protein domain (PF00388) - Phosphatidylinositol-specific phospholipase C, X domain	esterase	29331824, 265010, 265017, 264288, 21906764, 263981, 58526486
1968	88095841 (3935, 3936)	Novel Protein sim. GBank gi 2564953 (AF030001) - unknown [Mus musculus]	Contains protein domain (PF00008) - EGF-like domain	oncogene	35696286, 264905, 264509, 264908, 264907, 264908, 264909, 264511, 264512, 265008, 264910, 265009, 264594, 264757, 264758, 264604, 264605, 264760, 264762, 264682, 264764, 264685, 264766, 264767, 264689, 264691, 264693, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 18108380, 264584, 264585, 264586, 264587
1969	84328529 (3937, 3938)	Novel Protein sim. GBank gi 2911274 (U20329) - spidroin 1 [Nephila clavipes]		UNCLASSIFIED	22278995, 22278996, 35696052, 264906, 264908, 18108351, 264482
1970	80596049 (3939, 3940)	Novel Protein sim. GBank gi 4050087 (AF109907) - S164 [Homo sapiens]		UNCLASSIFIED	264908, 264288, 264766, 264636
1971	94843914 (3941, 3942)	Novel Protein sim. GBank gi 134208 sp P09593 SANT_PLAFV - S-ANTIGEN PROTEIN PRECURSOR		collagen	264486, 264489, 22278998, 264259, 60432049, 66714117, 29331826, 60432289, 29331827, 35696052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 264591, 264592, 60432229, 60433356, 264595, 264596, 264600, 264604, 264605, 264760, 18108351, 264448, 264764, 264288, 264766, 264768, 264769, 21908765, 33657023, 264692, 18108370, 264629, 35696423, 65274791, 35695855, 264632, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 60432113, 22278900, 264583, 264584, 264585, 264586, 264486
1972	87645444 (3943, 3944)	Novel Protein sim. GBank gi 4519623 db BAA75671.1 - (AB017616) homologous to the yeast YGR163 gene [Mus musculus]	Contains protein domain (PF01462) - Leucine rich repeat N-terminal domain		22278999, 264259, 29331822, 56182181, 60432289, 29331827, 52644045, 264909, 265006, 264511, 265008, 52644286, 265018, 265019, 264761, 264689, 21906768, 21906769, 264691, 264693, 33657109, 33657182, 264556, 52644332, 264558, 60432113
1973	88395533 (3945, 3946)			UNCLASSIFIED	29331826, 264692, 35696423, 264631, 264595, 264596, 264557, 264558, 264559
1974	80396629 (3947, 3948)	Novel Protein sim. GBank gi 3309543 (AF036382) - MLL [Fugu rubripes]		UNCLASSIFIED	264682, 264764, 264563

1975	04316479 (3949, 3950)			UNCLASSIFIED	264488, 66714117, 29331826, 29331828, 58182435, 265008, 264757, 55812038, 285010, 265017, 264369, 55811957, 65274791, 35895855, 58182323, 60432113
1976	95358914 (3851, 3952)			UNCLASSIFIED	264259, 35696052, 265018, 265020, 265021, 33657109, 56526486
1977	94852684 (3953, 3954)	Novel Protein sim. GBank gl 2499520 sp Q07782 NASU_RAT - SODIUM/SULFATE COTRANSPORTER (NA(+)/SULFATE COTRANSPORTER)		homeobox	264908, 264596, 265021, 264566
1978	87447845 (3955, 3956)	Novel Protein sim. GBank gl 103421 pir A33471 - transcription factor NTF1 - fruit fly (Drosophila melanogaster) (fragment)		transcriptfactor	60170831, 264566
1979	87627708 (3957, 3958)	Novel Protein sim. GBank gl 2244815 emb CAB10238.1 - (Z97336) hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	28331828, 29146498, 264905, 264907, 265007, 265009, 265010, 265018, 264686, 18108359, 21908788, 35695917, 265020, 60170815, 264693, 18108368, 18108370, 264631, 264635, 264556, 264558, 18108384, 22279000, 264585
1980	86577059 (3959, 3960)	Novel Protein sim. GBank gl 4759290 ref NP_004642.1 pUSP1 - Ubiquitin carboxyl-terminal hydrolase, X-linked		ubiquitin	264489
1981	87608874 (3961, 3962)	Novel Protein sim. GBank gl 4406693 pb AAD20060 - (AF131849) Unknown [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278999, 264259, 29331825, 29331828, 29146498, 29146499, 264107, 264908, 264910, 264595, 21906754, 265010, 265017, 265018, 265019, 264448, 264288, 21908787, 33657023, 27488284, 18108370, 18108374, 18108376, 264630, 264831, 264635, 18108385, 87168518, 22279000, 264482, 264584
1982	90995367 (3963, 3964)	Novel Protein sim. GBank gl 5689523 db BAA83045.1 - (AB029016) KIAA1093 protein [Homo sapiens]			65274572, 29331825, 35696052, 33656970, 264909, 265008, 55811386, 264760, 264686, 264691, 27486264
1983	95098668 (3965, 3966)	Novel Protein sim. GBank gl 3417297 (AC002310) - Unknown gene product [Homo sapiens]	Contains protein domain (PF00036) - Zinc finger, C2H2 type	transcriptfactor	22278996, 35696288, 264259, 29331822, 20281099, 29331824, 60432289, 29331827, 284509, 264905, 264906, 264907, 86712502, 264908, 52844045, 264909, 264510, 264512, 264910, 265009, 264591, 264592, 60433356, 60433438, 294758, 265010, 264600, 264603, 264604, 264780, 264762, 264763, 264764, 264766, 264687, 264768, 264769, 21908765, 55811957, 35695917, 264690, 264692, 264693, 264628, 264629, 263978, 18108379, 35698423, 35695855, 20281071, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 83373044, 18108385, 22279000, 22279002

1984	85760989 (3967, 3968)	Novel Protein sim. GBank gij2896695jemb[CAA17174.1] - (AL021897) fadD14 [Mycobacterium tuberculosis]		synthase	264688, 21906766, 55811957, 56984075, 265020, 265021, 22278999, 265022, 264259, 29331822, 33857182, 29148499, 264628, 18108370, 264908, 264628, 55811576, 35695855, 265008, 265007, 264591, 21908754, 33657084, 265010, 265017, 265019, 264288
1985	85636897 (3969, 3970)	Novel Protein sim. GBank gij5712131gbjAAD47379.1[AF12049 - (AF120499) DEM1 protein [Homo sapiens]		glycoprotein	264760, 264288, 263978, 55811576, 264637, 56182323, 18108385, 264584
1986	80200507 (3971, 3972)	Novel Protein sim. GBank gij4868443gbjAAD31319.1[AF14457 - (AF144573) Mx-interacting protein kinase PKM [Mesocricetus auratus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	UNCLASSIFIED	264488, 264629
1987	87011117 (3973, 3974)	Novel Protein sim. GBank gij4868443gbjAAD31319.1[AF14457 - (AF144573) Mx-interacting protein kinase PKM [Mesocricetus auratus]		UNCLASSIFIED	22278999, 29331830, 265007, 265018, 21906768, 33657023, 264692, 264693, 18108377, 264635, 60170384, 22279002
1988	94122108 (3975, 3976)			UNCLASSIFIED	264905, 264906, 264907, 264908, 264909, 264910, 264591, 264593, 264758, 264764, 264688, 264768, 265021, 264692, 264628, 264628, 35695855, 264630, 264635, 264636, 264637, 264638, 264639, 264483
1989	91225225 (3977, 3978)	Novel Protein sim. GBank gij2801701 (AF042379) - spindle pole body protein spc87 homolog GCP2 [Homo sapiens]		tubulin	60432049, 60432289, 52844045, 56182435, 264112, 265007, 33657402, 52644229, 21906765, 21906768, 21906769, 55811957, 33657023, 263967, 33657109, 18108370, 22279000, 22279002
1990	85699888 (3979, 3980)	Novel Protein sim. GBank gij5701727jdbjBAA83074.1] - (AB024728) alpha-1,3-D-mannoside beta-1,4-N-acetylglucosaminyltransferase IV-homologue [Homo sapiens]			264508, 264757, 264764, 18108381
1991	95353114 (3981, 3982)	Novel Protein sim. GBank gij4240287jdbjBAA74822.1] - (AB020706) KIAA0899 protein [Homo sapiens]	Contains protein domain (PF01802) - Adaptin N terminal region	glycoprotein	18108394, 56182575, 22278994, 35698288, 5694075, 22278997, 22278999, 29331822, 29331824, 29331825, 60432289, 29331828, 264508, 264906, 264907, 264908, 56182435, 264510, 265007, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264762, 18108351, 264763, 264683, 264369, 264288, 264885, 264766, 264687, 264768, 21906765, 21906768, 21906769, 55811957, 265020, 60431528, 263974, 18108379, 35695855, 264555, 264557, 264639, 83373044, 18108384, 87168518, 60432113, 22279000, 22279002, 264564, 264488
1992	95317232 (3983, 3984)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type	struct	29331827, 264906, 264907, 264909, 265007, 264603, 264766, 264688, 264768, 21906768, 264628, 264635, 264636, 18108385, 56528486, 264586, 264587
1993	80054763 (3985, 3986)	Novel Protein sim. GBank gij2565091 (U80761) - CTG28 alternate open reading frame [Homo sapiens]		UNCLASSIFIED	264592, 35698423

1984	84329114 (3987, 3988)	Novel Protein sim. GBank gi 5630077 gb AAD45822.1 AC00601 - (AC006017) similar to ALR; similar to AAC51735 (PID:g2358287) [Homo sapiens]	Contains protein domain (PF00856) - mapolymerase SET domain	264488, 22278997, 22278998, 22278999, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284905, 284907, 284908, 265008, 60432229, 33657402, 60433356, 264757, 60433438, 264758, 33109954, 265011, 265017, 265018, 265019, 284684, 284369, 284685, 284686, 264768, 21906765, 21906767, 21906768, 21906769, 265020, 284690, 18108362, 284693, 85274620, 18108370, 284635, 284555, 284556, 284557, 56182323, 83373044, 56528486, 22278900, 22278902, 264564
1995	85414353 (3989, 3990)	Novel Protein sim. GBank gi 4827040 ref NP_005110.1 pTRAP - thyroid hormone receptor-associated protein, 150 kDa subunit	UNCLASSIFIED	264488, 18108396, 22278994, 56984075, 22278996, 35896286, 22278997, 22278999, 264259, 29147620, 56182181, 29331824, 60432289, 29331828, 29331827, 35896052, 29148499, 284905, 284907, 66712502, 56182435, 265008, 265007, 265009, 60431735, 60433356, 33657402, 264595, 55812038, 33657084, 55811386, 85658542, 265010, 265011, 265017, 265018, 265019, 264761, 264762, 284448, 284683, 284764, 284288, 284766, 284686, 264768, 264769, 56181562, 264689, 21906765, 21906768, 21906767, 29148627, 21906768, 21908769, 29148629, 29148784, 265020, 265021, 264690, 18108361, 284693, 27486262, 27486264, 27486265, 18108370, 60431528, 18108374, 18108377, 35896423, 55811576, 65274791, 35895855, 284631, 264634, 264635, 264555, 284636, 60431850, 264557, 264558, 284559, 83373044, 20798451, 87188518, 264404, 60432113, 264567, 264564
1998	80254186 (3991, 3992)	Novel Protein sim. GBank gi 791146 emb CAA60020 - (X88028) extensin-like protein [Vigna unguiculata]	UNCLASSIFIED	
1997	87028423 (3993, 3994)	Novel Protein sim. GBank gi 2642034 (AF034547) - protein; phosphatase M130 myosin binding subunit [Ovis aries]	Contains protein domain (PF00023) - Ank repeat	264808, 264909, 264592, 264593
1998	85262704 (3995, 3996)	Novel Protein sim. GBank gi 4589634 db BAA76039.1 - (AB023212) KIAA0995 protein [Homo sapiens]	UNCLASSIFIED	264113, 264685, 284555, 284567

1899	94324903 (3897, 3998)	Novel Protein sim. GBank gi 5225312 gb AAD0846.1 AF07244 - (AF072441) catchneurin binding protein cabin 1 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	UNCLASSIFIED	18108394, 18108397, 35696286, 60424289, 29331827, 29331828, 35696052, 285008, 264512, 55811386, 265010, 265018, 265019, 55811150, 18108351, 264763, 264882, 264369, 264685, 264686, 56181562, 265020, 264691, 33657023, 264693, 33657109, 27486264, 18108370, 18108379, 35695855, 264634, 264635, 264636, 264555, 264557, 56182323, 18108382, 264559, 83373044, 60432113, 22279000, 264563, 264564, 264566
2000	95413705 (3998, 4000)	Novel Protein sim. GBank gi 1723232 sp Q10155 YATA_SCHPO - HYPOTHETICAL 90.6 KD PROTEIN C104.10 IN CHROMOSOME I		UNCLASSIFIED	52646365, 52646842, 22278994, 22278995, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 52645080, 28331822, 29331826, 29331827, 29331828, 35696052, 264106, 29331830, 52644045, 265007, 265008, 60170831, 264592, 264593, 33657402, 60433438, 21908754, 52644296, 265017, 265018, 265019, 264761, 264389, 264286, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 60170815, 52644150, 33657023, 85274620, 52645129, 27486261, 27486262, 27486284, 35695763, 35696423, 35695855, 264631, 52644332, 56182323, 60170394, 83373044, 56526488, 22279002, 264566, 264567
2001	95072534 (4001, 4002)	Novel Protein sim. GBank gi 107560 pir j B38637 - Ras inhibitor (clone JC285) - human (fragment)		UNCLASSIFIED	264769, 52644229, 65274572, 21908768, 22278996, 35696286, 35695917, 265020, 22278999, 264534, 264490, 264259, 264692, 60432289, 33657109, 35696052, 264508, 264509, 18108370, 60431528, 18108374, 35696423, 65274791, 35695855, 264510, 264511, 264512, 265009, 264634, 264636, 264555, 264556, 264638, 264557, 264558, 264559, 60433438, 83373044, 264759, 18108385, 265011, 264600, 264601, 60432113, 264603, 264604, 264605, 264448, 264288, 264765
2002	80236366 (4003, 4004)	Novel Protein sim. GBank gi 728433 sp P38657 ER60_BOVIN - PROBABLE PROTEIN DISULFIDE ISOMERASE ER-60 PRECURSOR (ERP60) (58 KD MICROSMAL PROTEIN) (P59)	Contains protein domain (PF00085) - Thioredoxin	isomerase	264907, 265006, 264810, 264803, 264692, 264629, 18108374, 264556, 264557
2003	80074449 (4005, 4006)	Novel Protein sim. GBank gi 86388 pir j A27040 - neurofilament triplet M protein - chicken (fragment)		UNCLASSIFIED	264905, 264906, 264908, 264910, 264596, 265017, 18108351, 264692, 264629, 264634, 264565

2004	95317318 (4007, 4008)	Novel Protein sim. GBank gi 4884249 emb CAB43230.1 - (AL049998) hypothetical protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	52645156, 52646842, 52646365, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 60432049, 284259, 32645080, 28331824, 29331826, 29331827, 35896052, 29331828, 33658970, 29331830, 284908, 284592, 60433356, 33657402, 52846317, 21906754, 33657084, 52644298, 87188474, 87168559, 285017, 285018, 285019, 284763, 284883, 284288, 52844228, 21906765, 21906786, 21906787, 21906789, 35695917, 265020, 265021, 265022, 52644150, 33657023, 52845129, 33657109, 33657182, 27486281, 27486282, 33657349, 27486265, 35895763, 18108374, 18108376, 18108377, 35898423, 35695855, 284631, 52844332, 284558, 18108385, 56826486, 87168518, 60432113, 284483, 284488, 284906
2005	87400884 (4009, 4010)	Novel Protein sim. GBank gi 3879501 emb CAA87795 - (Z47812) similar to ubiquitin carboxyl-terminal hydrolase; cDNA EST EMBL:D33388 comes from this gene; cDNA EST EMBL:D33965 comes from this gene; cDNA EST EMBL:D33822 comes from this gene; cDNA EST EMBL:D34547 comes from this ge...		ubiquitin	
2006	95351177 (4011, 4012)	Novel Protein sim. GBank gi 4106673 emb CAA22613 - (AL035064) queuine tRNA-ribosyltransferase [Schizosaccharomyces pombe]	Contains protein domain (PF01702) - Queuine tRNA-ribosyltransferase	UNCLASSIFIED	56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 22278999, 284259, 56182181, 60424269, 68714117, 35696052, 284908, 68712502, 284909, 284510, 60433356, 85658542, 285010, 285018, 285019, 284682, 284448, 284288, 284768, 28148627, 21906789, 29148784, 35695917, 60170615, 284691, 33657023, 65274620, 33657109, 55810784, 55811576, 35695855, 87168518, 60432113, 284583, 284482
2007	94325556 (4013, 4014)	Novel Protein sim. GBank gi 2662161 dbj BAA23712 - (AB007800) HH0452 cDNA clone for KIAA0440 has a 438-bp insertion at position 1711 of the sequence of KIAA0440. [Homo sapiens]		UNCLASSIFIED	284488, 263894, 35696052, 284508, 284905, 284906, 284907, 284908, 284909, 265007, 284910, 284592, 284595, 284758, 285011, 284760, 284782, 284784, 284786, 284685, 284787, 284788, 284789, 55811957, 35695917, 285020, 284691, 284693, 284628, 284629, 65274791, 35695855, 284631, 284632, 284634, 284635, 284637, 284638, 284839, 284586
2008	85084428 (4015, 4016)	Novel Protein sim. GBank gi 1550783 emb CAA69257 - (Y07860) homeodomain protein [Mus musculus]	Contains protein domain (PF00046) - Homeobox domain	homeobox	284909, 284768, 35695855

2008	85740240 (4017, 4018)	Novel Protein sim. GBank gll3882305[dbj]BAA34512.1] - (AB018335) KIAA0792 protein [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 264910, 264591, 265017, 264681, 264683, 21806788, 264691, 33857182, 33857348, 264631, 87168518, 264404, 22279002, 264583
2010	95422458 (4019, 4020)	Novel Protein sim. GBank gll5262829[emb]CAB45763.1] - (AL080164) hypothetical protein [Homo sapiens]	Contains protein domain (PF00057) - Low-density lipoprotein receptor domain class A	- eph	52844507, 52845156, 52846365, 52846842, 18108397, 65274572, 22278994, 56994075, 35986286, 22278996, 22278997, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 29331826, 29331827, 29331828, 264511, 265007, 264512, 265008, 265009, 60432228, 60433356, 21908754, 52846317, 33109954, 52844298, 87168474, 87168559, 265017, 265018, 265019, 264681, 264685, 264687, 52844229, 264689, 21908765, 21908766, 21908767, 21808768, 35895917, 265020, 52844150, 264691, 264692, 33857023, 263967, 52845128, 35895763, 18108376, 35896423, 65274791, 35895855, 264631, 264634, 60431850, 264637, 264638, 52844332, 80170394, 18108385, 87168518, 22279002, 264584, 264585, 264586, 264587, 56182575, 56994075, 22278999, 264259, 29331824, 29331826, 29331827, 29331828, 35896052, 264906, 66712502, 265006, 265007, 265008, 265010, 265011, 265017, 265018, 264681, 264448, 264683, 264389, 264288, 264685, 264766, 264687, 21908765, 21908767, 21908768, 21908769, 265020, 265022, 264691, 33857023, 65274620, 33857109, 264629, 264557, 264559, 89373044, 87168518, 60432113, 22279002, 264259, 29331822, 29331824, 29331825, 29146498, 87168558, 265019, 264682, 264288, 264686, 21908764, 265020, 265022, 33857023, 264693, 33857109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2011	94328149 (4021, 4022)	Novel Protein sim. GBank gll3347853 (AF076183) - cytosolic sorting protein PACS-1a [Rattus norvegicus]		UNCLASSIFIED	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692, 264488, 29331826, 264907, 264638, 264555, 264639, 264558
2012	87772137 (4023, 4024)	Novel Protein sim. GBank gll1086678 (U41020) - coded for by C. elegans cDNA yk100g4.5; coded for by C. elegans cDNA yk100g4.3; weakly similar to human SREBP-2 basic-helix-loop-helix-leucine zipper transcription factor [Caenorhabditis elegans]	Contains protein domain (PF00409) - Kinesin light chain repeat	UNCLASSIFIED	29146498, 87168558, 265019, 264682, 264288, 264686, 21908764, 265020, 265022, 33857023, 264693, 33857109, 55811576, 264632, 264558, 56182323, 264639, 18108383, 18108384, 18108388, 22279000, 22279002, 264587
2013	94843842 (4025, 4026)	Novel Protein sim. GBank gll4507985[ref]NP_003427.1]pZNF1 - zinc finger protein 135 (clone pHz-17)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	- dna_rna_bind	18108398, 264908, 265007, 265010, 265018, 265019, 264689, 21908767, 265020, 264692, 264488, 29331826, 264907, 264638, 264555, 264639, 264558
2014	87347940 (4027, 4028)	Novel Protein sim. GBank gll127720[epi]P20938[MYPO_HETFR - MYELIN P0 PROTEIN PRECURSOR		UNCLASSIFIED	

2015	88094822 (4029, 4030)	Novel Protein sim. GBank gl 81288 pir S22697 - extensin - Valvex carten (fragment)		UNCLASSIFIED	56182575, 35696286, 284259, 35696052, 284508, 284908, 284907, 284510, 284512, 87168474, 285010, 284681, 284288, 284689, 284628, 35698423, 35698555, 284639, 284663, 284564
2016	85298641 (4031, 4032)	Novel Protein sim. GBank gl 285046 pir S28413 - t-complex protein Tcp-10 - mouse	sinud		284102, 284508, 284110, 285009, 33109954, 21908768, 285021, 33657109, 27488282, 283972, 18108374, 283976, 284555, 284564
2017	79464293 (4033, 4034)			UNCLASSIFIED	284685, 284636
2018	78637067 (4035, 4036)	Novel Protein sim. GBank gl 124735 sp P18175 INVO_PIG - INVOLUCRIN			284683
2019	87787900 (4037, 4038)	Novel Protein sim. GBank gl 2143910 pir S68216 - phosphatase-1 glycogen-binding (GL)-chain - rat	phosphatase		284107, 284110, 284112, 285017, 283976
2020	94674476 (4039, 4040)	Novel Protein sim. GBank gl 2078483 (U43200) - antifreeze glycoprotein AFGP polypeptide precursor [Boreogadus saida]		UNCLASSIFIED	284259, 284508, 284591, 285018, 284682, 284288, 284688, 22278002
2021	88718818 (4041, 4042)	Novel Protein sim. GBank gl 585084 sp Q07803 EFGM_RAT - ELONGATION FACTOR G, MITOCHONDRIAL PRECURSOR (MEF-G)			56994075, 284593, 33109954, 21908754, 21908768, 33657023, 33657109, 27486261, 87168518
2022	85285665 (4043, 4044)	Novel Protein sim. GBank gl 4218005 (AC006135) - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]			284757, 284767, 60170615, 18108385
2023	87722976 (4045, 4046)	Novel Protein sim. GBank gl 5410230 gb AAD2892.1 AF07334 - (AF073344) ubiquitin specific protease 3 [Homo sapiens]	Contains protein domain (PF00442) - Ubiquitin carboxyl-terminal hydrolases family 2		18108394, 22278999, 284259, 284905, 284906, 284908, 284595, 284762, 284769, 284634, 284638, 87168518, 60432113, 22279000, 284482, 284585
2024	87868443 (4047, 4048)				60433438, 265017, 284686, 284692, 284693, 284636
2025	87858863 (4049, 4050)	Novel Protein sim. GBank gl 4755188 gb AAD29055.1 AC00701 - (AC007018) unknown protein [Arabidopsis thaliana]	Contains protein domain (PF00637) - 7-fold repeat in Clathrin and VPS	UNCLASSIFIED	22278997, 284509, 284906, 284909, 55812038, 265017, 265021, 285022, 60170815, 284558
2026	84122114 (4051, 4052)	Novel Protein sim. GBank gl 165569 emb CAA69032 - (Y07752) pterophorin-S [Valvex carten]		UNCLASSIFIED	56994075, 60432049, 284508, 66712502, 284112, 60170831, 87168559, 284288, 284688, 284689, 21908768, 33657109, 18108370, 284638, 18108385, 60432113, 22279000, 22278002, 284564, 284566, 284587
2027	80249001 (4053, 4054)			UNCLASSIFIED	283976, 284634, 284488

2028	84689884 (4055, 4056)	Novel Protein sim. GBank g11330345 (U58755) - coded for by C. elegans cDNA yk34b1.5; coded for by C. elegans cDNA yk13h10.5; coded for by C. elegans cDNA yk46e8.5; coded for by C. elegans cDNA yk46d5.5; coded for by C. elegans cDNA yk43c2.5; coded for by C. elegans cDNA yk46e8....	Contains protein domain (PF00632) - ubiquitin-HECT-domain (ubiquitin-transferase).	32644307, 52645156, 52646842, 56182575, 56994075, 55696266, 22278997, 22278998, 22278999, 80432049, 264259, 52645080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 35696052, 264908, 264907, 264908, 29331830, 52644045, 56182435, 265008, 265009, 60432229, 33657402, 264595, 264757, 55812038, 21906754, 52646317, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 18108354, 264288, 264369, 264766, 52644429, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644150, 33657023, 65274620, 33657109, 52645129, 18108368, 27486261, 27486262, 27486264, 27486265, 35695763, 264629, 55811576, 35696423, 35695855, 264635, 264636, 52644332, 264558, 83373044, 58526486, 22278000, 22279002, 264563, 265009, 264595, 85658542, 264555, 264556, 264557, 264558, 264559, 83373044
2029	95362032 (4057, 4058)	Novel Protein sim. GBank g13599940 (AF017368) - facicogenital dysplasia protein 2 [Mus musculus]	Contains protein domain (PF00621) - RhoGEF domain	UNCLASSIFIED
2030	91213734 (4059, 4060)	Novel Protein sim. GBank g15630080 [gb]AAD45825.1 (AC004890) similar to HUB1; similar to BAA24380 (PID:g2789430) [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor
2031	80245281 (4061, 4062)			18108394, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 80432289, 29331826, 264108, 66712502, 264828, 265009, 265018, 265019, 264681, 264682, 264684, 264685, 56181562, 264689, 21906769, 265022, 264692, 264693, 264628, 18108370, 18108374, 264634, 264636, 264556, 18108385, 87168518, 22279002, 264565
2032	91232607 (4063, 4064)	Novel Protein sim. GBank g15689491 [dbj]BAA83029.1 - (AB028000) KIAA1077 protein [Homo sapiens]	Contains protein domain (PF00884) - Sulfatase	hydrolase
2033	95000808 (4065, 4066)	Novel Protein sim. GBank g12494828 [sp]OP4686 [CAG7_RAT - ALPHA-N-ACETYL GALACTOSAMINIDE ALPHA-2-6-SIALYLTRANSFERASE (ST6GALNACIII) (STY)]		synthase
2034	91232528 (4067, 4068)	Novel Protein sim. GBank g14826894 [ref]NP_005147.1 [PROT1 - UNKNOWN]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	-dna_ma_bind

2035	83553451 (4099, 4070)				264369, 264686, 265022, 56526486, 264567
2036	87115833 (4071, 4072)				29331827, 29331828, 264682, 264369, 29148627, 60432113
2037	94324833 (4073, 4074)	Novel Protein sim. GBank gll2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 29331824, 60432289, 29331828, 29331828, 35698052, 264907, 29331830, 66712502, 56182435, 265008, 265009, 60170831, 264584, 5612038, 33109954, 21908754, 87168559, 265017, 265018, 265019, 264762, 264369, 264288, 21908765, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 265022, 52644190, 33657023, 33657109, 33657182, 35695763, 35695855, 264632, 264634, 264636, 56182323, 83373044, 60432113, 22279000, 22279002, 264583
2038	95422384 (4075, 4076)	Novel Protein sim. GBank gll3880625 (embjCAB07858) - (Z63785) predicted using GeneFinder; similar to RNA recognition motif (aka RRM, RBD, or RNP domain); cDNA EST EMBL: T01682 comes from this gene; cDNA EST EMBL: M75823 comes from this gene; cDNA EST EMBL: D27559 comes from this ge...	Contains protein domain (PF01412) - Putative GTP-ase activating protein for Arf	UNCLASSIFIED	22278995, 22278996, 56994075, 264259, 29331824, 35698052, 264905, 264906, 52644045, 265007, 265009, 87168559, 265017, 18108351, 264448, 264369, 264766, 264767, 264686, 18108358, 21906765, 21906769, 52644150, 33657023, 264692, 18108362, 33657109, 27486262, 18108370, 18108374, 18108379, 35698423, 65274791, 264632, 264636, 18108383, 83373044, 18108385, 87168518, 22279000, 22279002, 264563, 264584, 264586
2039	95514628 (4077, 4078)	Novel Protein sim. GBank gll2224653 (dbj BAA20813) - (AB002354) KIAA0358 [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	22278997, 264259, 29331822, 264905, 264906, 264907, 264908, 264909, 264510, 265009, 264910, 264593, 264758, 265011, 265018, 264762, 264288, 264766, 264768, 264769, 21906766, 33657023, 264692, 264693, 33657109, 35698423, 264631, 264632, 264634, 264635, 264636, 264637, 264639, 87168518, 264486
2040	95308417 (4079, 4080)			UNCLASSIFIED	264592
2041	95071736 (4081, 4082)	Novel Protein sim. GBank gll2500825 (sp P70700 RPA2_MOUSE - DNA-DIRECTED RNA POLYMERASE I 135 KD POLYPEPTIDE (RNA POLYMERASE I SUBUNIT 2) (RPA135)	mapolymerase		264488, 22278998, 35698052, 264905, 264907, 264908, 264910, 265018, 264605, 265019, 18108351, 264766, 264769, 21908766, 265021, 265022, 264692, 33657109, 264628, 264628, 35698423, 35695855, 264637, 264638, 264563, 264584, 264565, 264567

2042	95307447 (4083, 4084)	Novel Protein sim. GBank gi 4406590 gb AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]	Contains protein domain (PF00568) - WH1 domain	UNCLASSIFIED	60424179, 35696286, 264259, 29331826, 35696052, 29331828, 264508, 284509, 264907, 264909, 264510, 264511, 265009, 264910, 264591, 60433358, 284595, 265017, 265019, 264681, 264764, 264369, 264765, 264684, 264288, 264766, 264686, 52644229, 264769, 21908765, 35695917, 264535, 52644150, 264691, 264692, 18108385, 27486261, 27486262, 27486285, 18108374, 35696423, 65274791, 35695855, 264555, 284558, 60170394, 18108385, 264404, 22279000, 22279002, 264482, 264563, 264564, 264566
2043	94328076 (4085, 4086)	Novel Protein sim. GBank gi 502554 gb AAD38607.1 AF145632) BcDNA.GH06032 [Drosophila melanogaster]	Contains protein domain (PF00122) - E1-E2 ATPase	transport	264488, 52644507, 52646385, 56994075, 22278987, 22278998, 20281171, 264259, 29331822, 29331824, 66714117, 29331826, 29331828, 33656970, 28146498, 284509, 264908, 52644045, 56182435, 265006, 33657402, 21908754, 52644296, 87168559, 265017, 265018, 265019, 264681, 264288, 264766, 264685, 264686, 21906766, 21908767, 21908768, 21908769, 265020, 285021, 60170615, 264691, 33657023, 264693, 65274620, 33657109, 33657182, 27486261, 27486262, 33657349, 35695763, 18108374, 55811576, 35695855, 18108380, 18108381, 60170394, 56182323, 284558, 83373044, 18108385, 56526486, 87168518, 60432113, 22279000, 264567
2044	87106927 (4087, 4088)	Novel Protein sim. GBank gi 2248532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struc	264093, 29331827, 264905, 66712502, 264592, 264689, 21908765, 21908769, 265020, 264692, 264482, 264566
2045	79835532 (4089, 4090)	Novel Protein sim. GBank gi 4406698 gb AAD20062 - (AF131852) Unknown [Homo sapiens]			264259, 264906, 264683, 22278002
2046	87320849 (4091, 4092)	Novel Protein sim. GBank gi 4101720 (AF008466) - lymphocyte specific formin related protein [Mus musculus]			22278999, 29147620, 29331824, 29148498, 264508, 265007, 265008, 265019, 264605, 264681, 29148627, 29148628, 265021, 33657023, 18108365, 33657109, 33657182, 18108377, 264556, 264638, 264559, 18108388
2047	84578801 (4093, 4094)	Novel Protein sim. GBank gi 4598688 gb BAA78850.1 - (AB023223) KIAA1006 protein [Homo sapiens]		UNCLASSIFIED	264909
2048	84606378 (4095, 4096)			UNCLASSIFIED	264488, 264259, 29331824, 29331828, 35696052, 264906, 264907, 264908, 264909, 264910, 264603, 264763, 21908767, 21908768, 264628, 264634, 264637, 22278002, 264564, 264565, 264566, 264567

2050	79833835 (4098, 4100)			UNCLASSIFIED	284693
2051	87780188 (4101, 4102)			UNCLASSIFIED	284488, 284259, 284509, 284808, 284907, 284789, 18108374, 35698423, 284583, 284586, 284488
2052	88096383 (4103, 4104)	Novel Protein sim. GBank gij4529889[gb][AAD21812.1] - (AF134728) G8A [Homo sapiens]	Contains protein domain (PF00356) - SET domain	kinase	284488, 283994, 35698052, 284508, 284905, 284509, 284906, 284907, 284908, 284908, 284113, 284511, 285008, 284910, 60170831, 284592, 284758, 285010, 285011, 284605, 284780, 284682, 284784, 284389, 284786, 284686, 284788, 284789, 52844229, 284689, 35695917, 33857023, 33857109, 284828, 18108374, 35698423, 55811578, 35695855, 284830, 284631, 284632, 284634, 284635, 284636, 284556, 284638, 284639, 18108385, 58528486, 60432113, 284563, 284584, 35696052, 284508, 284905, 284509, 284906, 284586, 284488, 284587, 284488, 283994, 284907, 284908, 284909, 284113, 284511, 285009, 284810, 60170831, 284592, 284758, 285010, 285011, 284805, 284780, 284882, 284784, 284389, 284786, 284688, 284788, 284789, 52844229, 284689, 35695917, 33857023, 33857109, 284628, 18108374, 35698423, 55811578, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284556, 284638, 284639, 18108385, 58528486, 60432113, 284563, 284584, 284586, 284488, 284587
2053	87763078 (4105, 4106)	Novel Protein sim. GBank gij2895449[emb][CAA75113] - [Y14848] midline 1 protein [Mus musculus]		UNCLASSIFIED	22278998, 22278997, 284259, 29331822, 284102, 284508, 35695917, 283972, 284482, 60424178, 284094, 284259, 28331825
2054	95358937 (4107, 4108)	Novel Protein sim. GBank gij3876326[emb][CAB02080] - (Z78754) similar to C2 domain [Caenorhabditis elegans]	Contains protein domain (PF00168) - C2 domain		60424289, 284908, 60432229, 60433356, 87188559, 285019, 284780, 284288, 284686, 21908789, 33857023, 284893, 55810784, 55811578, 284635, 56182323, 60432113
2055	88258449 (4109, 4110)	Novel Protein sim. GBank gij5353748[gb][AAD42226.1][AF15913] - (AF159133) SIR2-like protein [Oryza sativa subsp. indica]		UNCLASSIFIED	284488, 29331828, 60432289, 29331828, 60433356, 285019, 284883, 284884, 285021, 33857109, 18108374, 284637, 18108385, 87188518, 60432113, 22278000, 284584

2056	88177398 (4111, 4112)	Novel Protein sim. GBank g 4826980 ref NP_005042.1 pQARS - glutamine-IRNA synthetase	Contains protein domain (PF00749) - IRNA synthetases class I (E and Q)	synthase	284488, 52845156, 56182575, 22278994, 35698286, 58694075, 22278998, 22278998, 22278999, 60432049, 284259, 29331824, 60432289, 29331827, 29331828, 33656970, 284104, 284908, 284908, 285006, 285008, 60170831, 264591, 60432229, 60433438, 18108348, 21908794, 33657084, 52844296, 87168474, 265010, 87168559, 265017, 265018, 284760, 18108351, 284881, 284882, 284448, 264883, 284389, 284288, 264685, 284887, 254888, 264689, 21908785, 21908766, 21908787, 21908769, 55811957, 35695917, 265022, 33657023, 18108362, 33657109, 18108388, 33657182, 27486281, 27486284, 27486285, 33657349, 264828, 18108370, 284629, 18108374, 18108377, 18108378, 35696423, 55811578, 20281152, 264838, 264852, 18108385, 18108388, 87168518, 284482, 284595, 284598, 284567 52846842, 52846365, 56182575, 35696286, 22278998, 22278997, 22278998, 264093, 52845080, 35698052, 29331828, 33656970, 285008, 52846317, 55811386, 52844296, 52844229, 21908788, 35695917, 265021, 60170815, 52844150, 33657109, 33657182, 27486261, 27486282, 35695763, 35696423, 35695855, 52844332
2057	87877805 (4113, 4114)	Novel Protein sim. GBank g 728850 p P08640 AMYH_YEAST - GLUCOAMYLASE S1/S2 PRECURSOR (GLUCAN 1,4-ALPHA- GLUCOSIDASE) (1,4-ALPHA-D-GLUCAN GLUCOHYDROLASE)		UNCLASSIFIED	
2058	86276898 (4115, 4116)	Novel Protein sim. GBank			285007, 265008, 284591
2059	79866684 (4117, 4118)	g 119714 p P13983 EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)		UNCLASSIFIED	29331825, 284682, 264686, 264691, 284693, 22278002
2060	83050800 (4119, 4120)	Novel Protein sim. GBank g 281122 (U87318) - NaDC-2 [Xenopus laevis]		UNCLASSIFIED	56182575, 29331824, 29331828, 284910, 55811957, 18108370, 55811578

2061	95362204 (4121, 4122)	Novel Protein sim. GBank gi 2486947 sp Q09289 YCO9_CAEEL - HYPOTHETICAL 141.2 KD PROTEIN EEED8.9 IN CHROMOSOME II	Contains protein domain (PF00009) - Eukaryotic protein kinase domain	kinase	22278997, 22278998, 284259, 29331822, 29331824, 29331828, 29331827, 35696052, 29331828, 284906, 68712502, 29331830, 284908, 284909, 284112, 284511, 285007, 285008, 284910, 284591, 33857402, 21906754, 85658542, 285017, 285019, 284448, 284883, 284288, 284684, 284369, 284886, 284887, 18108358, 284889, 21906785, 21906787, 21906788, 21906789, 285020, 285022, 284891, 33857023, 33857109, 20281149, 18108379, 35695855, 284634, 284558, 284557, 284558, 18108382, 284559, 83373044, 18108384, 58528488, 60432113
2062	87028440 (4123, 4124)	Novel Protein sim. GBank gi 4502091 ref NP_001139.1 pANK2 - ankyrin 2, neuronal	Contains protein domain (PF00023) - Ank repeat	struct	284905, 284628, 284907, 284628, 284908, 284909, 18108374, 283978, 35695855, 284512, 284635, 60431850, 284836, 284760, 284563, 18108351, 284782, 284585, 284784, 284487, 284788
2063	87801272 (4125, 4126)	Novel Protein sim. GBank gi 4589562 db BAA78803.1 - (AB023178) KIAA0959 protein [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	oncogene	22278994, 22278998, 284259, 29331827, 284906, 284909, 52844045, 284886, 21906767, 55811957, 284892, 18108365, 263972, 55811578, 18108384, 22279002, 284482, 284563, 284584, 284484
2064	95317253 (4127, 4128)	Novel Protein sim. GBank gi 1754515 db BAA13413.1 - (D87515) aminopeptidase-B [Rattus norvegicus]		hydrolase	284488, 52846365, 56994075, 35696286, 22278997, 22278998, 284259, 29331828, 60432289, 29331827, 29331828, 35696052, 284509, 285007, 285008, 60432229, 60433438, 21906794, 285010, 285011, 87188559, 285017, 285018, 284781, 18108351, 284682, 284369, 284286, 52844229, 21906785, 21906787, 21906788, 35695817, 33857109, 18108368, 18108374, 35698423, 35695855, 52844332, 284559, 60432113, 22279000, 22279002, 284586, 284488
2065	95082238 (4129, 4130)	Novel Protein sim. GBank gi 2507144 sp Q04205 TENS_CHICK - TENSIN		kinase	284569, 18108394, 56182181, 60432289, 29331828, 284905, 284906, 284908, 60431735, 60433356, 55811386, 85658542, 285018, 55811150, 284681, 284788, 284692, 60431828, 283974, 55810784, 35695855, 284631, 284634, 284635, 60431850, 284557, 83373044, 18108388, 22279000, 22279002, 56182575, 284259, 284906, 284784, 284288, 56182323, 284567
2066	85793402 (4131, 4132)	Novel Protein sim. GBank gi 160171 (M58295) - circumsporozoite protein, [Plasmodium yoelii]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	UNCLASSIFIED	

2067	95303892 (4133, 4134)				35686286, 22278997, 22278998, 60432049, 284259, 60432289, 60433438, 284682, 284448, 284369, 284288, 18108355, 21908765, 21908768, 265022, 33657109, 35686423, 35686555, 284558, 284404, 284583, 284488
2068	84344754 (4135, 4136)			UNCLASSIFIED	284687
2069	94316177 (4137, 4138)	Novel Protein sim. GBank gl 3152882 (AF084604) - KE03 protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	transcript factor	60424179, 56182575, 22278995, 22278996, 56994075, 264259, 29331822, 29331824, 29331825, 35686052, 29331828, 33656970, 284509, 284905, 56182435, 265009, 60433356, 87188559, 265017, 285018, 284604, 285019, 284448, 284764, 284766, 21908765, 21908767, 21908768, 21908769, 285020, 265021, 33657023, 33657109, 283976, 284555, 284557, 56182323, 83373044, 87188518, 60432113, 22278000, 22278002
2070	85791380 (4139, 4140)	Novel Protein sim. GBank gl 5712131(gb)AAD47379.1(AF12049) - (AF120499) DEM1 protein [Homo sapiens]		UNCLASSIFIED	35685917, 264805, 264828, 264908, 264638
2071	86946116 (4141, 4142)	Novel Protein sim. GBank gl 3551531(dbj)BAA33016] - (AB017437) avena [Gallus gallus]	Contains protein domain (PF00568) - WH1 domain		18108398, 265008, 265007, 265008, 265009, 284594, 265010, 265011, 18108351, 18108354, 18108364, 18108385, 18108368, 284634, 18108381, 18108385, 18108388, 18108391
2072	91718429 (4143, 4144)		Contains protein domain (PF00184) - Neurohypophyseal hormones, C-terminal Domain		22278995, 35686286, 22278997, 22278998, 22278999, 284480, 60432049, 284259, 29331822, 29331824, 29331826, 35686052, 265008, 33657402, 21908764, 285011, 285018, 18108351, 264682, 284389, 21908765, 21908766, 21908767, 21908768, 21908789, 35685917, 265020, 265021, 284680, 284692, 35686423, 264555, 264556, 284598, 22278000
2073	27825684 (4145, 4146)	Novel Protein sim. GBank gl 1504026(dbj)BAA13212] - (D86976) similar to C. elegans protein (Z37083) [Homo sapiens]		UNCLASSIFIED	284559
2074	94324787 (4147, 4148)	Novel Protein sim. GBank gl 4240317(dbj)BAA74837.1] - (AB020721) KIAA0914 protein [Homo sapiens]			28331822, 284809, 264511, 265009, 284594, 284595, 265010, 265011, 265017, 265018, 265019, 284448, 284683, 265020, 265021, 18108370, 284632, 83373044, 284587

2075	94314886 (4149, 4150)	Novel Protein sim. GBank gl 5138930 gb AA040382.1 - (AF093860) transcription factor IIB [Homo sapiens]			18108394, 22278994, 22278996, 35696286, 22278998, 22278999, 264259, 29331822, 29331825, 29331827, 35896052, 29331828, 264905, 264907, 264908, 264510, 265007, 264910, 265009, 33657084, 264760, 264448, 264288, 264766, 264767, 264688, 21908768, 21908767, 21908769, 265021, 265022, 60170615, 33657023, 27486282, 27486285, 35696423, 35695855, 264631, 264634, 264638, 87186518, 22279002, 264563, 264488, 18108391
2076	87594118 (4151, 4152)				264259, 29331828, 264508, 264908, 264510, 265007, 265011, 264288, 264637, 18108385
2077	11389877 (4153, 4154)			UNCLASSIFIED	264592
2078	87539384 (4155, 4156)	Novel Protein sim. GBank gl 4220350 gb BAA74578 - (D87908) nuclear protein np85 [Mus musculus]	Contains protein domain (PF00628) - PHD-finger		29331825, 265017, 265018, 264288, 265020, 265021, 264634, 58526488
2079	88095916 (4157, 4158)	Novel Protein sim. GBank gl 4240255 gb BAA74908.1 - (AB020890) KIAA0883 protein [Homo sapiens]	Contains protein domain (PF00098) - Zinc finger, CCHC class	UNCLASSIFIED	264768, 22278997, 265021, 264690, 264259, 264692, 29331822, 264693, 29331824, 29331828, 264508, 264509, 264908, 264907, 264628, 20281089, 264808, 265007, 265009, 264632, 264636, 264591, 264592, 264639, 264758, 264759, 33109954, 264604, 265018, 265019, 22279002, 264583, 264584, 264448, 264684, 264587, 264685
2080	84136889 (4159, 4160)	Novel Protein sim. GBank gl 240802 emb CAB18219.1 - (Z99162) putative vacuolar protein [Schizosaccharomyces pombe]	Contains protein domain (PF01363) - FYVE zinc finger	UNCLASSIFIED	56182575, 264092, 29331824, 29331826, 29331830, 265017, 265018, 265020, 83373044
2081	94847186 (4161, 4162)	Novel Protein sim. GBank gl 5524734 gb AA044360.1 AF166350 ST7 protein [Homo sapiens]	Contains protein domain (PF00431) - CUB domain	eph	22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 33657402, 85858542, 265011, 265018, 265019, 21908767, 21908768, 264693, 18108385, 22279000, 22279002
2082	87628628 (4163, 4164)	Novel Protein sim. GBank gl 3880558 emb CAA94234 - (Z70271) predicted using GeneFinder; similar to collagen; cDNA EST yk308e7.3 comes from this gene; cDNA EST yk308e7.5 comes from this gene; cDNA EST yk385a8.3 comes from this gene; cDNA EST yk385a8.5 comes from this gene [Caeno...]		collagen	264807, 265019
2083	94141000 (4165, 4166)	Novel Protein sim. GBank gl 2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Cryptotagus cuticularis]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	56182575, 22278996, 22278997, 264259, 29331822, 29331825, 264508, 264112, 265009, 264593, 21908764, 265018, 265019, 264448, 264288, 264885, 21908769, 265020, 265022, 264691, 18108370, 65274791, 264631, 264555, 264583
2084	95198288 (4167, 4168)	Novel Protein sim. GBank gl 7283689 p39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		UNCLASSIFIED	265018, 264763, 264683, 264691

2085	84988476 (4169, 4170)	Novel Protein sim. GBank gij1655699[embjCAA69032] - (Y07752) pherophorin-S [Volvox carter]	UNCLASSIFIED	56182575, 60432289, 264908, 56182435, 87168474, 264783, 264369, 264688, 264693, 18108370, 56182323
2086	91234404 (4171, 4172)	Novel Protein sim. GBank gij3875032[embjCAA8936] - (Z49125) similarity to Trichostromyolus colubriformis 11 kd secretory protein (Swiss Prot accession number P21937); cDNA EST EMBL:D33349 comes from this gene; cDNA EST EMBL:D37644 comes from this gene; cDNA EST EMBL:D36149 comes...	UNCLASSIFIED	35696286, 264259, 35696052, 264906, 264907, 264908, 264909, 264910, 264759, 264604, 264762, 264768, 264769, 35695917, 263978, 35695423, 35695555, 264632, 264634, 264637, 264638, 264639, 56182323, 18108385, 264482, 264486
2087	21436337 (4173, 4174)		UNCLASSIFIED	264489
2088	94111527 (4175, 4176)	Novel Protein sim. GBank gij3880930[embjCAA16334, 1]- (AL021481) similar to Phosphoglucosylase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST EMBL:T0080...		264488, 22278994, 35696286, 22278996, 29331827, 35696052, 33657402, 21906754, 33109954, 87168474, 265017, 265018, 265019, 264448, 264683, 264369, 264685, 264687, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 265022, 264692, 33657023, 33657109, 33657182, 27488261, 27488262, 33657349, 27488265, 35696423, 35695855, 83373044, 87168518, 22278000, 264567
2089	95422801 (4177, 4178)	Novel Protein sim. GBank gij4758118[refjNP_004623.1]pDAP3 - Death associated protein 3	cadherin	18108392, 264488, 52644507, 18108394, 18108397, 52646842, 18108398, 56182575, 22278994, 22278995, 35696286, 22278998, 56994075, 22278997, 22278998, 22278999, 264091, 264092, 264093, 264094, 60432049, 264259, 29331822, 20281099, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33856970, 29146498, 29146499, 284102, 284106, 284107, 264109, 264508, 264905, 264509, 264908, 264907, 264908, 68712502, 264628, 52644045, 264609, 56182435, 264110, 264112, 264510, 264511, 265006, 264512, 265007, 265008, 264910, 265009, 60170831, 264592, 264593, 60433356, 33657402, 60433438, 264595, 55812038, 264758, 21908754, 33657084, 55811368, 52644296, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264761, 55811150, 264762, 18108351, 264682, 264448, 264763, 264764, 264683, 264369, 18108354, 264288, 264685, 264766, 264686, 264687, 264768, 52644229, 264688, 18108356, 56181582, 264769, 18108359, 264689, 21908765, 21908766, 21908767, 21908768, 29148627, 21908769, 55811957, 29148628, 29148784, 35695917, 265020, 265021, 265022, 60170815, 264690

2080	88222470 (4179, 4180)				22278895, 22278898, 22278899, 264259, 29331826, 35686052, 264910, 33657402, 60433438, 33109954, 87168474, 87168559, 265018, 265019, 264681, 264684, 264686, 264687, 264688, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 265022, 60170815, 33657023, 35696423, 35695955, 264652, 18108387, 22279000, 263994, 264905, 264908, 264511, 264512, 265008, 264910, 55811386, 264288, 264768, 56181562, 21908765, 21908768, 21908769, 265022, 264628, 264563, 264587, 22278897, 22278899, 66712502, 87166559, 264683, 265021, 264488
2081	95309161 (4181, 4182)	Novel Protein sim. GBank glj4580987[gb]AAD24571.1[AF121081] cAMP Inducible 2 protein [Mus musculus]	UNCLASSIFIED		264905, 264908, 264907, 264908, 264510, 265008, 265007, 265009, 264910, 264596, 21908754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21908767, 21908768, 21908769, 265021, 264680, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2082	88223605 (4183, 4184)		homeobox		35696286, 265017, 265018, 265019, 18108388
2083	87406073 (4185, 4186)	Novel Protein sim. GBank glj2352427 (AF004161) - peroxisomal Ca-dependent solute carrier [Oryctolagus curticulus]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	265008, 265007, 265009, 264910, 264596, 21908754, 87168474, 265011, 264603, 265018, 265019, 264760, 264766, 264768, 264769, 21908767, 21908768, 21908769, 265021, 264680, 33657023, 264693, 264628, 264634, 264636, 264637, 264557, 56182323, 264564
2084	91230929 (4187, 4188)	Novel Protein sim. GBank glj4928451[gb]AAD34036.1[AF15179] CGI-40 protein [Homo sapiens]	MHC		35696286, 265017, 265018, 265019, 18108388
2085	95351528 (4189, 4190)	Novel Protein sim. GBank glj136323[pir]A57284 - spermatid perinuclear RNA-binding protein Spnr - mouse	Contains protein domain (PF00035) - Double-stranded RNA binding motif	dna_ma_bind	35696286, 52844045, 265008, 265007, 265008, 87168559, 18108351, 21908769, 29148784, 265020, 33657023, 27466262, 18108374, 18108388
2086	94110760 (4191, 4192)	Novel Protein sim. GBank glj3834423 (AF070688) - cytoplasmic dynein intermediate chain isoform DIC1a [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase_associated	264488, 264489, 65274572, 56182375, 22278896, 22278897, 22278899, 264259, 60432289, 29331826, 35696052, 264107, 264508, 264509, 264905, 264908, 264907, 264908, 52844045, 264909, 264510, 264511, 264512, 265008, 264910, 265009, 264592, 60433356, 60433438, 264758, 264596, 55812038, 21908754, 264601, 264602, 264605, 264762, 264681, 18108351, 264764, 264683, 264288, 264687, 264768, 264769, 264688, 21908765, 21908766, 21908767, 35695917, 265020, 265022, 52844150, 264681, 264682, 33657023, 264693, 27466261, 35695783, 264628, 264629, 35696423, 35695855, 264631, 264632, 264634, 264635, 264555, 264637, 263981, 264636, 264639, 264663, 264483, 264585, 264586, 264486, 264567

2097	95322772 (4193, 4194)	Novel Protein sim. GBank gi5174501[re]NP_008051.1 PLYF1 - zinc finger protein, subfamily 1A, 1 (Ikaros)	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	65274572, 264511, 265010, 264600, 265017, 264448, 264288, 265021, 60170815, 264692, 33957109, 18108370, 264636, 264483 56894075, 264259, 264288, 265020, 264563
2098	87780340 (4195, 4196)	Novel Protein sim. GBank gi4758209[re]NP_004081.1 pDUSP - dual specificity phosphatase 3 (varicella virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	phosphatase	
2099	95412827 (4197, 4198)	Novel Protein sim. GBank gi2685659 (AF026954) - pyruvate dehydrogenase phosphatase regulatory subunit precursor, PDP1 [Bos taurus]		phosphatase	65274572, 264805, 65274444, 264691, 264636, 264555
2100	95332656 (4199, 4200)	Novel Protein sim. GBank gi3681189[emb]CAB165141 - (Z98281) similar to ADP-ribosylation factor; cDNA EST EMBL: C08179 comes from this gene; cDNA EST EMBL: C08337 comes from this gene; cDNA EST EMBL: C08828 comes from this gene; cDNA EST yk291b4.5 comes from this gene; cDNA EST yk4...	Contains protein domain (PF00025) - ADP-ribosylation factor family	nud_rept	56182575, 22278995, 22278996, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 29331825, 29331827, 29331828, 26146498, 264908, 265008, 265009, 264910, 264591, 60432229, 60433358, 33657402, 264758, 21908754, 85658542, 87168474, 265017, 265018, 265019, 264681, 18108351, 264762, 264448, 264369, 264288, 18108355, 264686, 21908765, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 18108374, 35898423, 264558, 83373044, 87189518, 60432113, 22278900, 22279002 264091, 29331824, 264105, 265007, 265010, 18108380
2101	87782604 (4201, 4202)	Novel Protein sim. GBank gi4589468[db]BAA76761.1 - (AB012808) mBOCT [Mus musculus]		UNCLASSIFIED	
2102	87770461 (4203, 4204)	Novel Protein sim. GBank gi3874149[emb]CAA97423.1 - (Z73103) predicted using Genefinder [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264489, 35698286, 264259, 35698052, 264508, 264905, 264907, 264908, 264909, 264511, 264512, 264591, 264593, 60433358, 264758, 264601, 264605, 264760, 18108351, 264448, 264784, 264288, 264767, 264768, 21908769, 35695917, 18108374, 264634, 264555, 264559, 264583, 264482, 264486
2103	85413576 (4205, 4206)	Novel Protein sim. GBank gi4240159[db]BAA74858.1 - (AB020842) KIAA0835 protein [Homo sapiens]	Contains protein domain (PF01530) - Zinc finger, C2HC type	transcriptfactor	65274572, 56994075, 22278998, 264259, 29331824, 29331825, 35698052, 29331828, 66712502, 265008, 60170831, 264595, 33109954, 85658542, 87168559, 265017, 265019, 264448, 21908765, 21908768, 265022, 33657023, 27466262, 33657349, 35695763, 60431528, 18108374, 55811576, 56182323, 18108387, 87168518, 60432113, 264564
2104	85776161 (4207, 4208)			UNCLASSIFIED	264592, 264604, 22279000

2105	84848080 (4209, 4210)	Novel Protein sim. GBank gij1707032 (U80445) - coded for by C. elegans cDNA yk13g5.3; coded for by C. elegans cDNA yk21g8.3; coded for by C. elegans cDNA CEMSE18F; coded for by C. elegans cDNA yk126b1.3; coded for by C. elegans cDNA yk65h8.3; coded for by C. elegans cDNA yk65h8....	UNCLASSIFIED	284488, 56182575, 22278994, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 284259, 29331822, 29331824, 29331826, 60432289, 29331827, 29331828, 284508, 284905, 284509, 284907, 29331830, 52844045, 284510, 284511, 285007, 284512, 285009, 60170831, 60432229, 33857402, 60433356, 284595, 60433438, 284758, 33857084, 87168474, 285010, 87168559, 285017, 285018, 285019, 284782, 18108351, 284684, 18108354, 284288, 284688, 52844229, 18108359, 21908765, 21908766, 21908787, 21908788, 21908789, 35895917, 285020, 285022, 60170815, 52844150, 284682, 33857023, 284693, 33857109, 60431528, 18108374, 85274781, 35895855, 284635, 60170394, 284639, 284558, 18108385, 18108387, 58526488, 87168518, 60432113, 284564, 284568, 284567, 285008, 285019, 284908, 284639
2108	83385475 (4211, 4212)	Novel Protein sim. GBank gij3881524[embjCAA93883] - (Z70038) ZK1087.4 [Caenorhabditis elegans]	UNCLASSIFIED	284905, 284908, 284907, 284908, 284909, 284758, 285011, 284600, 284601, 284784, 284786, 284787, 284788, 284789, 284693, 284629, 35895855, 284632, 284634, 284635, 284638, 284639, 83373044, 284488
2109	80478719 (4217, 4218)	Novel Protein sim. GBank gij481043[pirj]S37671 - ba2	UNCLASSIFIED	18108348, 284789, 18108370, 18108374, 284555, 284558, 284557, 284558
2110	87728075 (4219, 4220)	Novel Protein sim. GBank gij481043[pirj]S37671 - ba2	UNCLASSIFIED	284584
2111	87818419 (4221, 4222)	Novel Protein sim. GBank gij2143639[pirj]I56542 - calmodulin-binding protein - rat	UNCLASSIFIED	284786, 35895917, 284630, 284587, 284486
2112	87283783 (4223, 4224)	Novel Protein sim. GBank gij4426629[gbjAAD20459] - (AF100980) protocadherin [Rattus norvegicus]	struct	284508, 284908, 284591, 284682, 22279002
2113	78941388 (4225, 4226)	Novel Protein sim. GBank gij3327184[dbj]BAA31660 - (AB014585) KIAA0885 protein [Homo sapiens]	cadherin	285008
2114	87889342 (4227, 4228)	Novel Protein sim. GBank gij3327184[dbj]BAA31660 - (AB014585) KIAA0885 protein [Homo sapiens]		86714117, 29331826, 29331827, 60433438, 55812038, 285017, 285019, 284689, 21908788, 55811957, 285020, 285021, 33857109, 60170394, 284558
2115	80983785 (4228, 4230)	Novel Protein sim. GBank gij4757890[refNP_004328.1]pc8OR - chromosome 8 open reading frame 1	UNCLASSIFIED	83274572, 284689, 284691, 284692, 60432113

2116	88258367 (4231, 4232)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		struct	35686286, 22278999, 56182181, 29331824, 29331825, 29331827, 35698052, 284907, 56182435, 285008, 284591, 55812038, 55811386, 87188559, 284288, 284369, 21908768, 29148629, 33657023, 35695763, 55811576, 35696423, 18108385
2117	87788804 (4233, 4234)	Novel Protein sim. GBank gij2330021 (AF019250) - kinesin-related protein; KRP; Costal2 [Drosophila melanogaster]		struct	28331824, 284511, 265009, 33109854, 285017, 285018, 284288, 284689, 265020, 284692, 58528488, 264482
2118	87078894 (4235, 4236)	Novel Protein sim. GBank gij1079307 (p1rjB56573) - nuclear pore complex glycoprotein p82 - African clawed frog		glycoprotein	284258, 284905, 284907, 284908, 284510, 284511, 285009, 284910, 285010, 284802, 284288, 284788, 284693, 263967, 263972, 284638, 284559
2119	86993317 (4237, 4238)	Novel Protein sim. GBank gij4321407 (gbAAD15748) - (AF047890) ATP-binding cassette protein M-ABC1 [Homo sapiens]		UNCLASSIFIED	284693, 18108385
2120	87789395 (4239, 4240)	Novel Protein sim. GBank gij485527 (refNP_005480.1) pNSP3 - novel SH2-containing protein 3	Contains protein domain (PF00017) - Src homology domain 2	eph	284091, 284259, 28331828, 29331828, 285017, 284604, 284288, 284885, 285020, 284691, 18108370, 55810764, 284555, 284638, 80432113
2121	80021375 (4241, 4242)	Novel Protein sim. GBank gij4757728 (refNP_004888.1) pAGTA - angiotensin/vasopressin receptor AII/AVP-like		UNCLASSIFIED	284601, 284766, 263978
2122	91230831 (4243, 4244)	Novel Protein sim. GBank gij4929551 (gbjAAD34036.1) (AF151799) CGI-40 protein [Homo sapiens]			18108394, 56182575, 22278997, 29331822, 29331824, 29331825, 29331826, 29331828, 284907, 56182435, 285007, 284910, 285010, 285018, 284686, 285020, 55811576, 284555, 284637, 18108382, 83373044, 18108383, 18108394, 56528488, 284985, 284587
2123	86787898 (4245, 4246)	Novel Protein sim. GBank gij2224551 (dbjBAA20764) - (AB002302) KIAA0305 [Homo sapiens]	Contains protein domain (PF01363) - FYE zinc finger	struct	18108386, 284757, 265011, 18108351, 284691, 284634, 18108385
2124	83005951 (4247, 4248)	Novel Protein sim. GBank gij5689455 (dbjBAA83011.1) - (AB028982) KIAA1059 protein [Homo sapiens]	Contains protein domain (PF00801) - PKD domain	transport	29331822, 284806, 284907, 284591, 284639, 284583
2125	95354041 (4249, 4250)	Novel Protein sim. GBank gij728831 (p1rjP39188) ALU1 - HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	284258, 284508, 284907, 284511, 85658542, 284783, 21808785, 35695917, 264636, 284488
2126	95084231 (4251, 4252)	Novel Protein sim. GBank gij4539284 (embjCAB39853.1) - (AL049495) conserved hypothetical protein [Schizosaccharomyces pombe]		UNCLASSIFIED	284488, 284489, 29331827, 35696052, 284905, 284509, 284908, 284909, 284510, 285009, 284591, 284592, 284593, 33657402, 284594, 284595, 284596, 284758, 284601, 284603, 285018, 284604, 284605, 284760, 284681, 284782, 284883, 284784, 284684, 284288, 284685, 284689, 80170615, 33657023, 33857109, 55810764, 284635, 284638, 284637, 284638, 284639, 83373044, 284584, 284586

2127	81110652 (4253, 4254)	Novel Protein sim. GBank gll4968435[gb]AAD31315.1[AF14323] - (AF143236) apoptosis related protein APR-2 [Homo sapiens]			35693286, 29331826, 35696032, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 284510, 285006, 284511, 284512, 285007, 285009, 284910, 284758, 285011, 284600, 284601, 284604, 284762, 284763, 284766, 284687, 284768, 284769, 284889, 35695917, 284690, 284891, 284892, 284893, 284629, 18108374, 35695855, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 18108385, 284563, 284564, 284567, 58182575, 35696288, 58182181, 29331824, 60432289, 35696052, 284905, 284907, 68712502, 284908, 284909, 284510, 284512, 285009, 284910, 284591, 55612038, 285016, 284784, 284288, 284369, 284687, 284788, 55811957, 284692, 18108368, 284628, 284832, 284634, 284635, 284637, 58182323, 284639, 18108384, 18108388, 284563, 284567
2128	87414282 (4255, 4256)				58182575, 35696288, 58182181, 29331824, 60432289, 35696052, 284905, 284907, 68712502, 284908, 284909, 284510, 284512, 285009, 284910, 284591, 55612038, 285016, 284784, 284288, 284369, 284687, 284788, 55811957, 284692, 18108368, 284628, 284832, 284634, 284635, 284637, 58182323, 284639, 18108384, 18108388, 284563, 284567
2129	95102089 (4257, 4258)		UNCLASSIFIED		68714117, 284828, 284595, 55812038, 55811150, 55811957, 284693, 18108374, 283978, 65274791, 18108381, 83373044, 22279000
2130	95417144 (4259, 4260)	Novel Protein sim. GBank gll2648265 (AE001012) - conserved hypothetical protein [Archaeoglobus fulgidus]	UNCLASSIFIED		263981
2131	85723065 (4261, 4262)	Novel Protein sim. GBank gll1086866 (U41276) - Similar to potassium channel protein. [Caenorhabditis elegans]		Contains protein domain (PF00805) - Pentapeptide repeats (8 copies)	264488, 22278988, 284259, 29331827, 29331828, 35696052, 284509, 284805, 284806, 284907, 284908, 284909, 284510, 285006, 284511, 285007, 284910, 284591, 284592, 284595, 284758, 21906754, 33109954, 87168474, 265011, 284600, 284601, 284605, 285018, 284760, 18108351, 284681, 284782, 284784, 284288, 284684, 284766, 284688, 284687, 284768, 284769, 284688, 21908769, 284690, 52644150, 284691, 284693, 18108370, 284628, 284629, 18108372, 18108374, 35696423, 35695855, 284631, 284634, 284635, 284636, 284555, 284637, 18108380, 284639, 284556, 58182323, 58528488, 284564, 284565, 284566, 284567
2132	95381096 (4263, 4264)	Novel Protein sim. GBank gll5689373[dbj]BAA82873.1 - (AB028944) KIAA1021 protein [Homo sapiens]		Contains protein domain (PF00122) - ATPase associated with E1-E2 ATPase	

2133	95351539 (4265, 4266)	Novel Protein sim. GBank gll4220489 (AC006089) - hypothetical protein [Arabidopsis thaliana]	UNCLASSIFIED	60424179, 52846365, 52646842, 56994075, 35986286, 22278997, 22278998, 60432049, 56182181, 66714117, 60424269, 29331826, 29331828, 35696052, 264905, 264906, 264907, 66712502, 29331830, 56182435, 265006, 264512, 265008, 60431735, 60433356, 33657402, 55812038, 33109954, 21908754, 55811386, 265010, 264603, 265017, 265018, 265019, 55811150, 18108351, 264682, 264368, 264288, 52844229, 56181582, 21908785, 21908786, 21908787, 21908788, 21908789, 55811957, 35895917, 265020, 265021, 60170815, 33857023, 33857109, 60431528, 18108374, 35898423, 65274791, 35695855, 264634, 60431650, 18108380, 56182323, 83373044, 18108385, 18108387, 60432113, 22279002, 264563, 264568
2134	95412697 (4267, 4268)	Novel Protein sim. GBank gll3875351[emb]CAB084151 - (Z96047) DY3.6 [Caenorhabditis elegans]		56181886, 35696286, 21908754, 55811386, 265011, 265017, 18108351, 264765, 264766, 264688, 21908788, 35895917, 265020, 33857023, 264628, 35695855, 264632, 264555, 264556, 264557, 264558, 18108382, 22279002
2135	88079813 (4269, 4270)	Novel Protein sim. GBank gll5689559[db]BAA83083.11 - (AB028034) KIAA1111 protein [Homo sapiens]	UNCLASSIFIED	22278999, 29331828, 35696052, 264906, 264908, 264910, 265009, 264591, 264759, 52846317, 265011, 87188559, 264601, 18108351, 264448, 264683, 264684, 264689, 18108359, 264691, 33857023, 264692, 35895763, 264629, 35695855, 264631, 264635, 264636, 264637, 56182323, 264639, 22279002, 264564
2136	84348478 (4271, 4272)	Novel Protein sim. GBank gll2662167[db]BAA237151 - (AB007903) KIAA0443 [Homo sapiens]	UNCLASSIFIED	284639
2137	87837718 (4273, 4274)	Novel Protein sim. GBank gll4884110[emb]CAB43282.11 - (AL050090) hypothetical protein [Homo sapiens]	UNCLASSIFIED	264569, 264909, 33109954, 264763, 21908788, 80170394, 18108385, 264563
2138	87395446 (4275, 4276)	Novel Protein sim. GBank gll5174779[db]AAD40696.11 - (U87804) 50 kDa protein [Caulobacter crescentus]	ATPass_associated	264259, 29331828, 35696052, 264908, 265006, 265017, 265018, 18108351, 264289, 21908788, 33857023, 33657109, 264628, 18108374, 35695855, 264634, 264555, 264556, 264557, 264558, 264559
2139	94843682 (4277, 4278)	Novel Protein sim. GBank gll3850821[emb]CAA771351 - (Y18350) U2 snRNP auxiliary factor, large subunit [Nicotiana glauca]		264905, 264910, 264591, 55812038, 55811386, 8569542, 264760, 18108351, 18108359, 55811957, 265020, 265021, 33857023, 18108384, 55811576, 83373044, 18108385, 56526488, 264482

2140	67845655 (4279, 4280)	Novel Protein sim. GBank glj417283[gbjAAD20418] - (AC007019) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264488, 264259, 29331824, 264104, 264109, 264509, 265008, 264759, 265018, 264448, 264288, 21908768, 55811957, 265021, 33857023, 27488265, 35898423, 264636, 264558, 264557, 264559, 264566
2141	79823886 (4281, 4282)		UNCLASSIFIED	265020, 264693
2142	80041222 (4283, 4284)		UNCLASSIFIED	263978
2143	94140051 (4285, 4286)	Novel Protein sim. GBank glj2135786[pij]S53382 - mucin 5AC (clone JER47) - human (fragment)	UNCLASSIFIED	22278997, 29331827, 264907, 265020, 60432113
2144	94320114 (4287, 4288)	Novel Protein sim. GBank glj2078483 (U43200) - antifeeze glycopeptide AFGP polypeptide precursor [Boreogadus salda]	UNCLASSIFIED	65274572, 264259, 29331824, 29331827, 264908, 264908, 264591, 265011, 87188559, 264600, 265018, 264288, 264768, 21908765, 21908767, 55811576, 35898423, 85274791, 22278002
2145	20564305 (4289, 4290)		UNCLASSIFIED	263978
2146	87010515 (4291, 4292)	Novel Protein sim. GBank glj1255871 (U53341) - short region of weak similarity to bovine membrane receptor p63 (PIR:S28503) [Caenorhabditis elegans]	UNCLASSIFIED	264909, 60433356, 264688
2147	80432911 (4293, 4294)	Novel Protein sim. GBank glj3080399[embjCAA18715.1] - (AL022803) putative protein [Arabidopsis thaliana]	UNCLASSIFIED	264807, 264768, 264769, 18108385
2148	80048811 (4295, 4296)	Novel Protein sim. GBank glj728837[spjP39194]ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III	UNCLASSIFIED	264593
2149	87382022 (4297, 4298)	Novel Protein sim. GBank glj119883[spjP20893]FCE2_MOUSE - LOW AFFINITY IMMUNOGLOBULIN EPSILON FC RECEPTOR (LYMPHOCYTE IGE RECEPTOR) (FC-EPSILON-RII) (CD23)	glycoprotein	29331824, 29331826, 35688052, 264758, 87168474, 265018, 52644150, 33857109
2150	94140059 (4299, 4300)	Novel Protein sim. GBank glj5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	22278998, 29331822, 29331824, 29331828, 264764, 264769, 21908768, 264488
2151	95353241 (4301, 4302)	Novel Protein sim. GBank glj5689407[dbj]BAA82887.1 - (AB028958) KIAA1035 protein [Homo sapiens]		22278998, 56894075, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 35688052, 29331828, 264508, 264511, 60433356, 264758, 264598, 33109954, 60174639, 265010, 265011, 87168559, 265017, 265018, 265019, 264448, 264288, 264689, 21908765, 21908768, 21908768, 265020, 60170816, 33857109, 33857182, 33857349, 18108370, 264635, 264557, 60170394, 18108385, 87168518, 22279000, 18108397, 18108398, 265007, 264591, 265011, 18108351, 18108368, 18108374, 18108388
2152	79321640 (4303, 4304)	Novel Protein sim. GBank glj3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	kinase	

2153	89313371 (4305, 4308)	Novel Protein sim. GBank gll4758704 ref NP_004216.1 pMASL - MFH-amplified sequences with leucine-rich tandem repeats 1	Contains protein domain (PF00560) - Leucine Rich Repeat	glycoprotein	264488, 263994, 5264842, 22278998, 22278998, 22278999, 264259, 29331822, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 56182435, 264510, 264511, 264512, 264758, 87168474, 87168559, 265017, 265018, 264760, 264288, 264389, 264768, 264887, 264789, 52644229, 21908768, 21908768, 35695817, 33857023, 33857109, 35695855, 264631, 264632, 264635, 264636, 264638, 18108385, 264483, 264584, 264488
2154	87408034 (4307, 4308)	Novel Protein sim. GBank gll225150 prf 1209265U - chorion protein B11 [Bombyx mori]		UNCLASSIFIED	56894075, 264084, 265009, 265019, 264288, 21908767, 35695817
2155	87424072 (4308, 4310)			UNCLASSIFIED	18108392, 18108398, 22278998, 264259, 29331824, 265008, 265010, 265011, 265017, 265019, 264288, 264686, 265020, 264693, 264628, 56182323
2156	84285205 (4311, 4312)	Novel Protein sim. GBank gll3970966 (ACQ04974) - spa-1-like; similar to AF026504 (PID:32555183) [Homo sapiens]			265007, 264684
2157	87316344 (4313, 4314)	Novel Protein sim. GBank gll1076211 prf S50765 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	264591
2158	86444218 (4315, 4316)	Novel Protein sim. GBank gll4650844 db BAA77027.1 - (AB026180) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain		264598
2159	80083729 (4317, 4318)	Novel Protein sim. GBank gll2878925 db BAA24826 - (AB007887) KIAA0437 [Homo sapiens]			29331822, 264112, 265008, 264681, 33857023, 264634
2160	16283674 (4319, 4320)	Novel Protein sim. GBank gll1504006 db BAA13202 - (D88968) simlarto human ZFY protein. [Homo sapiens]			264634
2161	87739131 (4321, 4322)			UNCLASSIFIED	265008
2162	84319528 (4323, 4324)			UNCLASSIFIED	85274572, 264508, 264905, 264906, 264907, 264908, 52644045, 264909, 265007, 264910, 264591, 264592, 264593, 55812038, 264598, 264758, 265011, 264600, 264762, 264763, 264683, 264764, 264288, 264766, 264686, 264768, 264769, 264689, 265020, 264691, 264628, 264629, 263978, 264632, 264634, 264557, 264638, 264639, 18108385, 264563, 264586, 264587
2163	95417158 (4325, 4326)	Novel Protein sim. GBank gll3876537 emb CAA98270 - (Z73974) cDNA EST yk2915.3 comes from this gene; cDNA EST yk2915.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	56182575, 22278998, 264093, 264683, 33857023, 85274620, 60432113
2164	80569456 (4327, 4328)		Contains protein domain (PF01008) - Hepatitis C virus non-structural protein NS4a	collagen	264603, 264637, 264585

2165	94328169 (4328, 4330)	Novel Protein sim. GBank gll1086784 (U41107) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	56994075, 22278998, 22278997, 22278999, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 264908, 29331830, 58182435, 265009, 21908754, 33857084, 285011, 265018, 264448, 264288, 264389, 21908765, 21908768, 21908769, 265020, 265021, 264691, 264692, 33857023, 65274820, 35695855, 264558, 60170394, 83373044, 60432113, 22279002, 284587, 52845158, 22278994, 22278998, 66714117, 29331828, 52844045, 265018, 265019, 264389, 21908765, 21908767, 21908768, 21908769, 265021, 285022, 264693, 27488262, 35695763, 18108376, 56528486, 87168518, 264587
2168	87618934 (4331, 4332)	Novel Protein sim. GBank gll2708522[emb]CAA75816] - (Y15885) ubiquitin activating enzyme [Drosophila melanogaster]	ubiquitin		56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2167	87716864 (4333, 4334)	Novel Protein sim. GBank gll2224713[db]BAA20840] - (AB002384) KIAA0388 [Homo sapiens]		UNCLASSIFIED	56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2169	88999334 (4335, 4336)	Novel Protein sim. GBank gll4321407[gb]AAD15748] - (AF047690) ATP-binding cassette protein M-ABC1 [Homo sapiens]	transport		56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2170	87888937 (4337, 4338)	Novel Protein sim. GBank gll5108521[gb]AAD39741.1[AF10538] K-Ci cotransporter KCC4 [Homo sapiens]		UNCLASSIFIED	56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2171	80194050 (4341, 4342)				56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2172	85452480 (4343, 4344)				56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2173	87038740 (4345, 4346)	Novel Protein sim. GBank gll4308681[gb]AAD15478] - (AC008930) R33423.1 [Homo sapiens]			56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587
2174	95003286 (4347, 4348)	Novel Protein sim. GBank gll2483778[sp]Q09456]YQ35_CAEEL - PUTATIVE CUTICLE COLLAGEN C09G5.5			56182575, 35696266, 29331824, 29331826, 28148498, 58182435, 265008, 265009, 264592, 264593, 33857402, 33109954, 265011, 265017, 265018, 18108351, 264389, 21908764, 21908765, 21908768, 29148827, 21908769, 52644150, 33857109, 35696423, 18108381, 18108384, 18108385, 60432113, 264587

2175	94325850 (4348, 4350)	Novel Protein sim. GBank gi 1263287 (U47855) - fibroin-3 [Araneus diadematus]		UNCLASSIFIED	264488, 35696286, 20281099, 29331826, 60432289, 35898052, 264109, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265006, 265007, 264512, 265008, 264910, 264591, 264594, 264595, 264596, 264758, 55812038, 265011, 264800, 264603, 264780, 264762, 264448, 264764, 264288, 264766, 264686, 264687, 21806788, 55811957, 35695917, 265020, 265022, 264691, 264692, 33657023, 264693, 264628, 264629, 55811576, 35696423, 65274791, 35695855, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 264639, 264558, 18108385, 60432113, 264563, 264584, 264585, 264566, 264486, 264597
2176	88223392 (4351, 4352)	Novel Protein sim. GBank gi 728837 ep F39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00805) - Penelopeptide repeats (8 copies)	oncogene	52644507, 52646842, 22278994, 35696286, 22278996, 22278999, 29331826, 29331827, 35696052, 29331828, 33656970, 29331830, 294910, 33657402, 264758, 52644298, 87188559, 265018, 264689, 21908765, 21908787, 21908789, 35695917, 52644150, 264690, 33657023, 33657109, 52645129, 33657182, 27486261, 27486262, 33657349, 18108378, 18108377, 35695855, 87168518, 60432113, 264404, 22278900, 264486 18108382, 22278997, 22278999, 264093, 33657402, 265018, 264448, 264766, 264689, 21908787, 21908788, 21908789, 265021, 33657023, 18108370, 18108374, 60432113, 22278902
2177	94128842 (4353, 4354)	Novel Protein sim. GBank gi 5454072 ref NP_008416.1 pSLU7 - step II splicing factor SLU7		kinase	
2178	87601557 (4355, 4356)	Novel Protein sim. GBank gi 473407 (U08215) - NST-1 [Mus musculus]	Contains protein domain (PF00012) - Hsp70 protein	eph	264488, 22278996, 22278999, 29331824, 29331825, 29331826, 29331827, 52644286, 87168474, 18108370, 35695855, 22279002, 60424299, 264760, 264628, 264632
2179	87316275 (4357, 4358)			UNCLASSIFIED	

2180	85351397 (4359, 4360)	Novel Protein sim. GBank gij3122317[sp]P90848[KMIH-DICDI - MYOSIN HEAVY CHAIN KINASE B (MHCK B)]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	52644507, 22278994, 35698286, 22278997, 22278998, 264259, 52645090, 29331822, 29331824, 29331825, 29331826, 29331828, 33656970, 264508, 264509, 264906, 264908, 29331830, 264909, 264510, 265006, 265007, 33657402, 55812038, 21906754, 87168474, 87168559, 265017, 265018, 265019, 264763, 264682, 264683, 264684, 264288, 264686, 21908765, 21908768, 21908769, 265020, 265021, 265022, 52644150, 33657023, 33657109, 27468265, 33657349, 18108374, 35686423, 35695955, 263981, 60170384, 18108385, 56526486, 87168518, 60432113, 22278000, 264482, 264568, 264567, 264486 29331827, 264369, 18108376, 264564
2181	85764930 (4361, 4362)	Novel Protein sim. GBank gij3024689[sp]Q15542ITD4_HUMAN - TRANSCRIPTION INITIATION FACTOR TFIIID 100 KD SUBUNIT (TAFII100)			
2182	87637731 (4363, 4364)	Novel Protein sim. GBank gij5420387[emb]CAB46678.1] - (AJ243459) proteophosphoglycan [Leishmania major]			
2183	85460649 (4365, 4366)	Novel Protein sim. GBank gij3873406[gib]AAC77482.1] - (U17129) unknown [Rhodococcus erythropolis]			
2184	87760680 (4367, 4368)	Novel Protein sim. GBank gij3114713 (AF081346) - Edp1 protein [Mus musculus]			
2185	87826463 (4369, 4370)	Novel Protein sim. GBank gij5106958[gib]AAD39908.1JAF11361 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		inf	29331822, 29331825, 29331826, 56182435, 265011, 264885, 264886, 21906768, 18108370, 264629, 264631, 264636, 264557 29331824, 264907, 86712502, 264757, 265018, 264288, 264692, 56526486
2186	87739227 (4371, 4372)	Novel Protein sim. GBank gij26864625[emb]CAA16972] - (AL021811) putative protein [Arabidopsis thaliana]		ATPase-associated	264259, 29331822, 29331824, 29331826, 56182435, 264592, 55812038, 264780, 264786, 55811957, 33657023, 55811576, 56182323, 264583
2187	87388173 (4373, 4374)			UNCLASSIFIED	35696052, 264905, 264906, 264907, 264808, 264510, 264511, 265008, 264910, 264758, 265019, 264762, 264681, 264766, 264769, 35695917, 264692, 35696423, 264631, 264635, 264637, 18108388, 264586, 264486
2188	87771708 (4375, 4376)	Novel Protein sim. GBank gij5107818[gib]AAD40129.1JAF14941 - (AF149413) contains similarity to histone deacetylases; Pfam PF00850, Score=13.3, E=5e-10, N=1 [Arabidopsis thaliana]		histone	18108388, 56994075, 264259, 29331824, 29331825, 86714117, 29331827, 264908, 29331830, 265018, 265020, 265021, 56182323, 264559, 22278000, 22278002
2189	85693573 (4377, 4378)	Novel Protein sim. GBank gij3452337 (AF075724) - unknown [Legionella pneumophila]	Contains protein domain (PF01598) - O-methyltransferase		22278998, 264259, 29331826, 21906754, 264369, 264286, 263987

2190	87639197 (4378, 4380)	Novel Protein sim. GBank gij132575jplP29315RINI_RAT - RIBONUCLEASE INHIBITOR		nucleaseinhib	22278998, 22278999, 28331822, 28331824, 28331826, 285008, 284910, 60170831, 55812038, 52844296, 285010, 285018, 284685, 284688, 56181562, 21906789, 35695917, 265022, 60170394, 22279000, 28331825, 28331826, 28331830, 264510, 264511, 284910, 264593, 284594, 284556, 284559, 284558
2191	95198828 (4381, 4382)	Novel Protein sim. GBank gij5327002jemb CAB46272.1 - (Y18503) XAP-5-like protein [Homo sapiens]			
2192	11126316 (4383, 4384)	Novel Protein sim. GBank gij462800jplP34400 MI10_CAEEL - MIG-10 PROTEIN	Contains protein domain (PF00169) - PH domain		
2193	94140073 (4385, 4386)	Novel Protein sim. GBank gij5420389jemb CAB46880.1 - (AJ243460) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	56181880, 28331825, 28331827, 264508, 284809, 285008, 264592, 60432229, 264288, 284684, 284786, 35695917, 33657023, 60431602, 60431528, 55810784, 55811576, 65274791, 35695855, 60431850, 56182323, 60432113, 284592
2194	21418714 (4387, 4388)	Novel Protein sim. GBank gij2773341 (AF040954) - putative protein phosphatase 1 nuclear targeting subunit [Rattus norvegicus]			
2195	88083023 (4389, 4390)	Novel Protein sim. GBank gij2832763jemb CAA15685.1 - (AL009191) /prediction=(method:; /match=(desc:; /molife=(desc:; [Drosophila melanogaster]		UNCLASSIFIED	22278998, 22278999, 35696052, 285008, 21908754, 285017, 35695917, 285021, 265022, 35695855
2196	95091631 (4391, 4392)	Novel Protein sim. GBank gij5262487jemb CAB45689.1 - (AL080076) hypothetical protein [Homo sapiens]		collagen	56182575, 35696286, 22278997, 22278999, 284259, 28331822, 66714117, 60432289, 28331827, 35696052, 28331828, 284508, 52844045, 56182435, 284510, 265007, 285008, 285009, 60433438, 55812038, 285010, 285011, 284448, 284288, 284686, 284687, 52844229, 21908785, 21908786, 21908787, 35695917, 265022, 264891, 33657023, 284693, 18108370, 18108376, 35696423, 55811576, 65274791, 35695855, 284636, 56182323, 18108385
2197	95073813 (4393, 4394)	Novel Protein sim. GBank gij4929587jbb AAD34044.1 AF15180 - (AF151807) CGI-49 protein [Homo sapiens]			284768, 284769, 21908785, 21908786, 21908787, 28148827, 55811857, 35696286, 265020, 22278998, 285021, 264259, 33657023, 284693, 28331824, 35696052, 28331828, 18108370, 35695855, 284113, 285008, 284910, 60432229, 56182323, 33657402, 264758, 63373044, 21908754, 285018, 285019, 22279002, 264482, 264448, 264565, 264288, 264369
2198	88080914 (4395, 4396)	Novel Protein sim. GBank gij3548787 (AC005622) - R30953.1 [Homo sapiens]		UNCLASSIFIED	

2199	88054355 (4397, 4398)	Novel Protein sim. GBank gll2739372 (AC002505) - hypothetical protein [Arabidopsis thaliana]				284105, 284110, 284112, 284688, 55811957, 33857023, 284892, 283967, 20281071, 58528488
2200	87405385 (4399, 4400)	Novel Protein sim. GBank gll3043634[db][BAA25481] - (AB011127) KIAA0555 protein [Homo sapiens]	struct			28331824, 284763, 284768
2201	94316872 (4401, 4402)	Novel Protein sim. GBank gll3913470[sp]Q57314[DPBX_ANAPL - PUTATIVE STEROID DEHYDROGENASE SPM2]	Contains protein domain (PF00108) - short chain dehydrogenase			29331824, 35696052, 284905, 284907, 33857402, 55811386, 285017, 285018, 285019, 284288, 21906788, 35695917, 285020, 285022, 33857023, 33857108, 27488281, 18108370, 35698423, 35695855, 284555, 284558, 83373044, 87188518, 60432113
2202	91872385 (4403, 4404)	Novel Protein sim. GBank gll5282665[emb][CAB43787.1] - (AL080186) hypothetical protein [Homo sapiens]	UNCLASSIFIED			284489, 284259, 29331824, 60432289, 35698052, 284905, 284909, 284592, 285017, 285018, 285019, 18108351, 284782, 284448, 284389, 284288, 284768, 21906785, 21908768, 284690, 284691, 284692, 33857109, 284634, 284636, 284555, 284639, 284558, 284559, 83373044, 18108385, 284404, 22279002, 284482
2203	87781832 (4405, 4406)	Novel Protein sim. GBank gll172845[sp]P46829[RB25_RABIT - RAS-RELATED PROTEIN RAB-25]	Contains protein domain (PF00071) - Ras family	glycoprotein		52846365, 56994075, 284259, 29331822, 29331826, 29331827, 29331828, 284910, 285010, 285011, 87188558, 285018, 285019, 284605, 284288, 21908768, 35695917, 33857023, 284892, 33857109, 35695783, 18108376, 284638, 22279000, 284566, 284567
2204	88088671 (4407, 4408)	Novel Protein sim. GBank gll121038[sp]P28348[GBT3_RAT GUANINE NUCLEOTIDE-BINDING PROTEIN GT], ALPHA-3 SUBUNIT (GUSTDUCIN ALPHA-3 CHAIN)	Contains protein domain (PF00503) - G-protein alpha subunit	UNCLASSIFIED		
2205	94147589 (4409, 4410)	Novel Protein sim. GBank gll4589480[db][BAA78768.1] - (AB023141) KIAA0924 protein [Homo sapiens]	Contains protein domain (PF00066) - dna_rna_bind Zinc finger, C2H2 type			18108394, 18108397, 56182575, 60432049, 284259, 29331822, 29331824, 29331825, 29331828, 29331827, 284606, 285007, 285008, 285009, 60432228, 285010, 285011, 285018, 284883, 284288, 284389, 284686, 21908768, 21908788, 21908789, 284690, 284691, 284893, 18108388, 55811576, 65274791, 284634, 18108381, 18108384, 60432113, 22279002, 284583, 284568, 284581
2206	20620008 (4411, 4412)	Novel Protein sim. GBank gll4557753[ref]NP_000372.1[pmid1 - midline 1 protein]	Contains protein domain (PF00622) - SPRY domain	UNCLASSIFIED		29331822, 56182181, 29331827, 35696052, 52844045, 285006, 285019, 56181562, 55811957, 285021, 33857023, 35695763, 35695855, 60170394, 60432113, 284568, 284908, 285019, 18108351, 21908789
2208	88100930 (4415, 4416)	Novel Protein sim. GBank gll3986748 (AF105228) - tuftelin [Bos taurus]		struct		284112, 285009, 284691, 18108385, 18108374, 284634, 20281166

2210	57152407 (4419, 4420)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		Kinase	284603
2211	87341720 (4421, 4422)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene	284685, 284686, 18108365, 22278002, 284482
2212	91223924 (4423, 4424)	Novel Protein sim. GBank gi 3776027 emb CAA08214 - (AJ010475) RNA helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	22278995, 22278997, 22278998, 284092, 284094, 29331822, 68714117, 29331826, 29331828, 284907, 52844045, 265009, 60170831, 21908754, 87188559, 285017, 285018, 18108351, 284683, 18108354, 264369, 284766, 284687, 52644228, 21908765, 21908768, 21908767, 21908768, 265021, 33657109, 18108370, 18108374, 284636, 56182323, 18108384, 18108387, 87168516, 284565
2213	91218309 (4425, 4426)	Novel Protein sim. GBank gi 5420387 emb CAB48678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			58182575, 22278996, 22278997, 35696052, 284805, 68712502, 284908, 284828, 58182435, 284112, 265008, 60431735, 60433438, 21908754, 265010, 285011, 285017, 265018, 265019, 18108351, 264765, 21908765, 21908768, 21908769, 265020, 265021, 284693, 264628, 263974, 263976, 18108379, 55811576, 264556, 264637, 284598, 83373044, 22278002, 284482, 284483

2214	95381453 (4427, 4428)	Novel Protein sim. GBank gij4504325jre NP_000173.1 pHADH - hydroxyacyl- Coenzyme A dehydrogenase/3-ketolacetyl-Coenzyme A thiolase/enoyl-Coenzyme A hydratase (trifunctional protein), alpha su	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	264488, 52844507, 18108394, 56182575, 22278894, 22278895, 35898288, 58994075, 22278897, 22278898, 22278899, 264490, 60432049, 264259, 62645080, 28331822, 29147620, 28331824, 66714117, 28331825, 60432289, 28331826, 28331827, 35898052, 28331828, 20281100, 264509, 284907, 68712502, 264908, 28331830, 52844045, 56182435, 264510, 265006, 264511, 264512, 265007, 265008, 265009, 60170831, 264593, 60433358, 60433438, 33109954, 33657084, 52844288, 87188474, 265010, 265011, 87188559, 264601, 265017, 265018, 265019, 18108351, 264448, 264682, 264763, 264288, 264687, 52844229, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35898917, 265020, 265021, 285022, 264532, 60170815, 264690, 52844150, 264691, 33857023, 264692, 18108384, 33857109, 33857182, 27488262, 27488284, 27488285, 35898763, 18108370, 264629, 60431528, 18108374, 18108378, 55810764, 35898423, 35898555, 264634, 264636, 52844332, 264638, 264558, 60170394, 18108381, 56182323, 83373044, 18108385, 18108387, 18108388, 56526488, 87188518, 60432113, 22278002, 264482, 264564, 264565, 264566, 264809, 265008, 264555, 264558, 87188518
2215	95418208 (4428, 4430)	Novel Protein sim. GBank gij1847160 (AF000298) - weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]		
2216	87614048 (4431, 4432)	Novel Protein sim. GBank gij1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388288) [Caenorhabditis elegans]		264693
2217	80589404 (4433, 4434)	Novel Protein sim. GBank gij5031707jre NP_005503.1 pGARP - glycoprotein A repetitions predominant	Contains protein domain (PF00560) - Leucine Rich Repeat	264288, 33657109, 264558
2218	85518264 (4435, 4436)	Novel Protein sim. GBank gij3878838jemb CAA88953 - (Z49128) similar to cAMP-dependent protein kinase; cDNA EST EMBL:700718 comes from this gene; cDNA EST YK465d8.3 comes from this gene; cDNA EST yk465d8.5 comes from this gene; cDNA EST yk49214.3 comes from this gene; cDNA EST y...	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	35898423, 264563
2219	87614048 (4437, 4438)	Novel Protein sim. GBank gij1572802 (U70854) - similar to Enterococcus faecalis TRAB (GI:388288) [Caenorhabditis elegans]	Contains protein domain (PF01963) - TraB family	264682, 264683, 264688, 264689, 264693, 18108370, 18108378

2220	95354165 (4438, 4440)	Novel Protein sim. GBank glj4507261[re]NP_003148.1[ps]STAT - elatlerin			284486, 18108394, 18108395, 35696286, 284259, 284097, 60432289, 284509, 284905, 284906, 284907, 28331830, 284908, 284909, 284510, 284511, 265007, 284512, 284910, 285008, 284593, 284594, 60433356, 284595, 55812038, 284758, 85658542, 265010, 284601, 284603, 265019, 284605, 284780, 284782, 284448, 284784, 284388, 284786, 18108357, 284788, 284687, 18108358, 284789, 55811957, 284690, 284691, 33657023, 284692, 18108362, 18108368, 284628, 284629, 18108374, 283976, 284634, 284635, 284636, 284637, 284638, 18108385, 284483, 284566, 284486, 284567
2221	88080827 (4441, 4442)	Novel Protein sim. GBank glj3549154 (AC005625) - R27328_1 [Homo sapiens]			
2222	84425892 (4443, 4444)			UNCLASSIFIED	284908, 285020, 35695855
2223	95081649 (4445, 4446)			UNCLASSIFIED	285010, 284685, 284680, 284693, 284628, 283974, 283976, 55811576, 284555, 284638, 83373044, 284483
2224	87388515 (4447, 4448)	Novel Protein sim. GBank glj3878005[emb]CAA84799] - (Z35719) cDNA EST EMBL:067419 comes from this gene; cDNA EST EMBL:C13853 comes from this gene; cDNA EST EMBL:C11578 comes from this gene; cDNA EST yk234a7.3 comes from this gene; cDNA EST yk234a7.5 comes from this gene; cDNA ES... Novel Protein sim. GBank glj1255847 (U53338) - C05E11.1 gene product [Caenorhabditis elegans] Novel Protein sim. GBank glj4826524[emb]CAB42852.1] - (AL040848) hypothetical protein [Homo sapiens]	Contains protein domain (PF01958) - Domain of unknown function	UNCLASSIFIED	284259, 284509, 56182435, 285008, 285009, 284757, 21906754, 18108351, 284693, 18108374, 18108385
2225	85749484 (4449, 4450)		transport		22278994, 22278995, 22278999, 52844045, 284600, 285019, 21906765, 21906789
2226	88878953 (4451, 4452)				284259, 29331822, 29331824, 28331825, 28331827, 284508, 284908, 285007, 284691, 284634, 284486
2227	87721135 (4453, 4454)			UNCLASSIFIED	22278999, 285006, 285008, 18108354, 28148629, 28148784, 27486261, 18108374, 284637, 18108384
2228	91227337 (4455, 4456)	Novel Protein sim. GBank glj808978 (U16800) - ribonucleoprotein [Xenopus laevis]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284081, 284092, 284094, 28331822, 29331825, 86714117, 284693, 283972, 284638, 83373044, 284563
2229	88080831 (4457, 4458)	Novel Protein sim. GBank glj3549155 (AC005625) - R27328_2 [Homo sapiens]		UNCLASSIFIED	

2230	95342815 (4459, 4460)	Novel Protein sim. GBank gij226154iprj 1412350A - DNA polymerase [Human adenovirus type 2]		UNCLASSIFIED	264468, 264768, 52644507, 264769, 21906765, 21906766, 21906767, 21906769, 22278995, 35695917, 22278996, 22278997, 22278998, 22278999, 265021, 264259, 52645129, 22278998, 265021, 264259, 264907, 18108370, 18108374, 35696423, 35695855, 265007, 264910, 264555, 33657402, 21906754, 18108387, 265010, 265018, 265019, 264760, 264288, 264567, 264563
2231	80060837 (4461, 4462)	Novel Protein sim. GBank gij3549154 (AC005625) - R27328 1 [Homo sapiens]		UNCLASSIFIED	
2232	87782561 (4463, 4464)	Novel Protein sim. GBank gij5281316ipb AAD41478.1 AF133124 - transcription factor IIC63 [Homo sapiens]		transcriptifactor	18108394, 56182575, 22278995, 35695286, 22278997, 22278999, 264259, 29331827, 35696052, 264907, 56182435, 265006, 265007, 265008, 264910, 264759, 55812038, 264803, 265018, 265019, 18108351, 264882, 264764, 264883, 264368, 264288, 264686, 264687, 264689, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 264680, 52644150, 264681, 33657023, 264693, 18108370, 18108374, 55811578, 35695855, 264639, 18108385, 264564, 264806, 33657402, 265018, 264288, 264686, 265020, 264635, 18108385, 56182435, 264368, 264688, 21906765, 265020, 264693, 264558, 56520486
2233	87755282 (4465, 4466)	Novel Protein sim. GBank gij4248733ipb AAD13780 - (AF109377) IdIPp [Mus musculus]			
2234	87771617 (4467, 4468)	Novel Protein sim. GBank gij1706559ipb P54352 EAS_DROME - ETHANOLAMINE KINASE (EASILY SHOCKED PROTEIN)		kinase	
2235	91012318 (4469, 4470)	Novel Protein sim. GBank gij4972734ipb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	
2236	88003131 (4471, 4472)	Novel Protein sim. GBank gij1082675iprj B53814 - p20 protein - human	Hsp20/alpha crystallin family		264569, 264687, 264769, 265022, 264259, 60432049, 264691, 29331826, 60432289, 20281149, 264906, 264907, 264511, 265008, 265009, 264634, 264635, 264636, 264555, 264556, 264557, 264558, 60433356, 264595, 264559, 60433438, 60432113, 264761, 264762, 264763, 264764
2237	91012318 (4473, 4474)	Novel Protein sim. GBank gij4972734ipb AAD34762.1 - (AF132174) unknown [Drosophila melanogaster]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264488, 264769, 21906765, 21906766, 21906767, 21906768, 21906769, 22278995, 22278996, 22278997, 22278998, 265020, 265021, 22278999, 264259, 29331824, 29331826, 29331827, 35695763, 18108376, 35695855, 265007, 60432229, 33657402, 60433356, 60433438, 83373044, 18108385, 21906754, 18108387, 60432113, 22276000, 265018, 22279002, 264482, 18108351, 264288

2238	9498857 (4475, 4476)		Contains protein domain (PF00286) - Viral coat protein	264509, 264907, 264628, 264634, 264564
2239	8779668 (4477, 4478)			29331825, 265009, 264389, 33657109, 18108370, 18108374, 264557, 264559
2240	84121471 (4479, 4480)	Novel Protein sim. GBank gij2882311 (AF051240) - probable ubiquitin-conjugating enzyme E2 [Picea mariana]	Ubiquitin protein domain (PF00179) - Ubiquitin-conjugating enzyme	264468, 65274572, 66182375, 35696266, 22278997, 22278999, 264259, 29331827, 35696052, 264508, 5264045, 56182435, 264511, 265007, 265008, 265009, 80433356, 80433438, 55812038, 21908754, 33657084, 55811388, 265018, 265019, 18108351, 264683, 264288, 264788, 264687, 264688, 264789, 21908785, 21908788, 21908789, 35695917, 265021, 265022, 60170615, 52644150, 33657023, 33657182, 33657349, 35695783, 18108370, 35696423, 35695855, 87188518, 22278000
2241	80031651 (4481, 4482)	Novel Protein sim. GBank	UNCLASSIFIED	264893, 264829
2242	81228075 (4483, 4484)	Novel Protein sim. GBank gij2484312 [p]705411E2BG, RAT - TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR)	synthase	22278995, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 264509, 265007, 265009, 264596, 21906754, 265010, 265011, 265017, 265018, 265019, 264448, 264389, 264288, 52644228, 21908785, 21908788, 21908787, 21908788, 21908789, 265020, 265021, 33657109, 27486282, 27486284, 18108374, 35695855, 264634, 264637, 56182323, 83373044, 56526486, 87188518, 264584
2243	78802028 (4485, 4486)	Novel Protein sim. GBank gij2291143 (AF016417) - Similar to BZIP transcription factor [Caenorhabditis elegans]	UNCLASSIFIED	265008
2244	85723527 (4487, 4488)	Novel Protein sim. GBank gij470340 (U00043) - similar to beta-mannosyltransferase [Caenorhabditis elegans]	UNCLASSIFIED	264604
2245	95318545 (4489, 4490)		Contains protein domain (PF00534) - Glycosyl transferases group 1	52645156, 22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331827, 264907, 264512, 80433438, 264758, 21908754, 265011, 264603, 264784, 264687, 21908787, 21908788, 21908789, 55811957, 265022, 264691, 264629, 35696423, 264638, 18108387, 80432113, 22279000, 22279002, 264568

2246	94846710 (4491, 4492)	Novel Protein sim. GBank gl 4996096[db][BAA78326.1] - (ABD28089) activator of S phase Kinase [Homo sapiens]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	65274572, 22278995, 35698288, 22278996, 22278997, 22278999, 284259, 35696052, 284108, 284905, 284907, 285006, 285007, 285008, 60433438, 33109954, 87168559, 285018, 285019, 284288, 21908765, 21908767, 21908768, 21908769, 55811957, 35695917, 285020, 285022, 27486264, 18108370, 18108374, 65274781, 35695855, 60432113
2247	87862542 (4493, 4494)	Novel Protein sim. GBank gl 854065[emb][CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	52845158, 52846385, 52845080, 35696052, 33656970, 52846317, 33657084, 285017, 21908768, 21908769, 35695917, 33657109, 52845129, 33657182, 27486261, 27486262, 33657349, 27486285, 18108387
2248	95412888 (4495, 4496)	Novel Protein sim. GBank gl 4756502[ref][NP_004123.1]pHABP - hyaluronan-binding protein 2	Contains protein domain (PF00089) - Trypsin	calhepsin	284488, 284259, 284907, 29331830, 284909, 285007, 285009, 284595, 21908754, 65274444, 284803, 285019, 284782, 284448, 284288, 284689, 21908768, 55811957, 285021, 284891, 18108374, 284634, 284635, 284636, 284555, 284638, 284557, 284558, 284559, 18108383, 83373044, 18108385, 284488
2249	94885662 (4497, 4498)	Novel Protein sim. GBank gl 4038461 (AF107772) - TcST11 [Trypanosoma cruzi]	Contains protein domain (PF00515) - TPR Domain	eph	284766, 284628, 284636, 284637
2250	78827508 (4499, 4500)	Novel Protein sim. GBank gl 3738140[emb][CAA21241] - (AL031852) velyl-tma synthetase, mitochondrial precursor [Schizosaccharomyces pombe]		UNCLASSIFIED	284908, 18108374
2251	87385883 (4501, 4502)	Novel Protein sim. GBank gl 3218467[emb][CAA07090.1] - (AJ008529) putative phosphatase [Gallus gallus]		UNCLASSIFIED	284259, 35696052, 284508, 58182435, 285009, 284592, 284593, 284780, 284448, 284884, 284288, 284690, 284628, 55811576, 284555, 284558, 284557, 284558, 284559, 284586
2252	87735887 (4503, 4504)	Novel Protein sim. GBank gl 4929325[gb][AAD33953.1]AF14531 - (AF145316) vacuolar proton pump delta polypeptide [Homo sapiens]	Contains protein domain (PF01813) - ATP synthase subunit D	synthase	284082, 284094, 284259, 28331822, 66714117, 29331828, 284102, 284103, 284104, 284105, 284109, 284112, 284511, 285007, 60433358, 285010, 18108351, 21908767, 21908768, 284691, 283974, 283977, 284488, 284567
2253	91010703 (4505, 4506)			UNCLASSIFIED	65274572, 285019

2254	95320031 (4507, 4508)	Novel Protein sim. GBank gij4502847re[NP_001271.1]pCIRB - cold inducible RNA- binding protein	Contains protein domain (PF00078) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	284589, 18108394, 18108398, 56182575, 58994075, 35698286, 22278999, 284094, 60432049, 284259, 28331822, 28331824, 28331825, 28331826, 60432288, 28331827, 28331828, 35698052, 284108, 284508, 284508, 284808, 284907, 28331830, 66712502, 284808, 284909, 284510, 285008, 284511, 285007, 285008, 285009, 60170831, 60432229, 60433358, 60433438, 284758, 65858542, 285010, 285011, 87188558, 285017, 285018, 285019, 284448, 284764, 284288, 284389, 284788, 284888, 284788, 284789, 21908785, 21908787, 55811957, 284691, 33657023, 284692, 18108362, 65274620, 283989, 284628, 18108370, 60431528, 283972, 284629, 18108372, 18108377, 18108379, 55811576, 35698423, 35698555, 284630, 284634, 284635, 284638, 284558, 283981, 284638, 56182323, 60170394, 284558, 18108381, 18108382, 83373044, 18108385, 87188518, 60432113, 22279002, 284482, 284584, 284585, 284488, 284587, 18108391
2255	91010548 (4508, 4510)	Novel Protein sim. GBank gij5541865[embjCAB51072.1] - (AL088658) hypothetical protein [Homo sapiens]	Contains protein domain (PF00078) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	struct	65274572, 56182575, 22278997, 22278999, 284258, 28331822, 28331825, 28331826, 28331827, 28331828, 284508, 284905, 284908, 284907, 66712502, 284908, 56182435, 284510, 284511, 285008, 284503, 284595, 21908754, 33109954, 87188474, 285011, 285017, 285019, 284882, 284784, 284389, 284288, 284788, 284888, 284888, 284788, 21908785, 21908788, 21908788, 21908789, 285020, 60170815, 52844150, 284690, 284692, 284693, 33657109, 33657348, 284632, 284638, 52844332, 56182323, 22279000, 22279002, 284788, 284688, 18108374
2256	87020531 (4511, 4512)	Novel Protein sim. GBank gij3327174[idbjBAA31655] - (AB014580) KIAA0880 protein [Homo sapiens]		UNCLASSIFIED	
2257	80088235 (4513, 4514)			UNCLASSIFIED	22278998, 22278999, 284681, 21908785, 21908788, 284587
2258	88080518 (4515, 4516)	Novel Protein sim. GBank gij3025446 (AC004828) - R32184_2 [Homo sapiens]	Contains protein domain (PF00080) - Ligand-gated ion channel	misc_channel	284908, 284592, 284784

2258	95364155 (4517, 4518)	Novel Protein sim. GBank gl 4884140 emb CAB43276.1 - (AL050110) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108388, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331827, 264905, 66712502, 264908, 264909, 56182435, 265007, 265008, 60432229, 33657084, 87186559, 18108351, 264448, 264883, 264288, 264369, 56181562, 265021, 60170615, 264890, 33657109, 60431528, 18108374, 52644332, 56182323, 18108385, 22278000, 22278002, 264482
2260	88084119 (4519, 4520)	Novel Protein sim. GBank gl 3080863 (AC004614) - similar to f-espandin proteins AB008086 (PID:g2529225) [Homo sapiens]	Contains protein domain (PF00009) - Thrombospondin type 1 domain	oxidase	56182575, 265020, 264905, 264908, 264908, 35698423, 264511, 264635, 55812038, 264758, 265018, 265019, 264805, 284760, 284583
2261	88074157 (4521, 4522)	Novel Protein sim. GBank gl 3334526 emb CAA18138 - (AL021308) predicted using FGENEH [Homo sapiens]		UNCLASSIFIED	
2262	91639292 (4523, 4524)	Novel Protein sim. GBank gl 487759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 [Homo sapiens]			56182575, 22278998, 29331822, 28331825, 80432288, 29331827, 35698052, 264508, 66712502, 52844045, 56182435, 265008, 265008, 265009, 60433356, 55812038, 265010, 265017, 265018, 264288, 264389, 21906785, 21906787, 55811857, 35695917, 52844150, 33657023, 33657109, 55811578, 65274791, 56182323
2263	87602495 (4525, 4526)	Novel Protein sim. GBank gl 3341697 (AC003672) - hypothetical protein [Arabidopsis thaliana]			22278994, 22278997, 264907, 264828, 52844150, 18108381, 264893, 18108374
2264	87756525 (4527, 4528)	Novel Protein sim. GBank gl 1657601 (U86220) - unknown [Nannocyathus exedens]		UNCLASSIFIED	264886, 264488, 264768, 264769, 264691, 264508, 264905, 264509, 264906, 264907, 264808, 264908, 35695855, 284510, 264511, 264512, 265007, 265009, 264638, 264639, 264757, 264758, 18108385, 265011, 264760, 264584, 264565, 264764, 264566, 264486, 264768
2265	86916663 (4529, 4530)	Novel Protein sim. GBank gl 477072 pir A48018 - mucin 7 precursor, salivary - human	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	264689, 264810, 264764
2266	87773458 (4531, 4532)	Novel Protein sim. GBank gl 3150478 (AF087212) - partial CDS [Caenorhabditis elegans]	Contains protein domain (PF01305) - Ribosomal protein L15 amino terminal region	ribosomal prot	22278995, 22278997, 22278999, 264259, 265008, 265007, 265009, 60433438, 21908754, 265010, 265011, 265017, 264448, 264883, 264288, 264689, 21908765, 21908768, 35695917, 265021, 18108374, 264638, 22278000, 22278002, 264566, 264487

2267	87395838 (4533, 4534)	Novel Protein sim. GBank gl 3560229 emb CAA20687.1 - (AL031630) hypothetical protein [Schizosaccharomyces pombe]	UNCLASSIFIED	35698286, 264259, 28331824, 29331825, 35698052, 29331828, 284905, 284509, 284907, 284908, 284909, 284512, 285009, 284910, 284593, 33657402, 285010, 285018, 284762, 284448, 284288, 284389, 284768, 32844229, 35695917, 284691, 33657023, 18108392, 33657108, 35698423, 284634, 18108381, 87188518, 284588
2268	85683867 (4535, 4536)	Novel Protein sim. GBank gl 728632 ep P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII	cadherin	284488, 264259, 284509, 284595, 285010, 285017, 284768, 18108385, 284486
2269	88177977 (4537, 4538)	Novel Protein sim. GBank gl 103418 pr J S17885 - Tcd37 protein - fruit fly (Drosophila melanogaster)	UNCLASSIFIED	56182575, 60432049, 265007, 265008, 284591, 87188559, 284605, 18108351, 21908764, 265020, 284628, 60431528, 284638, 18108385, 18108387, 60432113
2270	80410327 (4539, 4540)			284783
2271	91010392 (4541, 4542)		cyto450	284909, 56182435, 265008, 55812038, 55811957, 33657023, 284693, 33657109, 55810784, 55811578, 56182323
2272	84208220 (4543, 4544)		UNCLASSIFIED	284905, 284908
2273	95014271 (4545, 4546)	Novel Protein sim. GBank gl 4176370 (AC005058) - similar to calcium-independent phospholipase A2; similar to AC004392 (PID:g3367519) [Homo sapiens]	Contains protein domain (PF00462) - Glutaredoxin	52845156, 22278996, 22278999, 60432049, 284259, 29331822, 29331824, 29331825, 28331828, 29331827, 35698052, 284909, 285006, 284593, 60433438, 21908754, 285018, 284889, 21908765, 21908766, 21908767, 21908769, 285021, 285022, 60170815, 284691, 33657023, 284693, 33657109, 27488264, 18108376, 35698423, 35695855, 284630, 52644332, 284558, 56182323, 22278902
2274	91840217 (4547, 4548)	Novel Protein sim. GBank gl 1480112 emb CAA67981 - (X98842) HP1-8P74 protein [Mus musculus]	Contains protein domain (PF00538) - linker histone H1 and H5 family	52845156, 22278997, 22278999, 52645080, 29331824, 28331825, 29331828, 28331827, 29331828, 284905, 284908, 52644045, 284511, 285008, 285009, 80170831, 284591, 21908754, 33109954, 285011, 285018, 18108351, 284448, 284288, 284684, 284768, 21908765, 21908766, 21908767, 21908768, 52644150, 284693, 18108364, 35695763, 18108374, 35698423, 284634, 284557, 284638, 52644332, 83373044, 18108385, 56528488, 87188518, 22279002
2275	88082501 (4549, 4550)	Novel Protein sim. GBank gl 3165408 (AC004756) - (os37502_2 [Homo sapiens])	Contains protein domain (PF00122) - E1-E2 ATPase	
2276	11287447 (4551, 4552)		transport	
			UNCLASSIFIED	284555, 284556

2277	18084123 (4553, 4554)	Novel Protein sim. GBank gij280079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g138908) [Homo sapiens]	Contains protein domain (PF00580) - Leucine Rich Repeat	glycoprotein	2227899, 35696052, 265008, 285019, 284388, 265020, 265022, 59810784, 284404, 22279002
2278	94133079 (4555, 4556)	Novel Protein sim. GBank gij2818702 (AC002510) - unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	18108394, 22278997, 28331828, 60433356, 60433438, 21908754, 265018, 33657023, 284639, 83373044, 284565
2279	80419375 (4557, 4558)	Novel Protein sim. GBank gij119714 [sp]P13983 [EXTN_TOBAC - EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN)]		UNCLASSIFIED	284786, 284565
2280	84238723 (4559, 4560)				
2281	95293048 (4561, 4562)	Novel Protein sim. GBank gij424029 [dbj]BAA74928.1] - (A8020712) KIAA0805 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transport	265008, 33109954, 265010, 285019, 265020, 284092, 284259, 29331822, 29331824, 29331826, 35696052, 284107, 284806, 284908, 52844045, 265008, 33657402, 60433356, 264758, 265011, 265019, 284681, 284693, 284684, 284686, 21908785, 21908787, 21908788, 21908789, 60170615, 284690, 52844150, 18108382, 284692, 18108388, 18108374, 263978, 284631, 18108381, 284558, 18108385, 59528486, 22279000, 284566, 284567
2282	87602828 (4563, 4564)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]		UNCLASSIFIED	29331827, 29331828, 29331830, 33657402, 60433438, 87168474, 265019, 18108351, 21908787, 21908788, 55811957, 33657023, 52845129, 33657109, 33657182, 27486282, 263972, 55811578, 87168518, 20281189, 80424178, 56182575, 22278994, 35696286, 22278997, 22278999, 29331822, 29331824, 55182181, 29331825, 29331827, 35696052, 29148499, 284905, 66712502, 264908, 265007, 265009, 60432229, 264593, 60431735, 60433356, 33109954, 33657084, 55811366, 87168474, 265010, 265011, 265018, 285019, 55811150, 284683, 264369, 284288, 284898, 21908785, 21908787, 21908788, 29148627, 21908789, 55811957, 265020, 265022, 33657182, 27486281, 18108370, 284628, 18108374, 55810784, 18108378, 55811578, 35696423, 35695855, 284630, 60431850, 263981, 18108382, 83373044, 18108385, 18108387, 60432113, 22278000, 284482, 284587
2283	95322368 (4565, 4566)	Novel Protein sim. GBank gij2495729 [sp]Q82558 [Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA8725)]		UNCLASSIFIED	

2284	95414955 (4567, 4568)	Novel Protein sim. GBank gl 2498787 sp Q84311 PNAD_MOUSE - PROTEIN N-TERMINAL ASPARAGINE AMIDOHYDROLASE (PROTEIN NH2-TERMINAL ASPARAGINE DEAMIDASE) (NTN-AMIDASE) (PNAD) (PROTEIN NH2-TERMINAL ASPARAGINE AMIDOHYDROLASE) (PNAAD)			60424179, 52844507, 18108394, 52846842, 22278994, 35698286, 22278996, 22278997, 22278999, 284259, 80432048, 28331822, 28331824, 28331825, 60432289, 28331826, 28331827, 35698052, 28331830, 52844045, 56182435, 33657402, 60433438, 33109954, 21908754, 85658542, 87188559, 285018, 285019, 55811150, 284682, 284389, 21908765, 21908768, 21908787, 21908788, 21908789, 55811957, 35695917, 285020, 285021, 80170815, 33657023, 33657182, 27488262, 27488264, 27488265, 18108376, 55810764, 35696423, 35695855, 60431850, 87168518, 80432113, 284482, 284584
2285	87781484 (4569, 4570)	Novel Protein sim. GBank gl 3342234 (U83909) - nuclear antigen EBNA-1 (Carcopillhacine herpesvirus 15)		collagen	35696052, 284905, 284907, 284908, 284909, 284512, 285009, 284910, 284595, 284780, 18108351, 284682, 284763, 284685, 284768, 284686, 284768, 284683, 284684
2286	87737825 (4571, 4572)	Novel Protein sim. GBank gl 3873414 (U00043) - similar to D. melanogaster trithorax protein [Caenorhabditis elegans]		kinase	35696286, 58182435, 60170831, 284591, 60432229, 284592, 284593, 284594, 284595, 55812038, 284596, 87168474, 35695917, 284682, 55811578, 284555, 284557
2287	82986896 (4573, 4574)	Novel Protein sim. GBank gl 830805 pir S42731 - collagen alpha 1 chain - sea urchin (Hemicentrotus pulcherrimus) (fragment)	Contains protein domain (PF01381) - Collagen triple helix repeat (20 copies)	UNCLASSIFIED	284682
2288	94133083 (4575, 4576)	Novel Protein sim. GBank gl 728832 sp P39189 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	22278995, 56994075, 22278997, 22278999, 284259, 80432289, 284508, 284512, 285008, 33657402, 285017, 285018, 285019, 18108351, 284448, 21908765, 21908768, 21908787, 21908788, 33657023, 284557, 22279000, 22279002
2289	88084133 (4577, 4578)	Novel Protein sim. GBank gl 2887487 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	
2290	88084137 (4579, 4580)	Novel Protein sim. GBank gl 2887487 (AC004144) - R34001_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	284683
2291	84295281 (4581, 4582)	Novel Protein sim. GBank gl 3253120 (AC005175) - R31449_3 [Homo sapiens]		strudl	18108394, 284907, 285008, 285009, 33109954, 52846317, 285010, 18108351, 284681, 284688, 284692, 18108370, 18108374, 18108385

2292	94328634 (4583, 4584)	Novel Protein sim. GBank gi 4803672 emb CAB42643.1 - (AJ133769) nuclear transport receptor [Homo sapiens]		UNCLASSIFIED	58182575, 35898286, 56894075, 29331824, 29331825, 35898052, 56182435, 60433438, 55812038, 33109954, 87188474, 87188559, 265018, 18108351, 264763, 264448, 264369, 264288, 56181592, 264769, 21906765, 21906766, 21906767, 21906769, 265021, 265022, 33657023, 264693, 65274620, 33657109, 27488264, 264829, 55810764, 55811576, 35898555, 56182323, 56528486, 87188518, 22278000, 264567
2293	87759213 (4585, 4586)	Novel Protein sim. GBank gi 3252981 (AF088921) - Ras-binding protein SUR-8 [Mus musculus]	Contains protein domain (PF00560) - Leucine Rich Repeat	sinut	264488, 18108397, 35898286, 264092, 264259, 29331822, 29331826, 264906, 264908, 264511, 264512, 265009, 264610, 18108351, 264764, 264369, 264288, 264885, 264766, 265020, 265022, 264534, 35898423, 264631, 264637, 18108381, 56182323, 264839, 18108385, 264404, 264563, 264565, 22278997, 22278998, 22278999, 264259, 29331822, 60432289, 29331828, 35898052, 265018, 264684, 264288, 264686, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265021, 264692, 33657109, 18108376, 35898423, 35898555, 264634, 22278000, 22278002, 264563, 264488
2294	86693560 (4587, 4588)	Novel Protein sim. GBank gi 2062680 (U88984) - HEM45 [Homo sapiens]	Contains protein domain (PF00929) - Exonuclease	nuclease	22278996, 60432289, 264682, 264683, 264689, 18108374
2295	95312200 (4589, 4590)			UNCLASSIFIED	263974, 263978
2296	80030761 (4591, 4592)			transcriptfactor	264488, 65274572, 56182575, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 35898052, 264907, 264908, 52644045, 56182435, 264112, 265006, 265007, 264910, 265009, 60433356, 33657402, 264595, 55812038, 21906754, 265011, 265018, 265019, 264448, 264764, 264288, 264768, 21906765, 21906767, 21906768, 21906769, 55811577, 265020, 265021, 264690, 264691, 33657023, 264692, 264693, 33657109, 55811576, 56182323, 80170394, 83373044, 18108385, 56528486, 264564, 264488
2297	94321251 (4593, 4594)	Novel Protein sim. GBank gi 5689501 db BAA83034.1 - (AB028005) KIAA1082 protein [Homo sapiens]			

2298	95312207 (4595, 4598)	Novel Protein sim. GBank gl 3875051 emb CAB02849 - (Z81050) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D85564 comes from this gene; cDNA EST EMBL:D89048 comes from this gene; cDNA EST yk368b12.3 comes from this gene; cDNA EST yk368b12.5 comes from this gene ...	collagen	60424179, 56181686, 22278995, 35696268, 22278998, 22278998, 22278999, 264480, 264259, 29331822, 29331824, 66714117, 60424289, 35696052, 29331828, 66712502, 56182435, 264510, 265008, 60433438, 21908754, 33109954, 55811388, 265010, 265018, 55811150, 264782, 18108351, 264682, 264683, 264288, 264684, 264686, 264688, 56181562, 264689, 21908767, 29148629, 55811957, 29148784, 35695917, 265020, 18108362, 33657023, 18108364, 33657109, 60431602, 18108370, 60431528, 18108374, 55810764, 35696423, 35695855, 264630, 264634, 60431850, 18108380, 56182323, 264558, 83373044, 18108385, 60432113, 22278000, 264482, 264587, 264486
2299	80193720 (4597, 4598)		UNCLASSIFIED	264369
2300	94124348 (4599, 4600)	Novel Protein sim. GBank gl 2443888 (AC002284) - Unknown protein [Arabidopsis thaliana]		264488, 22278998, 22278999, 264259, 29331824, 66714117, 35696052, 264509, 264905, 264908, 264907, 264908, 264909, 265008, 264910, 265009, 264758, 265010, 87168558, 264600, 265018, 264760, 264762, 18108351, 264764, 264766, 264768, 264769, 21908768, 21908767, 35695917, 265021, 264691, 33657023, 35695783, 18108370, 18108374, 35696423, 35695855, 264631, 264638, 264638, 18108385, 22278002, 264583
2301	91235725 (4601, 4602)	Novel Protein sim. GBank gl 2143837 pir l 84505 - calcium-dependent actin-binding protein - rat	struct	264608, 264758, 265017, 21908765, 83373044, 264563
2302	88084141 (4603, 4604)	Novel Protein sim. GBank gl 2887497 (AC004144) - R34001_1 [Homo sapiens]	UNCLASSIFIED	52644045, 265019, 264288, 33657023, 18108370, 18108385
2303	94141439 (4605, 4606)	Novel Protein sim. GBank gl 4884194 emb CAB43220.1 - (AL049946) hypothetical protein [Homo sapiens]	Contains protein domain (PF00047) - Immunoglobulin domain	264259, 60432049, 264907, 264909, 264910, 60432229, 33657402, 265011, 265018, 264782, 264448, 264769, 264637, 264638, 83373044, 264486
2304	94840434 (4607, 4608)	Novel Protein sim. GBank gl 2484162 p Q10005 YRY1_CAEEL - HYPOTHETICAL 39.8 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	UNCLASSIFIED	264259, 29331824, 21908767, 33657182, 33657349
2305	90835911 (4609, 4610)	Novel Protein sim. GBank gl 4972686 gb AAD34738.1 - (AF132150) unknown [Drosophila melanogaster]		65274572, 22278998, 264908, 265006, 21908769, 264681, 264486

2308	95334940 (4611, 4612)	Novel Protein sim. GBank gi 4928595 gb AAD34043.1 AF15180 - (AF15180) CGI-48 protein [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	264488, 22278995, 22278996, 35698286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35698052, 264508, 264905, 264907, 29331830, 264908, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 33657402, 21906754, 8569842, 265010, 265011, 264801, 265017, 265018, 264604, 265019, 18108351, 264448, 264288, 264768, 264769, 21908785, 21908766, 21908787, 21908768, 29148629, 29148784, 35695917, 265020, 265021, 265022, 33657023, 264692, 18108370, 18108374, 18108376, 35698423, 35695855, 264630, 264634, 264635, 264636, 264637, 264638, 264639, 18108382, 18108385, 18108387, 264563, 264566, 264486 264828
2307	78415283 (4613, 4614)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCs - molybdenum cofactor synthesis 2		UNCLASSIFIED	264828
2308	87608409 (4615, 4616)	Novel Protein sim. GBank gi 4758732 ref NP_004522.1 pMOCs - molybdenum cofactor synthesis 2		synthase	35698288, 264259, 29331822, 29331824, 264112, 264512, 264757, 21908754, 264288, 264680, 27488264, 264631, 264634, 264404
2309	95357218 (4617, 4618)	Novel Protein sim. GBank gi 3878059 emb CAB17070 - (Z99842) cDNA EST EMBL:D73444 comes from this gene; cDNA EST EMBL:D70905 comes from this gene; cDNA EST EMBL:D72208 comes from this gene; cDNA EST EMBL:D75030 comes from this gene; cDNA EST EMBL:D72844 comes from this gene; cDN...		glycoprotein	18108397, 22278996, 22278997, 22278998, 22278999, 60432048, 29331822, 29331826, 60432289, 66712502, 60432228, 60433356, 60433436, 65274444, 265010, 264600, 264681, 264448, 264683, 264288, 21908766, 21908768, 265020, 264691, 264692, 264693, 65274620, 65274791
2310	79601668 (4619, 4620)	Novel Protein sim. GBank gi 2137337 pir j148281 - gene mCBP protein - mouse	Contains protein domain (PF00013) - KH domain	UNCLASSIFIED	264508
2311	87721189 (4621, 4622)	Novel Protein sim. GBank gi 2137337 pir j148281 - gene mCBP protein - mouse		transcriptfactor	18108397, 56182575, 22278998, 56994075, 264259, 29331824, 29331827, 264508, 264907, 56182435, 264510, 264511, 265008, 264512, 265007, 265008, 265009, 60433438, 33109954, 265010, 265011, 264603, 265017, 18108351, 264762, 264683, 264288, 264369, 264688, 33657023, 20281149, 20281069, 264628, 263972, 56811576, 35698423, 20281071, 264632, 264636, 18108385, 18108387, 87168516, 22278000, 264563, 264486

2312	87548881 (4823, 4824)	Novel Protein sim. GBank gll2911284 (AC002550) - Unknown gene product [Homo sapiens]			56182575, 56994075, 35686286, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 52844045, 60432228, 60433356, 55812038, 33109954, 21906754, 87168474, 265018, 18108351, 264288, 52844228, 21906765, 21906768, 21906767, 21906768, 21906769, 265022, 60170815, 33657023, 27486281, 27486284, 35686423, 35685855, 18108385, 22279000, 22279002, 263981
2313	80042533 (4825, 4828)	Novel Protein sim. GBank gll3043626[gb][BAA25477] - (AB011123) KIAA0551 protein [Homo sapiens]		UNCLASSIFIED	52844507, 52846365, 52848842, 22278996, 22278997, 22278998, 264259, 52845080, 29331822, 29331824, 60432228, 29331826, 29331827, 29331828, 35686052, 33656970, 52844045, 265008, 264593, 60433356, 60433438, 264758, 33109954, 265010, 265017, 265018, 265019, 264288, 264369, 21906765, 21906768, 21906769, 35685917, 52844150, 33657023, 33657109, 52845129, 33657349, 35685763, 18108374, 35686423, 35685855, 52844332, 22279000, 22278002, 264563, 264567
2314	94313401 (4627, 4628)	Novel Protein sim. GBank gll5598714[emb][CAB51401.1] - (AL035398) dJ79817.2 (CGI-51) [Homo sapiens]			264905, 264906, 264767, 264768, 264693, 55811576, 264635, 56182323, 18108385, 52844507, 52845156, 52846365, 22278994, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 22278999, 264259, 29331822, 52845080, 29331824, 29331825, 29331826, 29331827, 35686052, 29331828, 284906, 264807, 29331830, 52844045, 56182435, 264511, 265007, 265008, 265009, 60170831, 60433438, 21906794, 52846317, 33109954, 33657084, 52844288, 87168474, 265010, 87168558, 265017, 265018, 265019, 52844228, 21906764, 264689, 21906765, 264681, 264783, 264448, 264683, 264389, 21906768, 21906767, 21906768, 21906769, 35685917, 265020, 265021, 52844150, 33657023, 18108362, 52845129, 33657182, 33657348, 35685763, 18108370, 18108376, 35686423, 35685855, 264631, 264556, 52844332, 83373044, 18108385, 18108387, 87168518, 60432113, 22279000, 264566, 264567
2315	80430119 (4629, 4630)			UNCLASSIFIED	
2316	94312181 (4631, 4632)	Novel Protein sim. GBank gll5531827[gb][AAD44488.1] - (AF078856) p47 [Homo sapiens]	Contains protein domain (PF00789) - glycoprotein UBX domain		

2317	87020571 (4633, 4634)			UNCLASSIFIED	22278998, 60432049, 284910, 60432229, 284686, 264687, 264688, 264689, 264558, 18108385
2318	7969879 (4635, 4636)			UNCLASSIFIED	285006, 264910
2319	95101781 (4637, 4638)			UNCLASSIFIED	264488, 264569, 18108396, 52646365, 22278994, 22278995, 22278996, 56994075, 35686286, 22278997, 22278998, 264259, 52645080, 26331825, 26331826, 26331827, 26331828, 26331830, 56182435, 60170831, 60432229, 60431735, 33657402, 21808754, 52644286, 87188474, 265011, 87188559, 265017, 265018, 265019, 18108351, 264448, 18108354, 264288, 264369, 52644228, 21808764, 21808765, 21808766, 21808767, 21808768, 21808769, 265021, 265022, 52644150, 33657023, 52645129, 33637109, 27486284, 33657349, 35695763, 18108370, 18108376, 18108379, 35696423, 264558, 63373044, 18108385, 56526486, 87188518, 264564, 264565, 264566
2320	91822428 (4639, 4640)			kinase	22278994, 60432049, 60432289, 26331827, 264511, 265008, 52646317, 265017, 265019, 21808765, 18108372, 18108387, 22278902, 264486, 264687, 18108394, 264689
2321	94320377 (4641, 4642)	Novel Protein sim. GBank g 1728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY III Novel Protein sim. GBank g 3673837 emb CAB02700 - (261029) Similarity to S.pombe hypothetical protein C1D4.09C (SW:Q10154): cDNA EST EMBL:T00543 comes from this gene; cDNA EST EMBL:T01082 comes from this gene; cDNA EST EMBL:T01321 comes from this gene; cDNA EST EMBL:T02288 com...		UNCLASSIFIED	21808765, 18108397, 18108398, 21808767, 21808768, 65274791, 22278995, 35695855, 22278998, 265021, 265022, 264510, 265006, 264511, 264512, 265008, 60170815, 264555, 264636, 264556, 18108361, 264259, 60432229, 33657023, 264557, 264558, 264693, 60433356, 264559, 60433438, 26331824, 18108365, 18108346, 18108384, 26331825, 18108385, 33109954, 26331827, 56526486, 26146499, 265011, 60432113, 265017, 265018, 264508, 264563, 264482, 264509, 18108351, 264448, 264907, 264682, 18108370, 264683, 264908, 264288, 264909, 18108354, 264486, 264567
2322	87603165 (4643, 4644)	Novel Protein sim. GBank g 5678957 emb CAB51685.1 - (AL109630) BACR7A4.y [Drosophila melanogaster]	Contains protein domain (PF00106) - short chain dehydrogenase	dehydrogenase	18108351, 264788, 264638

2323	94840445 (4645, 4646)	Novel Protein sim. GBank gi2494162 epiQ10005 YRY1_CAEEL - HYPOTHETICAL 39.9 KD PROTEIN T15H8.1 IN CHROMOSOME II PRECURSOR	Contains protein domain (PF00228) - DnaJ domain	eph	22278984, 22278995, 22278997, 60432049, 264259, 29331822, 33656970, 264509, 58182435, 264511, 285008, 60433358, 60433438, 55812038, 33109954, 21908754, 85658542, 87168474, 265011, 87168559, 285017, 285019, 264780, 264681, 18108351, 284369, 284288, 18108355, 264687, 264688, 21908765, 21908767, 21908788, 55811957, 35695917, 285021, 33657023, 18108382, 27488262, 55811578, 264631, 264555, 83373044, 87168518, 60432113, 22279002
2324	86633607 (4647, 4648)	Novel Protein sim. GBank gi15419865 embjCAB46377.1 - [AL098732] hypothetical protein [Homo sapiens]		ATPase-associated	264592, 264593, 265020
2325	88165074 (4649, 4650)	Novel Protein sim. GBank gi231885 spP29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)	Contains protein domain (PF00087) - Cytochrome P450	Cyto450	285006, 284796, 35695855, 58182323
2326	84390962 (4651, 4652)	Novel Protein sim. GBank gi1231885 spP29881 CP4C_BLADI - CYTOCHROME P450 4C1 (CYP1VC1)		UNCLASSIFIED	
2327	88081648 (4653, 4654)	Novel Protein sim. GBank gi14240227 dbjBAA74892.1 - [AB020678] KIAA0869 protein [Homo sapiens]		UNCLASSIFIED	264259, 264508, 264905, 264908, 264907, 264908, 265007, 264512, 264910, 264758, 285010, 264786, 264788, 264769, 33657023, 284693, 284628, 264631, 264634, 264638, 264639, 264486
2328	83388428 (4655, 4656)	Novel Protein sim. GBank gi11245105 (U46463) - glutamine repeat protein-1 [Mus musculus]		UNCLASSIFIED	60433438, 264595, 265017, 284766, 264892, 264629, 264635, 264638, 264639, 58182323, 60432113, 264566
2329	87604478 (4657, 4658)	Novel Protein sim. GBank gi1169343 epP42209 DIF8_MOUSE - DIFF8 PROTEIN	Contains protein domain (PF00735) - Cell division protein	UNCLASSIFIED	285017, 264695, 60432113, 264088
2330	87333396 (4659, 4660)	Novel Protein sim. GBank gi15679136 gb AAD46674.1 AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	265009
2331	86980463 (4661, 4662)	Novel Protein sim. GBank gi12104452 embjCAB08779 - (Z95397) unknown [Schizosaccharomyces pombe]		ATPase-associated	35696265, 22278998, 29331824, 60424269, 265006, 265008, 265018, 264448, 264764, 21908765, 35695917, 35695855, 264636, 22279000, 264566
2332	87784182 (4663, 4664)	Novel Protein sim. GBank gi13879985 embjCAA92891.1 - (Z80318) cDNA EST CEMSD82F comes from this gene; cDNA EST EMBL:C07930 comes from this gene; cDNA EST EMBL:C09493 comes from this gene; cDNA EST yk415e8.3 comes from this gene; cDNA EST yk415e8.5 comes from this gene; cDNA EST...		UNCLASSIFIED	58182575, 56994075, 26331826, 29331828, 264107, 33657402, 87168559, 264693, 35695917, 285021, 33657023, 263976
2333	88206958 (4665, 4666)	Novel Protein sim. GBank gi14966270 gb AA02221.2 - (U87002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (hydrolase), Score=57.4, E- value=1e-13, N=1 [C...	Contains protein domain (PF00441) - Acyl-CoA dehydrogenase	dehydrogenase	58182575, 29331825, 21908788, 264636, 83373044
2334	94318788 (4667, 4668)	Novel Protein sim. GBank gi14966270 gb AA02221.2 - (U87002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh), Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (hydrolase), Score=57.4, E- value=1e-13, N=1 [C...			

2335	80046103 (4669, 4670)	Novel Protein sim. GBank gl 3283350 (AF062378) - calmodulin-binding protein SHA1 [Mus musculus]	Contains protein domain (PF00812) - struct	18108351, 21906769, 264555
2336	95196121 (4671, 4672)	Novel Protein sim. GBank gl 1929056 emb CAA72805 - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [Lycopersicon esculentum]	kinase	264807, 35695917, 18108379
2337	95345810 (4673, 4674)	Novel Protein sim. GBank gl 4495063 emb CAB39181.1 - (Z85986) dJ108K1.1.3 (similar to yeast suppressor protein SRP40) [Homo sapiens]	UNCLASSIFIED	35696286, 22278999, 56182181, 29331825, 60424289, 56182435, 33657402, 55812038, 55811386, 265017, 265018, 265019, 21906788, 35695917, 264891, 33657023, 33657109, 263972, 35696423, 35695855, 60432113
2338	87634045 (4675, 4676)	Novel Protein sim. GBank gl 2224689 db BAA20829 - (AB002372) KIAA0374 [Homo sapiens]	Contains protein domain (PF00323) - Mammalian defensin	18108394, 29331822, 66714117, 60432289, 264808, 56182435, 265009, 60433438, 264586, 265010, 265019, 18108354, 264288, 264389, 55811957, 265021, 33657023, 263976, 55811578, 264632, 56182323, 264639
2339	85663319 (4677, 4678)	Novel Protein sim. GBank gl 3873550 emb CAA22127 - (AL033534) serine-rich protein [Schizosaccharomyces pombe]	UNCLASSIFIED	35696286, 264592, 264389, 264691, 264558
2340	90937716 (4679, 4680)			
2341	8775261 (4681, 4682)			65274572, 22278994, 35696286, 22278997, 22278999, 264259, 29331822, 60432289, 29331828, 26331830, 265009, 33657402, 33109954, 265017, 265018, 264788, 264685, 21906789, 35695917, 264891, 264692, 35696423, 87188518, 22279000
2342	95334966 (4683, 4684)	Novel Protein sim. GBank gl 3874563 emb CAB02797 - (Z81042) similar to Yeast hypothetical protein YEY6 like; cDNA EST yk208h5.3 comes from this gene; cDNA EST yk208h5.5 comes from this gene; cDNA EST yk303h1.3 comes from this gene; cDNA EST yk303h1.5 comes from this gene; cDNA ...	Contains protein domain (PF00400) - kinase	264259, 264808, 264909, 264682, 22279000, 264488, 65274572, 22278995, 22278998, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 29331828, 60432289, 35696052, 264905, 264509, 29331830, 265008, 60170831, 60432229, 60433356, 87168474, 265017, 265018, 265019, 264448, 264389, 264288, 21906765, 21906766, 55811957, 35695917, 265020, 265022, 52644150, 33657023, 65274620, 33657109, 18108370, 18108376, 55810784, 35696423, 55811576, 264556, 264558, 18108385, 60432113, 264553, 264564, 264565, 264568, 264567, 264907, 264512, 265011, 264683
2343	8775448 (4685, 4686)	Novel Protein sim. GBank gl 492974 gb AAD34131.1 AF15189 - (AF15189) CGI-138 protein [Homo sapiens]	UNCLASSIFIED	
2344	79953198 (4687, 4688)			264758
2345	94319789 (4689, 4690)	Novel Protein sim. GBank gl 2506307 sp P13944 CA1C_CHICK - COLLAGEN ALPHA 1(XII) CHAIN PRECURSOR (FIBROCHIMERIN)	Contains protein domain (PF00092) - von Willebrand factor type A domain	264488, 264259, 66712502, 264759, 83373044, 264586

2348	84131820 (4891, 4892)	Novel Protein sim. GBank gll1255411 (U53153) - one short region of weak similarity to <i>S. cerevisiae</i> protease A inhibitor 3 (SP-P01094) and another short region of weak similarity to <i>S. cerevisiae</i> glucose repression mediator protein (SP-P14922) [<i>Caenorhabditis elegans</i>]	Contains protein domain (PF00515) - TPR Domain	proteaseinhib	35698286, 22278998, 284259, 35698052, 29331828, 33657402, 60433396, 33108954, 87168559, 284603, 265019, 18108351, 284881, 284688, 21906786, 285021, 33657109, 55811576, 35698585, 284637, 52844332, 284557, 83373044, 22279000, 22279002
2347	85330387 (4893, 4894)				22278997, 264511, 264683, 284684, 284768, 284687, 284688, 284691, 284892, 55811576
2348	85198133 (4895, 4896)	Novel Protein sim. GBank gll1929058[emb]CAA72805] - (Y12090) putative 3,4-dihydroxy-2-butanone kinase [<i>Lycopersicon esculentum</i>]		kinase	18108394, 35698286, 264259, 35698052, 284508, 284509, 284905, 284906, 284907, 284908, 284909, 264510, 264511, 285006, 265007, 264512, 285008, 265009, 284910, 284591, 284592, 284593, 284594, 264757, 264595, 284596, 284758, 265011, 284601, 284782, 18108351, 284784, 284286, 284766, 284788, 284689, 35695917, 284693, 284628, 18108370, 284628, 18108374, 35698423, 284631, 284635, 284638, 284637, 284638, 284639, 83373044, 18108385, 284587, 284488
2349	87776502 (4897, 4898)	Novel Protein sim. GBank gll4884108[emb]CAB43254.1] - (AL050062) hypothetical protein [Homo sapiens]			35698052, 29146499, 284909, 284369
2350	88280594 (4899, 4700)				22278998, 22278999, 284259, 29331822, 29331824, 29331825, 29331827, 29331828, 33108954, 21906754, 265010, 87168559, 265018, 265019, 284761, 284681, 284288, 18108357, 21906786, 21906787, 284691, 284692, 35695855, 87168518, 22279000, 22279002, 284482
2351	86868042 (4701, 4702)	Novel Protein sim. GBank gll728832[sp]P39189/ALU2_HUMAN - III ALU SUBFAMILY SB WARNING ENTRY III		kinase	56182575, 284909, 265006, 284558
2352	87337198 (4703, 4704)	Novel Protein sim. GBank gll731637[sp]P38780[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	284259, 284448
2353	91638784 (4705, 4706)	Novel Protein sim. GBank gll1346955[sp]P48809[RB27_DROME - HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN 27C (HNRNP 48) (HRP48.1)]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	29331826, 55812038, 265019, 284692, 284636
2354	87337198 (4707, 4708)	Novel Protein sim. GBank gll731637[sp]P38780[YHH5_YEAST - HYPOTHETICAL 75.9 KD PROTEIN IN SPO13-ARG4 INTERGENIC REGION]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	29331824, 284908, 265006, 265008

2355	81638788 (4708, 4710)	Novel Protein sim. GBank gl 4938503 emb CAB43881.1 - (AL078485) hnRNP-like protein [Arabidopsis thaliana]	Contains protein domain (PF00076) - dna_ma_bind RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	56994075, 22278998, 35686286, 22278999, 264259, 29331825, 29331826, 29331828, 29146488, 284905, 284908, 265008, 264758, 87168474, 265010, 265017, 264687, 21908765, 21908767, 21908769, 264691, 264692, 263987, 18108370, 87168518, 22278000
2356	95327688 (4711, 4712)	Novel Protein sim. GBank gl 5138320 gb AAC0377.1 - (AF092135) PTD014 [Homo sapiens]		52844507, 22278998, 35686286, 22278999, 22278997, 22278998, 22278999, 284259, 28331824, 66714117, 29331825, 60432289, 35696052, 29331828, 284908, 66712502, 284512, 285007, 285008, 60170831, 60432229, 60433358, 60433438, 264758, 52846317, 33109954, 21908754, 59811386, 87168474, 265017, 265018, 264605, 265019, 264681, 264682, 264448, 264389, 264288, 264686, 264768, 21908785, 21908768, 21908767, 21908768, 21908768, 265021, 60170816, 33657109, 27486284, 35695783, 55810764, 18108378, 35698423, 55811576, 35695855, 60170394, 56182323, 83373044, 18108385, 56526488, 284404, 60432113, 22279000, 264482, 264563, 264568, 264488, 284587
2357	87775458 (4713, 4714)	Novel Protein sim. GBank gl 4928741 gb AAD34131.1 AF15189 - (AF151894) CGI-136 protein [Homo sapiens]	UNCLASSIFIED	284488, 264769, 18108394, 264259, 29331822, 18108370, 18108374, 264510, 265017, 264482, 264563, 264762, 264565, 264568, 264389, 18108394
2358	87777078 (4715, 4716)	Novel Protein sim. GBank gl 4218005 AC008135 - putative vicilin storage protein (globulin-like) [Arabidopsis thaliana]	UNCLASSIFIED	22278997, 22278999, 264509, 264905, 264592, 18108351, 264681, 264682, 264769, 32833986, 18108374, 264556, 18108385, 264482
2359	87755858 (4717, 4718)	Novel Protein sim. GBank gl 1086830 UA1264 - coded for by C. elegans cDNA yk208.5; coded for by C. elegans cDNA yk4491.5; coded for by C. elegans cDNA yk12b7.5; coded for by C. elegans cDNA yk3698.5; coded for by C. elegans cDNA yk208.5; coded for by C. elegans cDNA yk18g12....	UNCLASSIFIED	35686286, 22278998, 264905, 264511, 265007, 265008, 60433438, 264288, 264686, 21908768, 265020, 264692, 35695855, 264558, 56526488, 264563
2360	80046125 (4719, 4720)	Novel Protein sim. GBank gl 3881545 emb CAA93779 - (Z68804) cDNA EST yk428d5.3 comes from this gene; cDNA EST yk428d5.5 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	22278997, 29331826, 263981, 22278000
2361	84232181 (4721, 4722)	Novel Protein sim. GBank gl 748487 U23514 - No definition line found [Caenorhabditis elegans]		22278995, 22278999, 264512, 265009, 264757, 21908785, 65274820, 18108370, 60431528, 18108374, 264635, 60170394, 284482

2362	91721193 (4723, 4724)	Novel Protein sim. GBank g11171083[sp19708]MYSB, ACACA - MYOSIN HEAVY CHAIN IB (MYOSIN HEAVY CHAIN IL)	UNCLASSIFIED	22278898, 264259, 29331822, 29331824, 60432289, 264509, 264512, 60432229, 60433356, 264448, 264862, 264883, 264389, 21908765, 21908768, 21908769, 60432113, 22279000, 22278002
2363	95006635 (4725, 4726)	Novel Protein sim. GBank g1854085[emb]CAA58337] - (X83413) U88 [Human herpesvirus 6]	UNCLASSIFIED	284907, 264629, 264635
2364	94827104 (4727, 4728)	Novel Protein sim. GBank g15639830[g1AAD45886.1]AF14601 - (AF146018) hydroxypyruvate reductase [Homo sapiens]	reductase	264488, 18108394, 264887, 18108398, 22278996, 56994075, 35698286, 22278997, 22278998, 264259, 66714117, 29331825, 35698052, 264509, 264905, 264908, 264907, 264908, 66712502, 264909, 264511, 285006, 284512, 265007, 265008, 33657402, 264758, 21908754, 87168474, 265010, 87168558, 264603, 265017, 265018, 265019, 264780, 264782, 18108351, 264448, 264784, 264683, 264684, 264288, 18108355, 264786, 18108358, 264689, 18108359, 21908765, 21908766, 21908767, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264691, 33657023, 264692, 18108384, 33657109, 18108388, 18108370, 18108374, 35698423, 35695855, 264635, 264556, 264557, 264639, 60170394, 83373044, 18108383, 18108384, 18108385, 18108388, 56526486, 264482, 264564, 264486, 22278996, 22278998, 22278999, 284907, 284909, 264910, 33657402, 264758, 264600, 264786, 264887, 264889, 21908769, 285021, 21908767, 21908768, 21908769, 285021, 33657023, 33657109, 83373044, 264586 52644507, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 264907, 29331830, 264909, 264511, 285008, 33657402, 264595, 52646317, 265017, 265018, 265019, 264605, 264685, 264788, 284689, 21908766, 21908769, 35695917, 265020, 265021, 265022, 52644150, 35695855, 52644332, 18108385, 18108387, 264584, 264586 35698286, 21908768, 56810764, 65274781, 284567 284628
2365	94140746 (4729, 4730)	Novel Protein sim. GBank g11840045 (U49082) - transporter protein [Homo sapiens]	transport	
2366	94312388 (4731, 4732)		UNCLASSIFIED	
2367	94140910 (4733, 4734)	Novel Protein sim. GBank g11065457 (U40410) - C54G7.4 gene product [Caenorhabditis elegans]	UNCLASSIFIED	
2368	94322180 (4735, 4736)			

2369	94314334 (4737, 4738)	Novel Protein sim. GBank gij5360901[dbj]BAA02158.1] - (AB020343) a-helix coiled-coil rod homologue [Homo sapiens]		struct	52844507, 52848842, 35686286, 264092, 264094, 52845080, 35686052, 264107, 29331830, 52844045, 265008, 285007, 265009, 52844298, 52844229, 264889, 21908765, 21908768, 35685917, 265020, 52844150, 263987, 33857109, 27486285, 35685763, 18108370, 263974, 18108374, 18108378, 52844332, 263981, 18108385, 264508, 264908, 264598
2370	79804120 (4739, 4740)			UNCLASSIFIED	264369
2371	57280408 (4741, 4742)			UNCLASSIFIED	263967, 263981
2372	87842413 (4743, 4744)			UNCLASSIFIED	29331826, 265010, 265019, 35685917, 264634, 60432113
2373	87418611 (4745, 4746)	Novel Protein sim. GBank gij4588582[dbj]BAA76813.1] - (AB023186) KIAA0989 protein [Homo sapiens]		UNCLASSIFIED	
2374	94123665 (4747, 4748)	Novel Protein sim. GBank gij5105131[dbj]BAA0445.1] - (AF000061) 248aa long hypothetical ribonuclease PH [Aeropyrum pernix]	Contains protein domain (PF01138) - 3' exoribonuclease family	UNCLASSIFIED	265008, 265007, 265008, 265009, 265011, 264768, 35685917, 35685855, 263981, 264557, 264585
2375	87731355 (4749, 4750)	Novel Protein sim. GBank gij1351115[sp]P47758[SRPB MOUSE - SIGNAL RECOGNITION PARTICLE RECEPTOR BETA SUBUNIT (SR-BETA)]		UNCLASSIFIED	60432049, 29331824, 264907, 52844045, 264512, 60433358, 21908754, 52844286, 87188559, 264448, 21908765, 21908768, 21908769, 33687023, 18108368, 55811578, 52844332
2376	87613744 (4751, 4752)	Novel Protein sim. GBank gij2645435 (AF007780) - CHD3 [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	ATPase-associated	264259, 29331830, 264908, 264910, 265009, 60433438, 21908754, 265017, 265018, 265019, 264882, 264288, 264685, 21908767, 283972, 35685855, 87168518, 60432113
2377	95319689 (4753, 4754)	Novel Protein sim. GBank gij5257005[gbj]AAD41239.1] - (AF083249) Rb binding protein homolog [Homo sapiens]	Contains protein domain (PF01388) - ARID DNA binding domain	UNCLASSIFIED	264095, 29331822, 29147620, 29331824, 66714117, 29331825, 29331826, 29331828, 33686970, 29148498, 29148499, 284509, 265008, 265007, 265008, 265009, 60170831, 265010, 265011, 265018, 55811150, 18108351, 284764, 264288, 21908767, 21908768, 29148627, 29148629, 265021, 33687023, 33687109, 18108370, 18108374, 18108379, 35686423, 284556, 83373044, 18108385, 18108388, 56528486, 22279000, 22279002, 284593
2378	94137032 (4755, 4756)	Novel Protein sim. GBank gij1072198 (U00942) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56182575, 35686286, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 80432289, 29331827, 56182435, 264510, 265009, 60433356, 87168474, 265011, 265018, 264288, 21908765, 33687023, 264557, 56182323, 83373044, 18108385, 22279002, 284482
2379	65444324 (4757, 4758)	Novel Protein sim. GBank gij3337357 (AC004481) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	285017, 264288, 21908768

2380	88823062 (4759, 4760)	Novel Protein sim. GBank gij4502839[ref]NP_001845.1[pcol.1 - collagen, type XI, alpha 1]	Contains protein domain (PF01410) - Fibrillar collagen C-terminal domain	collagen	284908, 284910, 285011
2381	87608241 (4761, 4762)	Novel Protein sim. GBank gij4455809[emb]CAB385551 - (AL031846) dJ742C19.5 (novel Chromobox protein) [Homo sapiens]	Contains protein domain (PF00385) - 'chromo' (CHR)romalin Organization Modifier domain	helicase	58182575, 284081, 284093, 284259, 29331825, 284105, 284908, 60433356, 21908754, 285017, 285019, 284883, 284288, 284885, 284688, 284687, 284691, 284692, 284693, 59811578, 284638, 284597 29331824, 60432289, 284905, 284596
2382	91225982 (4763, 4764)	Novel Protein sim. GBank gij4325130[gb]AAD172761 - (AF119716) dMI-2 protein [Drosophila melanogaster]	Contains protein domain (PF00628) - PHD-finger	transport	21908754, 284768, 285022, 284893, 283987, 33657109, 284629, 284831, 284558, 83373044, 60432113, 284482 285009, 21908765, 21908768
2383	87442841 (4765, 4766)	Novel Protein sim. GBank gij1902982[db]BAA190051 - (D89049) lectin-like oxidized LDL receptor [Bos taurus]	Contains protein domain (PF00059) - Lectin C-type domain	glycoprotein	
2384	95354768 (4767, 4768)	Novel Protein sim. GBank gij2482851 (AF018252) - Spinophilin [Rattus norvegicus]	Contains protein domain (PF00395) - PDZ domain (Also known as DHR or GLGF)	struct	284488, 52644507, 52645156, 52646385, 35898286, 22278999, 52645080, 29331824, 29331826, 35896052, 29331828, 284906, 284828, 52644045, 285006, 285008, 285009, 33109954, 33657084, 52644286, 285011, 285017, 285018, 284683, 52644229, 21908765, 21908767, 21908768, 285020, 52644150, 33657023, 284893, 65274820, 52645128, 33657109, 33657182, 27488261, 27488262, 27488264, 33657349, 27488265, 35895763, 18108374, 35895855, 284634, 284555, 284558, 284557, 52644332, 284558, 284559, 18108385, 22278900, 22279002 284488, 52644507, 52645156, 284887, 52646385, 22278995, 22278996, 22278997, 22278998, 284259, 52645080, 29331822, 29331826, 35896052, 52644045, 285006, 285007, 285008, 285009, 284910, 60432228, 60433356, 52646317, 21908754, 285018, 284448, 284683, 284686, 284687, 284689, 21908765, 21908766, 21908767, 21908769, 55811857, 285021, 285022, 284690, 284691, 284692, 65274620, 33657109, 18108370, 284631, 52644332, 22278900, 22279002, 284553, 284555, 284587 284488, 22278995, 22278996, 22278997, 284259, 28148498, 284112, 284511, 60170831, 60432229, 284595, 60433438, 87168474, 87168559, 284682, 21908765, 21908768, 21908767, 21908769, 28148828, 35895817, 285021, 284690, 33657109, 284628, 18108376, 83373044, 60432113, 22278900, 284564, 284566, 284487
2385	95419485 (4769, 4770)			UNCLASSIFIED	
2386	94742648 (4771, 4772)	Novel Protein sim. GBank gij482888[gb]AAD34110.1[AF15187 - (AF151873) CGI-115 protein [Homo sapiens]		glycoprotein	

2387	14987890 (4773, 4774)		UNCLASSIFIED	264634
2388	11424604 (4775, 4776)		UNCLASSIFIED	264595
2389	95310650 (4777, 4778)	Novel Protein sim. GBank gll4758058[ref]NP_004372.1 pCREB - cAMP responsive element binding protein-like 1	Contains protein domain (PF00170) - bZIP transcription factor	264468, 22278998, 22278999, 264509, 264895, 264908, 264907, 264908, 264909, 265006, 264511, 264512, 264810, 264591, 21908754, 264601, 264604, 264761, 18108351, 264784, 264288, 264766, 264768, 264789, 21908765, 21908768, 264692, 264693, 35698423, 264635, 264636, 264555, 83373044, 22278000, 264488
2390	94320912 (4776, 4780)	Novel Protein sim. GBank gll1644239[dbj]BAA122231 - (D84103) mitochondrial DNA polymerase gamma [Homo sapiens]	Contains protein domain (PF00476) - DNA polymerase family A	52644507, 56182375, 22278995, 35698286, 22278996, 22278997, 22278998, 29331822, 29331825, 29331826, 35698052, 264905, 52644045, 265009, 264758, 264759, 33109954, 52644296, 85658542, 285011, 265017, 265018, 264605, 52644229, 21908765, 21908767, 21908768, 21908769, 35695917, 52644150, 33657023, 33657109, 33657349, 35695763, 18108370, 18108374, 18108376, 35698423, 35695855, 264555, 52644332, 56182323, 60170394, 83373044, 56528486
2391	80036184 (4781, 4782)		UNCLASSIFIED	263978
2392	94245016 (4783, 4784)	Novel Protein sim. GBank gll4240169[dbj]BAA74863.11 - (AB020847) KIAA0840 protein [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	35698286, 35698052, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 264910, 265009, 264591, 264758, 264800, 264604, 264762, 264448, 264764, 264369, 264766, 264768, 264789, 264689, 35695917, 264629, 18108374, 263978, 35698423, 35695855, 264631, 264634, 264635, 264636, 264637, 264638, 60170394, 264639, 264565, 264486

2393	95302633 (4785, 4786)	Novel Protein sim. GBank gjk4506867[refINP_000983.1]pRPLP - ribosomal protein, large, PO	Contains protein domain (PF00486) - Ribosomal protein L10	ribosomalprot	18108392, 60424179, 284489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278998, 264093, 60432049, 264259, 29331822, 29147620, 20281098, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264509, 264905, 264907, 264908, 66712502, 52844045, 264828, 264909, 56182435, 264112, 264113, 264510, 265008, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52846317, 33109954, 21908754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264389, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 29146629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108388, 27486281, 27486282, 33657349, 35685763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810784, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264559, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265008, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21908765, 21908768, 21908769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264584, 264568, 264567
2394	94323268 (4787, 4788)	Novel Protein sim. GBank gjk4506867[refINP_000983.1]pRPLP - ribosomal protein, large, PO	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_ma_bind	18108392, 60424179, 284489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278998, 264093, 60432049, 264259, 29331822, 29147620, 20281098, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264509, 264905, 264907, 264908, 66712502, 52844045, 264828, 264909, 56182435, 264112, 264113, 264510, 265008, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52846317, 33109954, 21908754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264389, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 29146629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108388, 27486281, 27486282, 33657349, 35685763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810784, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264559, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265008, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21908765, 21908768, 21908769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264584, 264568, 264567
2395	95287212 (4789, 4790)	Novel Protein sim. GBank gjk4506867[refINP_000983.1]pRPLP - ribosomal protein, large, PO	Contains protein domain (PF00086) - Zinc finger, C2H2 type	dna_ma_bind	18108392, 60424179, 284489, 18108394, 18108397, 22278995, 56994075, 35696286, 22278996, 22278997, 22278998, 264093, 60432049, 264259, 29331822, 29147620, 20281098, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 35696052, 29146498, 264508, 264509, 264905, 264907, 264908, 66712502, 52844045, 264828, 264909, 56182435, 264112, 264113, 264510, 265008, 264511, 265007, 265008, 265009, 264910, 264591, 264593, 60433356, 264595, 60433438, 52846317, 33109954, 21908754, 55811386, 265010, 265011, 265017, 265018, 265019, 264681, 264762, 18108351, 264763, 264682, 264764, 264683, 264389, 264288, 18108354, 264766, 264686, 264687, 264688, 264689, 18108359, 21908765, 21908766, 21908767, 21908768, 21908769, 55811957, 29146629, 29148784, 35695917, 265021, 265022, 33657023, 264692, 264693, 18108364, 33657109, 18108388, 27486281, 27486282, 33657349, 35685763, 18108370, 263972, 264629, 18108374, 263977, 18108376, 263978, 55810784, 35696423, 35695855, 264634, 60431850, 264555, 264637, 264557, 263981, 264559, 18108381, 60170394, 35696286, 22278997, 22278998, 56182181, 35696052, 265008, 264592, 55811386, 265010, 265011, 265017, 265019, 264448, 264683, 264288, 21908765, 21908768, 21908769, 55811957, 35695917, 33657023, 65274620, 33657182, 33657349, 35695763, 18108374, 18108376, 55810764, 55811576, 35696423, 60170394, 18108385, 264584, 264568, 264567

2396	95086700 (4791, 4792)	Novel Protein sim. GBank gi 106322 pir B34087 - hypothetical protein (L1H 3' region) - human	Contains protein domain (PF00560) - nuclease Leucine Rich Repeat	52846355, 18108397, 56182575, 35698286, 22278997, 22278999, 60432049, 284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284108, 284907, 29331830, 68712502, 284110, 60170831, 264591, 33857402, 60433438, 55812038, 33109954, 21908754, 33857084, 87188474, 265017, 265018, 265019, 284760, 264448, 284288, 284766, 52844228, 21908766, 21908767, 265020, 265021, 60170815, 284692, 33857023, 65274620, 52845129, 33857182, 27486262, 27486264, 27486265, 284629, 18108374, 35698423, 35695855, 284631, 284556, 52844332, 284558, 83373044, 18108388, 87168518, 22279002, 284482
2397	87280854 (4793, 4794)			52844507, 52845156, 56182575, 264259, 29147620, 284905, 264907, 264908, 264909, 284910, 284758, 52844298, 264603, 284604, 264762, 284881, 284764, 18108357, 264769, 21908768, 264693, 264628, 264635, 264638, 284639, 284684
2398	88047689 (4795, 4796)	Novel Protein sim. GBank gi 3258809 (AC005178) - H53 GS1 (Homo sapiens)	UNCLASSIFIED	
2399	87738965 (4797, 4798)	Novel Protein sim. GBank gi 766117 (L41834) - nuclear protein [Ensis minor]	UNCLASSIFIED	56994075, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 66714117, 60432289, 284906, 29331830, 56182435, 264112, 264910, 33109954, 21906754, 87188474, 284600, 285017, 285018, 265019, 284764, 284765, 21908765, 21908766, 21908767, 21908768, 35695917, 265020, 265022, 60170815, 33857023, 18108370, 18108374, 284556, 60170394, 284558, 87168518, 22279000, 22279002, 284564, 264566, 284487
2400	91214116 (4799, 4800)	Novel Protein sim. GBank gi 2352822 gb AB69285.1 - (AF008945) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	21908766, 52846842, 56994075, 33657182, 27488262, 52844298, 265017

2401	91214118 (4801, 4802)	Novel Protein sim. GBank gl 2352822 gb AA689285.1 - (AF008845) glucose-6-phosphatase [Haplochromis nubilus]	phosphatase	52644507, 52645156, 52644228, 264688, 21908764, 21908785, 52646385, 52646842, 21908766, 21908787, 21908768, 22278995, 35695917, 56994075, 35696286, 22278996, 22278997, 285020, 22278998, 22278999, 264259, 33657023, 52645080, 264693, 28331824, 33657109, 52645129, 28331826, 33657182, 28331827, 35696052, 27466281, 27466282, 33656970, 33657349, 27466285, 35695763, 264108, 264905, 35698423, 35695955, 265006, 265007, 265008, 265009, 264637, 52644332, 55812038, 52646317, 18108385, 52644298, 87168474, 265010, 87168559, 60432113, 265017, 265018, 265019, 264563, 264288, 264907, 264908, 264909, 264566
2402	91221408 (4803, 4804)	Novel Protein sim. GBank gl 4689258 gb AAD27832.1 AF12185 - (AF121859) sorting nexin 9 [Homo sapiens]		
2403	94135432 (4805, 4806)	Novel Protein sim. GBank gl 4929575 gb AAD34048.1 AF15181 - (AF151811) CGI-53 protein [Homo sapiens]	Contains protein domain (PF00082) - C-type lysozyme/alpha-lactalbumin family	22278999, 35698052, 265018, 264686, 264693, 83373044, 264567
2404	95312605 (4807, 4808)	Novel Protein sim. GBank gl 2315796 (AF018885) - similar to short chain-type dehydrogenases [Caenorhabditis elegans]	Contains protein domain (PF00106) - short chain dehydrogenase family	35696286, 28331826, 35696052, 265008, 265018, 21908769, 264564
2405	94311851 (4809, 4810)	Novel Protein sim. GBank gl 464178 db BAA03581 - (D14853) polyprotein [Hepatitis C virus]	UNCLASSIFIED	35696286, 28331822, 265007, 21906754, 265017, 265018, 265019, 264783, 264389, 21906785, 35695917, 265020, 265021, 52644150, 264693, 35695855, 264632, 52644332, 22279002
2406	86094501 (4811, 4812)	Novel Protein sim. GBank gl 2773363 (AF041382) - microtubule binding protein D-CLIP-190 [Drosophila melanogaster]	Contains protein domain (PF01302) - struct CAP-Gly domain	52646842, 22278994, 22278996, 35696286, 22278997, 22278998, 22278999, 264092, 264093, 60432049, 264259, 28331822, 28331824, 28331825, 28331827, 35696052, 28331828, 264102, 264108, 264906, 52644045, 265007, 265008, 265009, 264910, 264592, 60433356, 60433438, 33109954, 265010, 265011, 265018, 265019, 264389, 264685, 264686, 21906768, 21906769, 52644150, 264693, 52645129, 264628, 35696423, 264632, 56182323, 264639, 22279000, 22279002, 264563
2407	79465005 (4813, 4814)		UNCLASSIFIED	264685, 264686
2408	87381503 (4815, 4816)	Novel Protein sim. GBank gl 423442 pir IS33513 - gene Fil protein - mouse	UNCLASSIFIED	264910, 265010, 264448, 264557

2409	84741770 (4817, 4818)	Novel Protein sim. GBank gll1178601[sp]P45988[YNZ8, CAEEL - HYPOTHETICAL 20.8 KD PROTEIN T08A5.6 IN CHROMOSOME III]		UNCLASSIFIED	22278995, 22278996, 22278997, 264097, 29331822, 29331824, 29331827, 29148498, 52844045, 60433438, 33857084, 87168474, 264780, 21906787, 29148627, 29148629, 52844150, 33857023, 263987, 20281089, 18108374, 20281071, 56182323, 83373044, 18108385, 87168518 22278998, 264259
2410	87604860 (4819, 4820)	Novel Protein sim. GBank gll4966262[gb]AAC48052.21 - (UB4849) Contains similarity to P1am domain: PF00848 (F- box), Score=28.7, E-value=4.3e-05, N=1 [Caenorhabditis elegans]	Contains protein domain (PF00080) - Copper/zinc superoxide dismutase (SODC)		
2411	87534633 (4821, 4822)	Novel Protein sim. GBank gll3114713 (AF061346) - Edp1 protein [Mus musculus]	Int		29331824, 29331827, 29331828, 264784, 264369, 33857108, 56182323
2412	87778332 (4823, 4824)	Novel Protein sim. GBank gll54103338[gb]AAD43038.11 - (AF106685) myelin gene expression factor 2 [Homo sapiens]	Contains protein domain (PF00076) - dna_ma_bind RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)		22278998, 29331827, 264807, 265011, 265017, 285018, 285019, 18108351, 21906788, 285020, 33857109, 264559, 18108385
2413	84133820 (4825, 4826)	Novel Protein sim. GBank gll5282705[emb]CAB45778.11 - (AL080214) hypothetical protein [Homo sapiens]	Contains protein domain (PF00039) - Intermediate filament proteins	sinud	264488, 284259, 29331828, 264508, 264905, 264309, 264906, 264907, 264908, 264510, 264511, 264512, 285008, 285009, 264910, 265011, 264682, 264784, 264788, 264688, 264788, 264688, 265021, 33857023, 18108370, 264628, 35685855, 264832, 264634, 264635, 264636, 83373044, 264563, 264564, 264565, 264568, 264587, 264488
2414	84312590 (4827, 4828)	Novel Protein sim. GBank gll1082340[pir]S52863 - DNA- binding protein R kappa B - human		ubiquitin	52845158, 52846842, 52846365, 18108398, 56182575, 22278994, 22278995, 56994075, 22278996, 35686286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35686052, 33856970, 29331830, 264909, 60433356, 33857402, 264594, 52846317, 21906754, 33857084, 265010, 87168558, 285017, 285018, 285019, 264369, 264684, 264687, 264688, 56181562, 21906764, 264689, 21906785, 21906786, 21906787, 29148627, 21906789, 285020, 265021, 60170615, 33857023, 264693, 52845128, 33857109, 33857182, 27486281, 27486282, 27486285, 33857349, 18108370, 60431528, 264629, 18108374, 18108376, 55810764, 264636, 52844332, 264638, 264558, 56182323, 83373044, 18108385, 87168518, 22278902

2415	88089002 (4829, 4830)	Novel Protein sim. GBank gij423915 pir A45438 - myosin I heavy chain - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	264259, 264908, 60433356, 33657402, 21908754, 265018, 264687, 264689, 21908769, 55811957, 265021, 264690, 264691, 33657023, 264693, 33698423, 56182323, 56526486
2416	94118336 (4831, 4832)	Novel Protein sim. GBank gij3025445 (AC004528) - R32184_1 [Homo sapiens]			264638
2417	87733334 (4833, 4834)	Novel Protein sim. GBank gij1084944 pir S54495 - hypothetical protein YPR021c - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00153) - Mitochondrial carrier proteins		264094, 29331822, 29331824, 29331827, 264369
2418	94234349 (4835, 4836)	Novel Protein sim. GBank gij1176572 sp P45895 YNA4_CAEEL - HYPOTHETICAL 91.0 KD PROTEIN PAR2.4 IN CHROMOSOME III	Contains protein domain (PF00411) - Ribosomal protein S11	UNCLASSIFIED	56994075, 264091, 264259, 29331824, 29331825, 60432286, 29331828, 264905, 264907, 264511, 265008, 60432228, 21908754, 87168559, 265019, 264862, 21908768, 21908769, 265020, 265021, 33657023, 65274620, 18108370, 55811576, 264634, 60170394, 18108385, 22279000, 22279002, 264568
2419	82374249 (4837, 4838)	Novel Protein sim. GBank gij284008 pir S18732 - autoantigen, 84K - human		struct	264569, 264762, 264448, 264691, 264631, 264634, 264555, 264556, 264638, 264558
2420	94844244 (4839, 4840)	Novel Protein sim. GBank gij1076211 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	29331824, 29331825, 29331828, 60432229, 33109954, 85658542, 87168474, 265018, 264288, 265020, 264564
2421	87805345 (4841, 4842)	Novel Protein sim. GBank gij224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]	Contains protein domain (PF00617) - RasGEF domain	UNCLASSIFIED	264909, 264768, 264638
2422	88084714 (4843, 4844)	Novel Protein sim. GBank gij224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]		transport	18108392, 18108394, 18108398, 264906, 265008, 265010, 18108351, 18108374, 18108385
2423	88058390 (4845, 4846)	Novel Protein sim. GBank gij4505153 ref NP_002392.1 pMEKK - MAP/ERK kinase kinase 3	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 60432049, 29331822, 29331828, 60432289, 29331828, 265008, 265009, 60433356, 21908754, 265017, 265018, 265019, 21908768, 21908769, 21908769, 265020, 265021, 20281149, 263971, 60432113
2424	94854047 (4847, 4848)	Novel Protein sim. GBank gij2988398 (AC004381) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	56182575, 35686286, 22278997, 60432049, 264259, 29331828, 29331828, 264905, 66712502, 29331830, 60433356, 265011, 265019, 264768, 21908768, 55811957, 264692, 33657023, 33657109, 55811576, 56182323, 83373044, 18108385, 18108388, 60432113, 22278900
2425	87415981 (4849, 4850)	Novel Protein sim. GBank gij2077832 dbj BAA16878 - (D86558) Protein Kinase [Rattus norvegicus]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264634
2426	87813945 (4851, 4852)	Novel Protein sim. GBank gij2039368 gb AA853003.1 - (U94619) circulating cathodic antigen [Schistosoma mansoni]		UNCLASSIFIED	22278996, 22278998, 264259, 264102, 264512, 265008, 21908767, 18108370, 18108374, 263976

2427	87622693 (4853, 4854)	Novel Protein sim. GBank gij4680695jibjAAD27737.1jAF13296 - (AF132962) CGI-28 protein [Homo sapiens]	Contains protein domain (PF00573) - Ribosomal protein L4/L1 family	- ribosomalprot	264259, 20281099, 35686052, 265008, 264594, 265011, 264780, 18108351, 264682, 264683, 264389, 264684, 264686, 264687, 264689, 21906768, 264691, 264692, 18108374, 18108377, 264557, 264639, 18108385
2428	85732889 (4855, 4856)	Novel Protein sim. GBank gij1537070 (U63840) - nucleoporin p54 [Rattus norvegicus]			22278996, 22278998, 35686052, 21906754, 264286, 21906765, 21906768, 21906769, 35695917, 265020, 263972, 22278002
2429	87769276 (4857, 4858)	Novel Protein sim. GBank gij601931 (M94316) - neurofilament-H [Oryctolagus cuniculus]	Contains protein domain (PF00711) - Beta defensins	UNCLASSIFIED	22278999, 29331824, 264606, 264909, 264511, 265008, 21906754, 265017, 265018, 265019, 264448, 264683, 264288, 21906765, 21906768, 265021, 264693, 18108381
2430	86848827 (4859, 4860)	Novel Protein sim. GBank gij3860729jembjCAA14630] - (AJ235270) CELL DIVISION PROTEIN FTSJ (fts-J) [Rickettsia prowazekii]	Contains protein domain (PF01728) - FtsJ cell division protein	UNCLASSIFIED	264112, 264631
2431	87648884 (4861, 4862)	Novel Protein sim. GBank gij3876367jembjCAA93287] - (Z89380) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89268 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]		protease	29331826, 29331827, 35686052, 29148499, 264905, 264908, 264681, 264288, 264689, 21906765, 264692, 35686423 264634, 264558
2432	80083033 (4863, 4864)	Novel Protein sim. GBank gij3876367jembjCAA93287] - (Z89380) Weak similarity to Elmeria thrombospondin (PIR Acc. No. A45517); cDNA EST EMBL:M89268 comes from this gene; cDNA EST yk295b9.5 comes from this gene [Caenorhabditis elegans]			
2433	80055092 (4865, 4866)	Novel Protein sim. GBank gij2224593jdbjBAA20784] - (AB002324) KIAA0326 [Homo sapiens]	Contains protein domain (PF00086) - Zinc finger, C2H2 type	transcriptfactor	264569, 264805, 265018, 264762, 264683, 264691, 264558, 264557, 264639, 264558 264563
2434	19520148 (4867, 4868)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	264555
2435	20759044 (4869, 4870)	Novel Protein sim. GBank gij3641352 (AF081234) - putative transcription factor [Mus musculus]		UNCLASSIFIED	265008, 264758, 265010, 264689, 27486261, 263972, 18108374, 18108381
2436	88044008 (4871, 4872)	Novel Protein sim. GBank gij3860014 (AF091086) - unknown [Homo sapiens]	Contains protein domain (PF01256) - Uncharacterized protein family UPF0031	UNCLASSIFIED	29331828, 265007, 265009, 265017, 264760, 264685, 264693, 264565
2437	83363424 (4873, 4874)	Novel Protein sim. GBank gij3860014 (AF091086) - unknown [Homo sapiens]		UNCLASSIFIED	26331826, 264508, 264805, 264509, 264906, 264907, 264908, 264809, 264511, 265008, 264512, 264910, 265009, 264591, 33657402, 21906754, 265011, 264760, 264764, 264685, 264686, 264768, 35695917, 33657023, 264693, 264631, 264632, 56182323, 264556, 83373044, 264563, 264564, 264565, 264566, 264567

2439	94850850 (4877, 4878)	Novel Protein sim. GBank gl 4283519 gb AAD15345 - (AC004044) small nuclear riboprotein Sm-D1 [Arabidopsis thaliana]	Contains protein domain (PF01423) - Sm protein	UNCLASSIFIED	60424178, 18108397, 56182575, 56181886, 56984075, 22278998, 35698286, 22278997, 22278999, 264259, 52645080, 29331822, 56182181, 29331824, 60424269, 88714117, 29331825, 60432288, 29331826, 29331827, 29331828, 35698052, 29146488, 264509, 264905, 264906, 52644045, 60431735, 33109854, 21806754, 33657084, 55811386, 52644296, 87188474, 265017, 265018, 285019, 18108351, 264448, 264288, 264768, 52644229, 56181582, 21906764, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 33657109, 33657182, 27486282, 27486284, 33657349, 27486285, 35695783, 18108370, 60431528, 263977, 55810764, 35696423, 85274791, 35695855, 60431850, 56182323, 60432113, 22278000, 22279002, 264587
2440	87641733 (4878, 4880)			UNCLASSIFIED	29331822, 29331824, 29331825, 29331827, 35696052, 264508, 264907, 264510, 265018, 285019, 264448, 264389, 265020, 265021, 56182323, 264639, 22279002
2441	87623814 (4881, 4882)	Novel Protein sim. GBank gl 3024889 pf 56524 Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)		UNCLASSIFIED	264488, 264629, 16108374, 264564
2442	87273590 (4883, 4884)	Novel Protein sim. GBank gl 4508013 ref NP_002703.1 pPPP1 - protein phosphatase 1, regulatory subunit 7	Contains protein domain (PF00560) - Leucine Rich Repeat	UNCLASSIFIED	22278998, 22278999, 29331822, 264768, 264683
2443	84305949 (4885, 4886)	Novel Protein sim. GBank gl 1170858 pf Q02975 KID1_RAT - RENAL TRANSCRIPTION FACTOR KID-1 (TRANSCRIPTION FACTOR 17)	Contains protein domain (PF01352) - KRAB box	transcriptfactor	264908
2444	88086345 (4887, 4888)	Novel Protein sim. GBank gl 4758824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	264259, 18108382, 18108383, 18108385, 22278000
2445	87338636 (4889, 4890)	Novel Protein sim. GBank gl 2135950 pf S58222 - PQ-rich protein - human			264259, 35698052, 264389, 18108381
2446	88059293 (4891, 4892)	Novel Protein sim. GBank gl 4753887 emb CAA05408.2 - (AJ002424) p65 protein [Rattus norvegicus]	Contains protein domain (PF00085) - WAP-type (Whey Acidic Protein) 'four-disulfide core'	proteaseinhb	265011, 264689, 33657023, 263981, 18108385
2447	94845149 (4893, 4894)	Novel Protein sim. GBank gl 4885813 ref NP_005409.1 pST5l - suppression of tumorigenicity 5	cadherin		56182575, 264259, 29331824, 29331825, 29331827, 60433356, 60433438, 264758, 285018, 264682, 85274620, 60431528, 85274791, 56182323

2448	87748680 (4895, 4898)			UNCLASSIFIED	22278996, 22278997, 22278998, 29331826, 35698052, 264107, 264110, 87168474, 87188559, 18108351, 21906787, 21908769, 27486262, 263978
2449	87869075 (4897, 4898)	Novel Protein sim. GBank gll728637 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		cadherin	284259, 284828, 265007, 284595, 265021, 56526488
2450	86597784 (4899, 4900)			UNCLASSIFIED	264906
2451	81014563 (4901, 4902)	Novel Protein sim. GBank gll1710021 sp P35280 RB24_MOUSE - RAS-RELATED PROTEIN RAB-24 (RAB-16)	Contains protein domain (PF00071) - Ras family	glycoprotein	264093, 29331822, 29331824, 29331825, 68714117, 29331828, 29331828, 35696052, 264907, 68712502, 29331830, 264910, 265009, 264758, 265017, 265018, 264762, 264448, 264288, 21908767, 265021, 33657023, 264693, 33657109, 263969, 83373044, 18108385
2452	81230509 (4903, 4904)	Novel Protein sim. GBank gll1504034 db BAA13216 - (D86980) KIAA0227 [Homo sapiens]		isomerase	264102, 264112, 264688, 263972, 18108374, 83373044, 264593
2453	84201088 (4905, 4906)	Novel Protein sim. GBank gll2880079 (AC004142) - similar to murine leucine-rich repeat protein; possible role in neural development by protein-protein interactions; 93% similarity to D49802 (PID:g1369908) [Homo sapiens]	Contains protein domain (PF00580) - Leucine Rich Repeat	nglrecep	264509, 264512, 18108385
2454	95310691 (4907, 4908)	Novel Protein sim. GBank gll1076802 p H549915 - extensin like protein - maize	Contains protein domain (PF00170) - bZIP transcription factor	UNCLASSIFIED	263994, 68714117, 29331827, 264508, 264509, 264903, 264906, 264907, 264908, 264909, 264510, 264511, 264512, 265009, 264910, 264591, 264758, 264759, 265010, 265011, 264603, 264604, 264760, 264761, 264762, 18108351, 264764, 264765, 264766, 264688, 264768, 264769, 264534, 264691, 264692, 33657023, 264693, 33657109, 264628, 263978, 35695855, 264634, 264635, 264637, 264638, 264639, 83373044, 18108385, 264583, 264584, 264486
2455	95288301 (4909, 4910)	Novel Protein sim. GBank gll543617 sp P35585 AP47_MOUSE - CLATHRIN COAT ASSEMBLY PROTEIN AP47 (CLATHRIN COAT ASSOCIATED PROTEIN AP47) (GOLGI ADAPTOR AP-1 47 KD PROTEIN) (HA1 47 KD SUBUNIT) (CLATHRIN ASSEMBLY PROTEIN ASSEMBLY PROTEIN COMPLEX 1 MEDIUM CHAIN)	Contains protein domain (PF00928) - Adaptor complexes medium subunit family	glycoprotein	264486, 22278998, 264259, 35696052, 264905, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264758, 265019, 264760, 264681, 18108351, 264683, 264764, 18108354, 264766, 264768, 264769, 264689, 21908768, 21908767, 21908769, 29148629, 35695817, 265020, 265022, 33657023, 33657109, 18108370, 264628, 264629, 264631, 264632, 264635, 56182323, 60170394, 18108385, 264583, 264584, 264586, 264587
2458	88166700 (4911, 4912)	Novel Protein sim. GBank gll2568630 (AC003079) - Ankyrin-like; 54% similar to 2022340A (NID:g1092123) in exons spanning 43974 to 11551 of clone. [Homo sapiens]	Contains protein domain (PF00023) - kinase Ank repeat	kinase	264693

2457	94118375 (4913, 4914)	Novel Protein sim. GBank gl 3025447 (AC004528) - R32184_3 [Homo sapiens]		UNCLASSIFIED	58181688, 264905, 264907, 264511, 264598, 5581388, 264882, 264884, 264885, 264887, 264891, 33857023, 264893, 35695855, 264636, 264555, 58182323, 264558, 58528486, 264563
2458	85075304 (4915, 4916)	Novel Protein sim. GBank gl 2384942 (AF022885) - Similar to collagen [Caenorhabditis elegans]		UNCLASSIFIED	264681, 264693, 264634, 264559
2459	87551913 (4917, 4918)	Novel Protein sim. GBank gl 5441942 gb AAD43187.1 AC004897 supported by mouse EST AA538043 (NID: g2284036) [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)	transport	27486265
2460	94315289 (4919, 4920)	Novel Protein sim. GBank gl 4929701 gb AAD34111.1 AF15187 - (AF151874) CGI-116 protein [Homo sapiens]		kinase	65274572, 35688286, 22278996, 22278997, 80432049, 29331822, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 29331828, 33856970, 29146499, 264102, 264109, 60433438, 265017, 265018, 265019, 264288, 21908785, 21908786, 21908789, 35695917, 265020, 264891, 33657023, 27486281, 18108374, 35695855, 87168518, 80432113
2461	87645147 (4921, 4922)	Novel Protein sim. GBank gl 4428882 gb AAD20833 - (AF128082) Arf-like 2 binding protein BART1 [Homo sapiens]		UNCLASSIFIED	264259, 29331828, 264910, 18108351, 18108370, 18108374
2462	86988002 (4923, 4924)	Novel Protein sim. GBank gl 5420387 emb CAB46678.1 - (AJ243459) proteophosphoglycan [Leishmania major]			264809, 264758, 264884, 18108374, 264637, 18108385
2463	84386543 (4925, 4926)	Novel Protein sim. GBank gl 5052518 gb AAD38588.1 AF14561 - (AF145613) BcDNA.GH03108 [Drosophila melanogaster]	Contains protein domain (PF00098) - Zinc finger, C2H2 type	UNCLASSIFIED	264681, 264586
2484	91219857 (4927, 4928)	Novel Protein sim. GBank gl 5410300 gb AAD43021.1 - (AF100757) COP9 complex subunit 4 [Homo sapiens]	Contains protein domain (PF01398) - PCI domain	protease	264489, 52648842, 22278995, 35696286, 22278998, 22278997, 22278999, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 264509, 52644045, 264510, 264511, 264512, 265008, 60170831, 264593, 52846317, 33109954, 33657084, 265017, 265018, 265019, 264782, 264448, 264784, 264288, 264788, 21908765, 21908768, 21908767, 21908789, 265021, 33657023, 33657109, 18108370, 18108381, 60170394, 18108385, 22279002, 264488

2465	85357483 (4928, 4930)	Novel Protein sim. GBank gi 4506401 ref NP_002871.1 pRAF1 - v-rat-1 murine leukemia viral oncogene homolog 1	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	1810392, 52844507, 52845156, 52846385, 22278994, 22278995, 35696288, 22278998, 22278998, 284259, 29331822, 29331824, 29331825, 60424289, 60432289, 29331827, 35696032, 29331828, 284907, 29331830, 52844045, 284909, 56182435, 284511, 285007, 285008, 285009, 284910, 33857402, 60433438, 55812038, 21908754, 33109954, 285010, 285011, 87168559, 284600, 285017, 285018, 285019, 18108351, 284369, 284288, 284685, 284787, 21908765, 21908767, 21908768, 55811957, 35695917, 285020, 285021, 60170615, 52844150, 33657023, 52845128, 33857109, 27488261, 27488264, 35695763, 284628, 283972, 18108374, 35695855, 284636, 284637, 80170394, 56526488, 87168518, 60432113, 284563, 284564, 284566, 284487 284389
2466	85681366 (4931, 4932)	Novel Protein sim. GBank gi 4321619 gb AAD15788.1 - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		
2467	85059465 (4933, 4934)	Novel Protein sim. GBank gi 3513300 (AC005595) - F18801.1, partial CDS [Homo sapiens]	UNCLASSIFIED	56894075, 284908, 21906768, 33657023
2468	87614686 (4935, 4936)	Novel Protein sim. GBank gi 2143455 pir j158108 - gene [DMR-N9 protein - mouse (fragment)]	Contains protein domain (PF00400) - WD domain, G-beta repeat	29331824, 52844045, 285008, 284910, 285019, 21908765, 21908769, 285021 284288, 284628
2469	86284397 (4937, 4938)	Novel Protein sim. GBank gi 5420389 emb CAB46880.1 - (AJ243480) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	284592, 284692, 284555, 284558, 284557, 284558, 284559, 18108385, 284482
2470	80223831 (4939, 4940)	Novel Protein sim. GBank gi 5419882 emb CAB46424.1 - (AL088749) DKFZp434G153 [Homo sapiens]	UNCLASSIFIED	65274572, 35696288, 29331827, 285007, 284592, 33109954, 285018, 285019, 284288, 55811957, 285020, 284693, 55811576, 56182323
2472	95080811 (4943, 4944)	Novel Protein sim. GBank gi 4929747 gb AAD34134.1 AF15189 - (AF151897) CGI-139 protein [Homo sapiens]	UNCLASSIFIED	284092, 60432049, 28331825, 60433356, 285010, 285011, 18108351, 284764, 284288, 284692, 65274820, 18108370, 18108372, 18108374, 284634, 18108385
2473	95421508 (4945, 4946)	Novel Protein sim. GBank gi 4538009 emb CAB39830.1 - (AL049461) putative protein [Arabidopsis thaliana]		80424179, 65274572, 22278999, 60424289, 29331826, 285008, 60433356, 60433438, 285010, 18108351, 284448, 284288, 284687, 284689, 285021, 284692, 65274820, 60431528, 65274791, 284558, 56182323, 60432113
2474	94315616 (4947, 4948)	Novel Protein sim. GBank gi 3252827 (AC004382) - Unknown gene product [Homo sapiens]		65274572, 56994075, 284259, 29331826, 60170831, 285017, 285018, 285019, 284683, 284389, 285020, 284693, 284563, 284564

2475	94321693 (4949, 4950)	Novel Protein sim. GBank gll1218486 (U48852) - HT protein [Cricetulus griseus]	Contains protein domain (PF00008) - IGF EGF-like domain		284259, 29331822, 265008, 265007, 285010, 285011, 284448, 264288, 264369, 264685, 264686, 18108357, 264768, 18108382, 264693, 18108370, 18108374, 18108379, 35688423, 83373044, 18108383, 18108385, 264584, 264585, 264587
2476	94315618 (4951, 4952)	Novel Protein sim. GBank gll3252827 (AC004382) - Unknown gene product [Homo sapiens]	UNCLASSIFIED		284259, 60424269, 66714117, 284905, 285008, 264511, 265008, 265009, 264768, 285010, 285011, 18108351, 264681, 264369, 264288, 264689, 21908767, 265020, 18108374, 264639, 18108382, 83373044, 18108385, 87168518
2477	20718974 (4953, 4954)		UNCLASSIFIED		263978
2478	17659165 (4955, 4956)		UNCLASSIFIED		285017
2479	94314568 (4957, 4958)	Novel Protein sim. GBank gll1644232[dbj BAA11082] - [D87086] N-WASP [Bos taurus]	Im7		56984075, 22278999, 21906764, 264682, 21906785
2480	95295605 (4959, 4960)		UNCLASSIFIED		284905, 284907, 264765
2481	94718481 (4961, 4962)	Novel Protein sim. GBank gll5689489[dbj BAA63018.1] - (AB028889) KIAA1066 protein [Homo sapiens]	collagen		65274572, 56182575, 22278997, 264084, 284259, 29331822, 29331824, 66714117, 28331827, 35688052, 264508, 284905, 284906, 284907, 284908, 52644045, 264909, 58182435, 265008, 264910, 33657402, 55812038, 264758, 265010, 285011, 265017, 285018, 264760, 264762, 18108351, 264764, 264288, 264766, 264886, 264768, 21906788, 55811957, 265020, 264691, 264692, 264693, 264628, 55811576, 264630, 264634, 264635, 264636, 264637, 264556, 264558, 56182323, 83373044, 60432113, 22278002
2482	87393165 (4963, 4964)	Novel Protein sim. GBank gll321249[pir S28407] - guanine nucleotide-exchange activator CDC25 homolog - mouse	UNCLASSIFIED		29331822, 29331824, 29331825, 29331827, 264508, 264905, 264509, 264906, 264907, 264908, 264511, 264591, 264768, 264693, 264631, 264632, 264636, 264638, 264639, 264583
2483	87731583 (4965, 4966)		UNCLASSIFIED		264488, 22278995, 264083, 264095, 60432049, 60433356, 60433438, 264448, 264288, 263967, 18108370, 18108385, 18108386, 264482
2484	94187774 (4967, 4968)	Novel Protein sim. GBank gll728831[sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Kinase		264563
2485	87786556 (4969, 4970)	Novel Protein sim. GBank gll1185367 (U23281) - SH3 domain binding protein [Rattus norvegicus]	UNCLASSIFIED		22278995, 22278996, 22278997, 22278999, 264259, 60432049, 29331824, 60432289, 29331827, 265007, 264910, 264593, 264600, 264603, 264604, 265018, 264448, 264288, 264685, 264686, 264768, 264689, 35695917, 265022, 264692, 264693, 56182323

2486	87748978 (4971, 4972)	Novel Protein sim. GBank gij2862167[dbj BAA23715] - (AB007903) KIAA0443 [Homo sapiens]			265017, 264555
2487	95343105 (4973, 4974)	Novel Protein sim. GBank gij484559[sp P35287 RB14_RAT RAS-RELATED PROTEIN RAB-14	Contains protein domain (PF00071) - Ras family	glycoprotein	22278996, 35688286, 22278997, 22278998, 22278999, 264092, 264259, 29331822, 35696052, 264106, 264905, 264907, 29331830, 264909, 265008, 264511, 265008, 265009, 60433436, 21908754, 33108954, 87188558, 265018, 264681, 264288, 264687, 21908769, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 264534, 33657023, 264692, 33657109, 263972, 18108377, 35688423, 35695855, 60170394, 18108385, 56526486, 22279000, 22279002, 264583, 264482, 264565, 20281169, 18108391
2488	87652451 (4975, 4976)			UNCLASSIFIED	264910, 264448, 264288, 264684, 264691, 264634
2489	82990585 (4977, 4978)	Novel Protein sim. GBank gij4886439[emb CAB43355.1] - (AL050253) hypothetical protein [Homo sapiens]	Contains protein domain (PF00084) - Sushi domain (SCR repeat)	complementrecept	264888, 264693, 55811576, 22279002
2490	88089609 (4978, 4980)	Novel Protein sim. GBank gij2588624 (AC003083) - Rap2 Interacting protein-like; similar to U73941 (PID:g1916018) [Homo sapiens]		UNCLASSIFIED	264907, 265008, 22279002
2491	81242116 (4981, 4982)	Novel Protein sim. GBank gij728632[sp P39169 ALU2_HUMAN - IIII ALU SUBFAMILY SB WARNING ENTRY IIII		tm7	264259, 29331828, 265008, 264782, 18108370, 18108376, 18108379
2492	95308202 (4983, 4984)	Novel Protein sim. GBank gij3355303 (AF001549) - Unknown gene product [Homo sapiens]		transcriptfactor	264488, 22278998, 22278999, 29331828, 264591, 33109954, 265017, 55811150, 21908784, 21908788, 264692, 60431528, 87188518, 60432113, 22279000

2493	95422415 (4985, 4988)	Novel Protein sim. GBank gl 4240307 dbj BAA74932.1 - (AB020716) KIAA0809 protein [Homo sapiens]	Contains protein domain (PF01424) - struct R3H domain	18108394, 264887, 65274572, 56182575, 22278985, 56994075, 60432048, 28331822, 29331824, 29331825, 29331826, 29331827, 29146498, 264508, 264905, 264509, 264906, 264907, 29331830, 264909, 264510, 265006, 264511, 265007, 264512, 265008, 265009, 264910, 21908754, 265011, 264600, 265017, 265018, 264604, 264805, 265019, 55811150, 264762, 18108351, 264891, 264448, 264683, 264389, 264288, 18108355, 18108357, 264687, 21908765, 21906788, 21906767, 21906768, 21908769, 265020, 264691, 264692, 33657023, 33657348, 18108370, 18108374, 18108376, 55810764, 18108379, 65274791, 264630, 264632, 264634, 264635, 264636, 264555, 264637, 264557, 264558, 264639, 264559, 83373044, 18108385, 87168518, 60432113, 22279000, 22279002, 264482, 264586, 264486
2494	30783118 (4987, 4988)		UNCLASSIFIED	284907, 284601
2495	94234551 (4989, 4990)	Novel Protein sim. GBank gl 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	collagen	263994, 22278997, 35696032, 284509, 264905, 264906, 264907, 264908, 264909, 265006, 265009, 264595, 264604, 264448, 264682, 264764, 264288, 264685, 264768, 264769, 264689, 265020, 264692, 65274620, 264629, 55810764, 35696423, 55811576, 264636, 264637, 18108385, 22279000, 264584, 264587, 264486
2496	80018765 (4991, 4992)	Novel Protein sim. GBank gl 4808220 emb CAB42832.1 - (AL022316) dJ117715.1 (PUTATIVE novel protein) [Homo sapiens]	struct	29147620, 264905, 265006, 265007, 18108348, 18108362, 18108370, 18108374, 264555, 264556, 18108381, 18108383, 18108388
2497	81723554 (4993, 4994)		UNCLASSIFIED	52644507, 22278996, 22278999, 28331824, 29331826, 33657402, 21906754, 87168474, 265019, 264389, 264689, 21906785, 21906786, 21906787, 21906788, 265020, 33657023, 18108376, 18108387
2498	87724633 (4995, 4996)	Novel Protein sim. GBank gl 1200503 (U47824) - B [Homo sapiens]	UNCLASSIFIED	29331827, 264512, 264910, 264288, 18108374, 35695855
2499	94685125 (4987, 4988)	Novel Protein sim. GBank gl 3510234 (AC005561) - R31237.1, partial CDS [Homo sapiens]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	264809, 55812038, 264631, 264637, 264558

2500	84849324 (4898, 5000)	Novel Protein sim. GBank gll3881275[emb]CAA21725] - (AL032655) predicted using GeneFinder; similar to Inositol monophosphatase family; cDNA EST yk255a11.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00459) - Inositol monophosphatase family	transport	52644507, 52645158, 22278995, 56994075, 35898286, 22278998, 264259, 52845080, 29331824, 29331825, 68714117, 60432289, 29331826, 29331827, 35898052, 29331828, 264508, 264509, 264510, 264512, 33857402, 60433438, 21906754, 52844288, 87188474, 87188559, 264603, 264681, 264448, 264883, 264288, 264389, 52844229, 264889, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 35895917, 265020, 265021, 52844150, 33857023, 264693, 33657182, 35895783, 35896423, 35895855, 52644332, 83373044, 18108387, 87188518, 22279002
2501	94303888 (5001, 5002)	Novel Protein sim. GBank gll4829815[gb]AAD34088.1[AF15183] CGI-73 protein [Homo sapiens]	Contains protein domain (PF00851) - BTB/POZ domain	dna_rna_bind	65274572, 56182575, 35898286, 22278998, 56994075, 22278997, 60432048, 264259, 29331822, 29331824, 29331826, 29331827, 35898032, 264905, 264908, 264907, 264908, 264909, 56182435, 264510, 264511, 285007, 264910, 264591, 60432229, 33857402, 80433356, 264595, 55812038, 264758, 264598, 87188474, 87188559, 264600, 264601, 264602, 265017, 264604, 265018, 264605, 265019, 18108351, 264448, 264389, 264288, 264788, 18108357, 21908765, 21908768, 21908767, 21908769, 29148629, 35895917, 264692, 33857023, 264628, 35898423, 55811576, 35895855, 264630, 264634, 264635, 264555, 264636, 264638, 264558, 60170394, 83373044, 18108385, 18108387, 87188518, 60432113, 22279002, 264388
2502	90893718 (5003, 5004)	Novel Protein sim. GBank gll3041847 (AC004542) - OXYSTEROL-BINDING PROTEIN-like; similar to P22059 (PID:g128308) [Homo sapiens]	Contains protein domain (PF01237) - UNCLASSIFIED Oysterol-binding protein		65274572, 264907, 56182435, 265007, 264592, 264760, 18108351, 264448, 264369, 264288, 264684, 264686, 55811957, 265021, 264692, 33857109, 263973, 55811576, 264635, 264555, 264556, 264557, 264558, 56182323, 264559, 87188518, 264563, 264482
2503	87878345 (5005, 5006)	Novel Protein sim. GBank gll2188974[emb]CAA72838] - (Y11888) BRX protein [Mus musculus]			264905, 264907, 264512, 265008, 265011, 18108351, 264448, 264288, 29148627, 264693, 18108370, 18108374, 18108385

2504	87868708 (5007, 5008)	Novel Protein sim. GBank gij550420[emb]CAA48220] - (X88101) trg [Rattus norvegicus]			264488, 52844507, 52845156, 52846842, 22278994, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 29331827, 35696052, 264808, 264808, 52844045, 265009, 60433356, 33857402, 60433438, 264595, 33109954, 87168474, 265017, 265019, 264448, 264288, 264766, 52844229, 21908765, 21908766, 21908767, 21908768, 52844150, 264892, 27486261, 27486262, 27486264, 27486265, 35695763, 35696423, 35695855, 52844332, 58182323, 18108387, 87168518, 60432113, 22279002, 264584
2505	8760559 (5008, 5010)			UNCLASSIFIED	264488, 52844507, 52845156, 52846365, 5274572, 22278995, 36994075, 22278996, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 29331825, 29331828, 29331828, 264508, 56182435, 264112, 264593, 60433356, 55812038, 21908754, 265011, 265017, 265018, 265019, 264605, 264762, 18108351, 264448, 264288, 264768, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 265022, 60170815, 33857023, 27486264, 18108378, 35695855, 264637, 83373044, 18108385, 87168518, 60432113, 22279000, 264563, 264482, 264585
2506	87232328 (5011, 5012)	Novel Protein sim. GBank gij2137562[pil]49635 - mouse Dhml protein - mouse		nuclease	264488, 263994, 264592, 264595, 264369, 264886, 264768, 35695917, 35696423, 264563
2507	95316233 (5013, 5014)	Novel Protein sim. GBank gij5174489[ref]NP_006035.1[pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone Histone deacetylase family		22278995, 22278999, 60432049, 264259, 29331828, 265008, 265007, 60433438, 33857084, 265010, 265017, 265018, 265019, 18108351, 264448, 18108354, 264369, 18108359, 21908765, 21908769, 55811857, 265020, 265022, 27486281, 33857349, 18108377, 35695855, 60432113, 22279002, 264563, 264585
2508	95315505 (5015, 5016)	Novel Protein sim. GBank gij4826433[emb]CAB42889.1] - (AL031447) dJ128A5.2.1 (novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	
2509	87813741 (5017, 5018)	Novel Protein sim. GBank gij1263289 (U47856) - fibroin-4 [Araneus diadematus]		UNCLASSIFIED	265007, 265008, 18108357, 264558, 264567

2510	95421379 (5018, 5020)	Novel Protein sim. GBank gl 3293537 gb AAC25762.1 - (AF071059) zinc finger RNA binding protein [Mus musculus]		dna_ma_bind	65274572, 22278994, 22278996, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331828, 33656970, 264908, 66712502, 265007, 264910, 60170831, 60432229, 60433356, 60433438, 21908754, 87188474, 265017, 265018, 264448, 264288, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265022, 264891, 33657023, 264693, 85274820, 33657109, 33657182, 27486282, 33657349, 18108370, 35695855, 264555, 58182323, 83373044, 60432113, 22279002, 265017, 21908764, 265020, 264692
2511	67384281 (5021, 5022)	Novel Protein sim. GBank gl 4323152 gb AAD18228.1 - (AF098863) Ets-protein Spi-C [Mus musculus]			
2512	98084771 (5023, 5024)	Novel Protein sim. GBank gl 4502075 ref NP_001135.1 pAMFR - autocrine motility factor receptor	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	transport	22278999, 284259, 29331825, 29331826, 29148499, 264907, 264909, 265008, 264591, 60432229, 21908754, 264763, 264683, 264766, 18108357, 264689, 21908769, 264693, 18108370, 263972, 18108374, 264558, 22279000
2513	95357843 (5025, 5026)	Novel Protein sim. GBank gl 3004657 (AF017777) - bobby sox [Drosophila melanogaster]		UNCLASSIFIED	60424178, 52845156, 18108394, 22278994, 35696286, 56994075, 22278996, 29331822, 29331824, 60424268, 29331825, 29331827, 33656970, 60431735, 33657084, 87168559, 265017, 264448, 264389, 56181562, 21908766, 21908767, 21908768, 21908769, 265020, 265021, 33657023, 18108366, 33657109, 27486281, 27486282, 33657349, 18108374, 55810784, 35696423, 58182323, 264558, 18108385
2514	88094578 (5027, 5028)	Novel Protein sim. GBank gl 2258437 (AF008197) - syncollin [Rattus norvegicus]		UNCLASSIFIED	264510
2515	87894509 (5029, 5030)	Novel Protein sim. GBank gl 3757727 emb CAA18783 - (AL022727) dJ8018.7 (olfactory receptor-like protein (hs8M1-3)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	- tm7	
2516	87786908 (5031, 5032)			UNCLASSIFIED	264259, 29148498, 264905, 264288, 29148929, 35695917, 27486281, 264634
2517	87784988 (5033, 5034)	Novel Protein sim. GBank gl 4220527 emb CAA23000 - (AL035356) putative protein [Arabidopsis thaliana]		UNCLASSIFIED	264091, 29331824, 29331825, 29331826, 29331828, 35696052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264511, 264910, 33657402, 264757, 33106954, 265017, 265018, 264605, 264760, 264762, 264763, 264768, 264769, 33657109, 33657182, 264628, 55811576, 35696423, 264631, 264634, 264637, 264638, 264639, 87168518, 22279002, 264584

2518	94147410 (5035, 5036)	Novel Protein sim. GBank gi 4928591 gb AAD34056.1 AF15181 - (AF151819) CGI-81 protein [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	UNCLASSIFIED	35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 284907, 284909, 284511, 285007, 60432228, 60433356, 60433438, 58812038, 285010, 285017, 284446, 284288, 264889, 21806768, 21806769, 285022, 52644150, 284693, 18108370, 263972, 264555, 56182323, 83373044, 18108385, 60432113, 264088, 264259, 66714177, 29331826, 29331827, 29331828, 264907, 68712502, 285006, 265008, 264594, 265010, 265011, 265018, 264288, 21806769, 285020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22276902, 264564
2519	94328180 (5037, 5038)	Novel Protein sim. GBank (AC004893) similar to KIAA0768, similar to PID:g3882253 [Homo sapiens]	kinase		264259, 66714177, 29331826, 29331827, 29331828, 264907, 68712502, 285006, 265008, 264594, 265010, 265011, 265018, 264288, 21806769, 285020, 60431528, 55811576, 65274791, 264632, 264555, 264636, 22276902, 264564
2520	87413235 (5039, 5040)	Novel Protein sim. GBank gi 4826722 ref NP_005085.1 pFATP - fatty acid transport protein 4	transport		264259, 264808, 264810, 264682, 21806769, 285020, 264563
2521	95318244 (5041, 5042)	Novel Protein sim. GBank gi 5174488 ref NP_008035.1 pKIAA - histone deacetylase 6	Contains protein domain (PF00850) - histone Histone deacetylase family		264488, 264489, 263994, 65274572, 22278995, 22278996, 264259, 29331822, 29331826, 264508, 264905, 264509, 264906, 284907, 66712502, 284511, 265006, 285007, 284591, 284592, 264593, 264594, 284595, 264596, 264681, 264448, 264763, 264682, 264784, 264684, 264369, 264288, 264685, 264686, 21806768, 55811957, 264692, 264693, 27486261, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 284632, 264558, 18108385, 65274727, 60432113, 264563, 264564, 264585, 264586, 264587
2522	87754052 (5043, 5044)	Novel Protein sim. GBank gi 4580011 gb AAD24201.1 U81002 - (U81002) TRAF4 associated factor 1 [Homo sapiens]	transport		264489, 22278997, 20281171, 21806754, 35695917, 263967, 263976, 263981, 20281169
2523	95340467 (5045, 5046)				263969
2524	95340469 (5047, 5048)	Novel Protein sim. GBank BOP2 [Mus musculus]	Contains protein domain (PF01753) - MYND finger		35694075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331828, 29331830, 56182435, 284512, 265006, 60170831, 33657402, 265010, 87168559, 285019, 264288, 21806765, 21806769, 35695917, 285020, 265021, 265022, 52644150, 264691, 33657023, 33657109, 27486281, 35696423, 65274791, 264559, 83373044, 56526486, 87168518, 264567

2525	94126928 (5049, 5050)	Novel Protein sim. GBank gl 2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]		kinase	264488, 22278997, 22278998, 60432049, 60432289, 29331828, 284905, 285008, 55812038, 21908754, 265019, 264369, 21908785, 21908786, 21908787, 21908789, 35695917, 265020, 265021, 33657109, 60431528, 83373044, 60432113, 22279000, 22278002, 264565
2526	95269404 (5051, 5052)	Novel Protein sim. GBank gl 4589628(dj BAA78836.1) - (AB023209) KIAA0982 protein [Homo sapiens]	Contains protein domain (PF00238) - Ribosomal protein L14	ribosomal prot	60424179, 264768, 264687, 264769, 264689, 65274572, 21908787, 58182575, 21908788, 21908789, 55811957, 22278994, 22278995, 35696288, 35695917, 22278996, 22278997, 265020, 22278998, 265021, 22278999, 265022, 264690, 264691, 60432049, 264259, 264097, 33657023, 29331822, 29331824, 26432289, 29331828, 29331827, 29331828, 27486282, 284508, 284509, 284905, 284907, 18108370, 66712502, 60431528, 264828, 264908, 18108372, 18108374, 56182435, 18108376, 55810784, 55811578, 35696423, 35695855, 265008, 265007, 264512, 265008, 265009, 264634, 264635, 60431850, 264636, 264555, 264592, 60431735, 264638, 33657402, 56182323, 60433356, 60433438, 264595, 55812038, 264596, 264758, 83373044, 52648317, 18108385, 33657084, 18108387, 55811386, 65274727, 56526486, 87168518, 60432113, 265017, 22278000, 265018, 265019, 264504, 18108351, 264448, 264566, 264289, 264486, 264587, 264766
2527	88094580 (5053, 5054)	Novel Protein sim. GBank gl 2258437 (AF008197) - synocollin [Rattus norvegicus]		UNCLASSIFIED	264510, 264512, 264630, 264591, 264592, 264259, 264594, 264595, 264603, 264605, 18108351, 264565, 264369, 18108354
2528	88078380 (5055, 5056)	Novel Protein sim. GBank gl 2085786 (AC002066) - similar to zinc finger 5 protein from Gallus gallus, U51640 (P Dg1399185) [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	dna_ma_bind	55812038, 265017, 264689, 35695917, 35695763, 60431528, 60432113, 22278002
2529	86670826 (5057, 5058)	Novel Protein sim. GBank gl 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW:Q08891) [Caenorhabditis elegans]		synthase	264908, 264769, 265020, 265021, 18108383
2530	80259978 (5059, 5060)				264369, 264556
2531	87768931 (5061, 5062)			UNCLASSIFIED	28331822, 29331824, 60432289, 264508, 264509, 264906, 265011, 264769, 21908768, 33657023, 87168518, 22279000, 264593
2532	87419778 (5063, 5064)	Novel Protein sim. GBank gl 2664625(jemb CAA16972) - (AL021811) putative protein [Arabidopsis thaliana]			
2533	87000255 (5065, 5066)	Novel Protein sim. GBank gl 437181 (U02289) - GTPase-activating protein [Caenorhabditis elegans]		UNCLASSIFIED	264555

2534	87332322 (5087, 5088)	Novel Protein sim. GBank gll3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	UNCLASSIFIED	284259, 35698052, 284905, 285017, 21908789, 285020, 285022, 33657109, 22278000
2535	91225056 (5069, 5070)	Novel Protein sim. GBank gll4488311 (emb CAB37992) - (AL031432) dJ485N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		65274572, 35698286, 60432289, 29331828, 68712502, 285008, 60432228, 285017, 285018, 285019, 284288, 284369, 284689, 21908788, 285020, 285021, 284636, 60170394, 22278002
2536	94218540 (5071, 5072)	Novel Protein sim. GBank gll728836 (sp P39193 ALU8_SP WARNING ENTRY IIII	kinase	18108388, 58182875, 35698286, 22278997, 22278999, 60432049, 284259, 29331824, 29331826, 29331827, 29331828, 284905, 284511, 285008, 284910, 284998, 52846317, 18108351, 284681, 284683, 18108354, 284288, 284687, 284788, 284689, 21908765, 21908786, 21908787, 285021, 52845129, 33657109, 18108374, 18108380, 56182323, 18108381, 18108388, 87188518, 60432113, 22279000, 22279002, 284567, 18108381
2537	95422283 (5073, 5074)	Novel Protein sim. GBank gll4557028 (p NP_003913.1 pHERC - guanine nucleotide exchange factor p32	ubiquitin	65274572, 35698286, 29331822, 29331825, 29331827, 29331828, 35698052, 284905, 68712502, 284909, 285008, 285011, 284760, 284288, 284685, 35698917, 60170815, 284681, 33657023, 65274620, 33657109, 18108374, 35698423, 35698585, 284636, 284558, 60170394, 56182323, 83373044
2538	36853454 (5075, 5076)		UNCLASSIFIED	
2539	84144816 (5077, 5078)		UNCLASSIFIED	22278996, 22278999, 29331822, 29331825, 29331828, 28148499, 284908, 284112, 60170831, 87168559, 284604, 285019, 284685, 284766, 87168518, 22278000, 284565, 284566
2540	94218545 (5079, 5080)	Novel Protein sim. GBank gll1362647 (p p S53878 - sex-regulated protein janus A - fruit fly (Drosophila pseudoobscura)	UNCLASSIFIED	22278997, 29331828, 285008, 285009, 284758, 285010, 18108351, 284683, 284288, 21908765, 35698917, 285020, 18108374, 284567
2541	95308238 (5081, 5082)	Novel Protein sim. GBank gll1711858 (sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DGCR REGION	UNCLASSIFIED	284488, 284768, 284689, 284511, 20281771, 284634, 284635, 284691, 284639, 29331824, 284603, 284604, 284905, 284907, 284908, 284768

2542	95298162 (5083, 5084)	Novel Protein sim. GBank gi 5225320 gb AAD40850.1 AF083110 - (AF083107) sirtuin type 2 [Homo sapiens]	Contains protein domain (PF00220) - Neurohypophyseal hormones, N- terminal Domain	UNCLASSIFIED	284488, 18108394, 52846385, 52846842, 85274572, 22278994, 35898288, 22278998, 284259, 52845080, 29331822, 29331824, 29331827, 35898052, 33858970, 284907, 284909, 52844045, 284510, 285008, 284512, 285007, 285008, 285009, 284910, 60431735, 52846317, 52844288, 285010, 285011, 285018, 285019, 18108351, 284883, 284288, 284885, 284887, 52844229, 284789, 21908768, 21908787, 21908789, 52844150, 33857023, 33857109, 52845129, 33857182, 27488281, 27488284, 33857349, 35895783, 18108374, 35896423, 35895855, 284831, 284834, 284835, 284558, 83373044, 18108385, 18108387, 87168518, 284563, 284564
2543	94139088 (5085, 5086)	Novel Protein sim. GBank gi 5419857 emb CAB46374.1 - (AL088723) hypothetical protein [Homo sapiens]	Contains protein domain (PF00078) - RNA recognition motif (e.k.a. RRM, RBD, or RNP domain)		85274572, 58182575, 22278999, 284259, 29331826, 284907, 284510, 284511, 284592, 284595, 284784, 284389, 284288, 284884, 284786, 284889, 21908765, 21908787, 21908789, 80170815, 284892, 284893, 55811578, 85274791, 284836, 284558, 18108381, 60170394, 284638, 18108385, 60432113, 22278900
2544	94218548 (5087, 5088)	Novel Protein sim. GBank gi 2498110 sp Q83181 AEGP_RAT - APICAL ENDOSOMAL GLYCOPROTEIN PRECURSOR	Contains protein domain (PF00629) - MAM domain.	glycoprotein	18108397, 52846385, 22278997, 284259, 60432049, 29331822, 28331825, 29331828, 29331827, 29331828, 284905, 284908, 285006, 285007, 285008, 87168559, 285017, 285018, 285019, 18108351, 284448, 284888, 284887, 284889, 21908785, 285020, 285021, 18108370, 18108374, 18108378, 18108381, 18108385, 18108387, 56528486, 22278900, 284482, 284563, 284567
2545	87742845 (5089, 5090)	Novel Protein sim. GBank gi 3327048 dbj BA3159.1 - (AB014516) KIAA0618 protein [Homo sapiens]			29331825, 284908, 285009, 60170831, 285017, 284389, 21908787, 60170815, 284892, 33857109
2546	88093861 (5091, 5092)	Novel Protein sim. GBank gi 2996032 (AF054588) - brain finger protein [Rattus norvegicus]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284892, 33857109 29331824, 285007, 22278902

2547	94143868 (5083, 5094)	Novel Protein sim. GBank gi 4929607 gb AAD34084.1 AF15182 - (AF151827) CGI-69 protein [Homo sapiens]	Contains protein domain (PF00153) - transport Mitochondrial carrier proteins	UNCLASSIFIED	264488, 18108394, 52646842, 18108397, 56182575, 22278995, 56984075, 22278996, 22278997, 22278998, 264259, 29331822, 29331824, 29331826, 60432289, 29331827, 35696052, 29331828, 264104, 264508, 264905, 264906, 264908, 66712502, 264909, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432228, 60431735, 264594, 60433438, 21906784, 52646317, 265010, 265011, 264600, 264601, 265018, 265019, 264760, 18108351, 264682, 264448, 264288, 264369, 264684, 264686, 264687, 56181562, 264688, 264689, 21906785, 21906786, 21906787, 21906788, 29148627, 21906789, 55811957, 265020, 265021, 265022, 264690, 264691, 18108362, 264692, 264693, 27486281, 18108370, 18108374, 55810764, 55811576, 35696423, 35695855, 264635, 264636, 264555, 264637, 263981, 264557, 18108380, 264638, 56182323, 264556, 264559, 83373044, 18108385, 87168516, 22278002, 264564, 264566, 264486
2548	66179079 (5085, 5086)			UNCLASSIFIED	264488, 18108394, 52646365, 22278994, 35696266, 56984075, 22278997, 22278999, 264259, 29331822, 26331824, 29331825, 29331826, 60432289, 26331827, 29331828, 56182435, 264511, 265007, 264512, 60433356, 87168559, 264684, 264369, 52644229, 265021, 35657023, 264692, 18108374, 52644332, 264557, 18108380, 18108381, 18108382, 18108384, 18108385, 60432173, 22278000, 22279002, 264563, 264567
2549	94186863 (5087, 5090)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00412) - struct LIM domain containing proteins	struct	56182575, 22278996, 22278997, 22278998, 22278999, 264259, 264508, 264908, 29331830, 265009, 265010, 265016, 264688, 21906784, 21906785, 21906786, 21906787, 21906788, 265020, 265021, 52644150, 264691, 18108368, 60431802, 18108376, 35696423, 56182323, 18108387, 264587
2550	87775584 (5089, 5100)	Novel Protein sim. GBank gi 2143886 pir J152523 - nucleoporin p62 homolog - rat (fragment)		UNCLASSIFIED	56182575, 29331822, 264105, 264512, 18108351, 35695917, 264637, 264638

2551	95308400 (5101, 5102)	Novel Protein sim. GBank gl 4337103 gb AAD18079 - (AF129756) NG28 [Homo sapiens]	Contains protein domain (PF00561) - alpha/beta hydrolase fold	UNCLASSIFIED	18108396, 65274572, 22278995, 22278998, 22278999, 284259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 284905, 56182435, 265007, 60433438, 55812038, 21906754, 65274444, 265017, 265018, 284605, 265019, 284288, 21906766, 21906768, 21906769, 265020, 60170815, 284693, 33657108, 35696423, 284638, 56182323, 83373044, 22279000
2552	95332820 (5103, 5104)			UNCLASSIFIED	56182375, 35696286, 29331824, 29331826, 35696052, 29331828, 284508, 284907, 56182435, 285008, 284591, 33109954, 284760, 55811957, 35695917, 33657023, 33657109, 18108374, 55811578, 35696423, 35695855, 56182323, 284558
2553	95308243 (5105, 5106)	Novel Protein sim. GBank gl 1711658 sp P54797 T10_MOUSE - SER/THR-RICH PROTEIN T10 IN DCCR REGION		UNCLASSIFIED	284686, 284488, 283976, 284766, 29331826, 35696052, 35696423, 284601, 284511, 284602, 284910, 284634, 284760, 284555, 284762, 284908, 284592, 284891, 284566, 284908, 284684, 284567, 284909, 284766
2554	87761520 (5107, 5108)	Novel Protein sim. GBank gl 728835 sp P38192 ALUS_HUMAN - III ALU SUBFAMILY SC WARNING ENTRY IIII		cadherin	22278997, 29331822, 284508, 21906769, 33657023, 33657109, 56182323
2555	87627551 (5109, 5110)	Novel Protein sim. GBank gl 4884319 emb CAB43260.1 - (AL050084) hypothetical protein [Homo sapiens]		nuclease	29331824, 263972
2556	87645533 (5111, 5112)	Novel Protein sim. GBank gl 4106984 (AC003038) - R30923_1 [Homo sapiens]	Contains protein domain (PF00514) - Armadillo/beta-catenin-like repeats	UNCLASSIFIED	22278998, 284509, 33657402, 284683, 284684, 284766, 284889, 33657023, 33657109, 35695855, 284558, 284567, 284595
2557	79437803 (5113, 5114)			UNCLASSIFIED	22278997, 29331824, 66714117, 29331825, 284908, 284511, 265018, 284448
2558	87617591 (5115, 5116)	Novel Protein sim. GBank gl 119110 sp P03211 EBN1_EBV - EBNA-1 NUCLEAR PROTEIN		UNCLASSIFIED	22278997, 29331822, 29331828, 60433356, 265011, 284288, 284765, 284766, 284769, 21906765, 21906766, 60432113, 284482
2559	88096382 (5117, 5118)	Novel Protein sim. GBank gl 453999 emb CAB39618.1 - (AL049481) AIG1-like protein [Arabidopsis thaliana]		UNCLASSIFIED	
2560	87994530 (5119, 5120)	Novel Protein sim. GBank gl 5051399 emb CAB44995.1 - (AL078630) 573K1.3 (nm17M1-4) (novel 7 transmembrane receptor (rhodopsin family) (olfactory receptor LIKE) protein)) [Mus musculus]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)		
2561	88176575 (5121, 5122)	Novel Protein sim. GBank gl 5326825 gb AAD42056.1 AF044955 - (AF044953) NADH:ubiquinone oxidoreductase PGIV subunit [Homo sapiens]		UNCLASSIFIED	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 284259, 29331822, 29331824, 29331826, 29331827, 29331828, 285007, 60432229, 87168559, 285017, 265018, 285019, 284689, 21906768, 21906769, 35695917, 265020, 33657023, 33657109, 18108374, 284634, 284559, 18108385, 87168518, 22279002

2562	07845539 (5123, 5124)	Novel Protein sim. GBank gi 4106984 (AC003038) - R30923_1 [Homo sapiens]		UNCLASSIFIED	56994075, 22278996, 22278997, 22278999, 264259, 29331822, 60432289, 33657402, 60433356, 21906765, 55811957, 60170615, 33657023, 264693, 35895855, 87188518, 264488, 35896286, 22278999, 264259, 29331822, 29331824, 35896052, 264508, 264907, 264908, 264909, 52844045, 264510, 264511, 265009, 264910, 264591, 264593, 33657402, 265017, 265018, 265019, 18108351, 264686, 21906767, 21906768, 55811957, 35695917, 265020, 264691, 264693, 27486262, 264628, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264639, 264558, 18108384, 87168518, 22279000, 22279002, 264482, 264563, 264565, 264566, 264486, 29331822, 265007, 265010, 265019, 264769, 55811576, 56182323
2563	80095497 (5125, 5126)	Novel Protein sim. GBank gi 4886447[emb]CAB43371.1] - (ALD50270) hypothetical protein [Homo sapiens]		UNCLASSIFIED	
2564	80502783 (5127, 5128)	Novel Protein sim. GBank gi 1352844[sp]P47179 YJP_YEAST - HYPOTHETICAL 118.4 KD PROTEIN IN BAT2-DALS INTERGENIC REGION PRECURSOR		sulfoltransferase	
2565	85530906 (5129, 5130)			UNCLASSIFIED	66714117, 264909, 263978, 264632
2566	80224956 (5131, 5132)	Novel Protein sim. GBank gi 628012[pi]A53933 - myosin I myr 4 - rat	Contains protein domain (PF00063) - Myosin head (motor domain)	struct	18108370, 35695855, 264558, 264558, 18108383
2567	88143580 (5133, 5134)	Novel Protein sim. GBank gi 460009[sp]P34548 YJN4_CAEEL - HYPOTHETICAL 33.8 KD PROTEIN R10E11.4 IN CHROMOSOME III		synthase	265020, 60170615
2568	91233099 (5135, 5136)				60424179, 18108394, 56181686, 56994075, 22278999, 264490, 264259, 29331822, 56182181, 29331824, 60424269, 29331825, 29331826, 29331828, 264509, 29331830, 265007, 265008, 265009, 33657402, 265010, 265011, 265019, 264448, 264683, 264288, 18108354, 264769, 21906766, 21906767, 35695917, 265021, 33657023, 18108362, 33657109, 33657182, 35695763, 60431528, 55810784, 18108379, 83373044, 18108385, 60432113, 264482

2569	95313784 (5137, 5138)	Novel Protein sim. GBank gl 2599560 gb AAB84168.1 - (AF029874) basic leucine zipper protein LZIP [Homo sapiens]	Contains protein domain (PF00170) - bZIP transcription factor	transcriptfactor	18108394, 56182575, 56181886, 22278995, 22278996, 56994075, 35896286, 22278997, 22278998, 22278999, 264259, 60432049, 29331822, 56182181, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35896052, 264905, 264908, 56182435, 265008, 265009, 264910, 60432229, 264592, 60433356, 60433438, 21908754, 87188559, 265017, 265018, 265019, 264682, 264448, 264288, 21908765, 21908766, 21908767, 21908768, 29148827, 21908769, 35895917, 265021, 265022, 52644150, 264690, 264691, 264692, 264693, 65274620, 263967, 35895763, 20281089, 263974, 18108374, 55810764, 35898423, 35898585, 264558, 18108381, 56182323, 18108382, 83373044, 18108385, 56526486, 87168518, 22279000, 22279002, 264566
2570	94138754 (5139, 5140)	Novel Protein sim. GBank gl 4758954 ref NP_004587.1 ppp2 - protein phosphatase 2 (lormeny 2A), regulatory subunit B (PR 52), beta isoform	Contains protein domain (PF01240) - Protein phosphatase 2A regulatory subunit PR55	phosphatase	22278998, 29331822, 29331824, 66714117, 29331825, 60432289, 29331827, 35896052, 264907, 264510, 265007, 265009, 264758, 33109954, 265019, 264686, 264689, 265020, 265021, 264691, 264692, 264693, 18108374, 35895855, 264634, 56182323, 264639, 60170394, 83373044, 22279002, 264482
2571	87733750 (5141, 5142)	Novel Protein sim. GBank gl 732218 sp P34609 YO60. CAEEL - HYPOTHETICAL 128.6 KD PROTEIN ZK1098.10 IN CHROMOSOME III		struct	264508, 264905, 264907, 264828, 18108351, 264555, 264556, 264557, 264558, 264559
2572	87627560 (5143, 5144)	Novel Protein sim. GBank gl 4884319 emb CAB43280.1 - (AL050084) hypothetical protein [Homo sapiens]		UNCLASSIFIED	35896286, 29331827, 35896052, 264100, 264104, 264110, 264592, 21905754, 29148627, 29148629, 263972, 263974, 18108374, 263976, 35895855, 60170394, 264559, 18108385

2573	95313928 (5145, 5146)	Novel Protein sim. GBank gi1399138 sp P02745 C1QA_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, A CHAIN PRECURSOR	Contains protein domain (PF00386) - complement C1q domain	264488, 60424179, 65274572, 56182575, 56181886, 22278995, 56994075, 22278987, 60432049, 264259, 29331822, 29331824, 29331825, 60432288, 29331828, 29331827, 29331828, 264104, 264107, 264508, 264806, 29331830, 264909, 264510, 265006, 264512, 265008, 265009, 264910, 264591, 264592, 60432229, 264593, 60433356, 264594, 60433438, 264595, 55812038, 264759, 21906754, 87188474, 265010, 265011, 87188559, 265017, 265018, 265019, 264761, 264762, 264763, 264764, 264369, 264288, 264685, 264766, 264686, 264687, 264688, 264769, 56181562, 264689, 21906765, 21906766, 21906767, 29148627, 21906768, 21906769, 265020, 265021, 265022, 60170815, 264690, 52644150, 264691, 264692, 33637023, 65274620, 18108365, 18108368, 27486265, 60431602, 264629, 60431528, 263976, 65274791, 35695855, 20281071, 60431850, 264637, 264638, 264558, 264639, 56182323, 60170394, 83373044, 18108384, 87168518, 80432113, 264482, 264564, 264565, 264566, 264567, 22278995, 264259, 60432289, 29331827, 29331828, 33656970, 264908, 265008, 264910, 264591, 33657402, 265018, 265019, 264448, 264784, 264369, 264288, 18108357, 21906765, 21906766, 21906768, 55811957, 60170815, 264691, 33657023, 264693, 33657109, 33657182, 27486261, 27486264, 33657349, 264636, 264555, 83373044, 18108385, 264482
2574	94748814 (5147, 5148)	Novel Protein sim. GBank gi13334982 (AC005306) - R27216_1 [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	UNCLASSIFIED
2575	87754408 (5149, 5150)	Novel Protein sim. GBank gi14929729 gb AAD34125.1 AF151888 - (AF151888) CGI-130 protein [Homo sapiens]		UNCLASSIFIED
2576	95357881 (5151, 5152)	Novel Protein sim. GBank gi14680881 gb AAD27730.1 AF132955 - (AF132955) CGI-21 protein [Homo sapiens]	Contains protein domain (PF00442) - ubiquitin	284259, 35696052, 264908, 80433438, 264681, 18108351, 264288, 52644150, 264628, 35696423
2577	86996621 (5153, 5154)	Novel Protein sim. GBank gi14337103 gb AAD18079 - (AF129756) NG26 [Homo sapiens]	Ubiquitin carboxyl-terminal hydrolases family 2	UNCLASSIFIED
2578	87786841 (5155, 5156)			UNCLASSIFIED
2579	87282879 (5157, 5158)			UNCLASSIFIED

2580	88168788 (5159, 5180)	Novel Protein sim. GBank gi 2568828 (AC003080) - Similar to KIAA0289; 80% similarity to AB002297 (PID:g2224539) [Homo sapiens]			265007, 265018, 264762
2581	87888048 (5181, 5182)	Novel Protein sim. GBank gi 4406642 gb AAD20049 - (AF131809) Unknown [Homo sapiens]	Contains protein domain (PF00595) - collagen PDZ domain (Also known as DHR or GLGF).		5694075, 29331824, 29331826, 29331828, 264905, 60433356, 60433438, 264758, 87168539, 21908769, 265022, 35695855, 263981
2582	87788789 (5183, 5184)	Novel Protein sim. GBank gi 2739387 (AC002505) - putative phosphatidylinositol-4-phosphate 5-kinase [Arabidopsis thaliana]	eph		264488, 264907, 264908, 264910, 264764, 264684, 264766, 264636, 264555, 264565
2583	91220850 (5165, 5166)	Novel Protein sim. GBank gi 4378112 emb CAA16521.1 - (AL021578) dJ453C12.2 (similar to transcription factor RBP-L) [Homo sapiens]	transcript factor		56181688, 264259, 264510, 264512, 264591, 264592, 264593, 264594, 264595, 264596, 264603, 264629, 55810764, 264630, 264637, 264565
2584	80430841 (5167, 5168)		UNCLASSIFIED		264808, 264910, 264768, 264693, 18108374, 55811576, 56182323
2585	80436126 (5169, 5170)	Novel Protein sim. GBank gi 2738151 (AF021935) - myotonic dystrophy kinase-related Cdc42-binding kinase [Rattus norvegicus]	kinase		264768
2586	91226138 (5171, 5172)				
2587	80430943 (5173, 5174)				22278998, 264259, 29331822, 29331824, 29331827, 29331828, 264906, 265007, 265009, 264591, 60433358, 33657402, 265018, 264782, 264288, 21908766, 21908767, 21908769, 265022, 264691, 83373044, 58528486, 22279002
2588	80074385 (5175, 5176)		UNCLASSIFIED		264908, 265019, 264768, 264693, 55811576, 56182323
2589	85515607 (5177, 5178)	Novel Protein sim. GBank gi 302159 emb CAA71415 - (Y10389) nuclear protein [Xenopus laevis]	UNCLASSIFIED		264564
2590	87054526 (5179, 5180)	Novel Protein sim. GBank gi 2104689 (U92793) - alpha glucosidase II, alpha subunit [Mus musculus]			35696052, 264905, 264906, 264907, 264908, 264909, 265009, 265018, 264768, 35698423, 264636
2591	94192187 (5181, 5182)	Novel Protein sim. GBank gi 570202 gb AAD47189.1 AF129166 (AF129166) long-chain acyl-CoA synthetase 5 [Homo sapiens]	glucoamylase		22278995, 29331830, 265008, 265010, 265017, 264639
			eph		264259, 29331822, 264106, 264906, 56182435, 265007, 265008, 33109954, 264448, 55811957, 265020, 18108370, 55811576, 22279002

2592	95332848 (5183, 5184)	Novel Protein sim. GBank gi 3024888 sp Q80936 YAB1_MOUSE - HYPOTHETICAL HEART PROTEIN		transport	18108397, 56182575, 35696286, 56994075, 264259, 29331822, 29331824, 29331826, 60432288, 29331827, 29331828, 264906, 264908, 265007, 265008, 264910, 60432229, 264594, 60433356, 60433438, 59812038, 18108348, 21908754, 265011, 87168559, 265017, 265019, 264784, 264389, 264288, 264786, 265021, 60170615, 33657023, 33657109, 264628, 35698423, 35695855, 264557, 264638, 60170394, 56182323, 83373044, 56526486, 87168518, 264563, 264482, 264585
2593	87754416 (5185, 5186)	Novel Protein sim. GBank gi 4929729 gb AAD34125.1 AF15188 - (AF15188) CGI-130 protein [Homo sapiens]		Im7	22278999, 29331825, 264758, 21906754, 52646317, 265010, 18108351, 264288, 264389, 21908768, 264693, 18108370, 264637, 264638, 264482
2594	95305758 (5187, 5188)	Novel Protein sim. GBank gi 4929587 gb AAD34054.1 AF15181 - (AF15181) CGI-59 protein [Homo sapiens]		UNCLASSIFIED	264488, 18108398, 56182575, 35696286, 22278997, 264093, 264259, 29331822, 29331825, 66714117, 29331826, 264905, 264909, 52644045, 56182435, 264510, 264512, 265007, 264757, 21906754, 87168474, 265017, 264760, 264448, 264764, 264288, 264766, 264689, 21908768, 33657109, 263975, 263977, 264634, 264556, 60170394, 56182323, 56526486, 264482, 264563, 264564, 264566, 264567 264892
2595	78561878 (5189, 5190)	Novel Protein sim. GBank gi 4309881 gb AAD15478 - (AC008930) R33423.1 [Homo sapiens]		UNCLASSIFIED	22278999, 264259, 265018, 264448, 265021, 80431528
2596	87538637 (5191, 5192)			UNCLASSIFIED	264905, 264509, 264908, 284762, 264766, 35695917, 35695855, 264635, 264636, 83373044, 264488
2597	94784089 (5193, 5194)	Novel Protein sim. GBank gi 1001351 db BAA10838 - (D84008) hypothetical protein [Synecocystis sp.]		UNCLASSIFIED	22278998, 264259, 29331824, 87168474, 264683, 21908766, 35695917, 264891, 33657023, 33657109, 18108370, 18108374, 264564, 264585
2598	88084848 (5195, 5196)	Novel Protein sim. GBank gi 3941737 (AF103719) - BAT2 [Mus musculus]		MHC	264766, 264769, 21908768, 33657182, 35695763, 18108370, 18108374, 264635, 264636, 56526486, 22279000, 264569 35696286, 264093, 264288, 21906769, 35696423, 35695855
2599	87842888 (5187, 5188)				
2600	87787848 (5198, 5200)	Novel Protein sim. GBank gi 4283521 gb AAD15347 - (AC004044) putative WD-repeat protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinasereceptor	

2601	81243070 (5201, 5202)	Novel Protein sim. GBank g 1728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	56182575, 22278999, 264259, 28331822, 29331824, 60432289, 29331826, 29331827, 264908, 265007, 265008, 264591, 60433356, 33657402, 60433438, 21906754, 265011, 265018, 265019, 18108351, 264448, 264369, 21906769, 265020, 60170615, 264693, 33657109, 18108370, 18108376, 56182323, 18108381, 18108385, 22278002, 264563, 60433438, 21906754, 87168559, 264601, 264369, 264288, 21906767
2602	88180022 (5203, 5204)	Novel Protein sim. GBank g 1408632 pb AAD200471 - (AF1131801) Unknown [Homo sapiens]			264488, 65274572, 22278995, 22278996, 56994075, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 60432289, 29331826, 29331827, 29331828, 35696052, 56182435, 264113, 265008, 265009, 60433356, 264757, 60433438, 284759, 33657084, 87168474, 265010, 285011, 87168559, 265017, 265018, 265019, 264448, 264883, 18108354, 264288, 264767, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265020, 265021, 265022, 60170615, 264691, 33657023, 264893, 33657109, 27486282, 18108374, 35696423, 65274791, 35695855, 264555, 264638, 264637, 56182323, 83373044, 56526486, 87168518, 60432113, 22279000
2603	94325821 (5205, 5206)	Novel Protein sim. GBank g 13122367 sp Q61211 LIGA_MOUSE - LIGATIN		UNCLASSIFIED	264259, 35696052, 264508, 264906, 264907, 264908, 264909, 264510, 264512, 265008, 264910, 33657402, 264604, 264605, 264762, 264763, 264682, 264764, 264683, 264768, 264769, 264689, 33657023, 264693, 18108365, 264628, 35696423, 264631, 264632, 264634, 264635, 264637, 18108381, 264639, 83373044, 264565
2604	94876801 (5207, 5208)	Novel Protein sim. GBank g 15454030 ref NP_008488.1 pRRP2 - RAS-related on chromosome 22		oncogene	22278998, 264490, 60432049, 264259, 60432289, 264909, 265008, 60433356, 60433438, 264756, 21906754, 265010, 265011, 265018, 264681, 18108351, 264288, 264766, 264685, 21906765, 21906768, 21906769, 264691, 264692, 264693, 65274791, 264634, 264555, 264636, 22278996, 264510, 264512, 265009, 264768, 22279002, 264566
2605	94316756 (5209, 5210)	Novel Protein sim. GBank g 13628745 db BAA33366 - (AB013721) mltugumin 23 [Oryctolagus cuniculus]		UNCLASSIFIED	
2606	87748408 (5211, 5212)				

2607	87627742 (5213, 5214)	Novel Protein sim. GBank gl4828626[gb AAD30202.1] - (AF135022) mediator [Homo sapiens]			29331822, 29331825, 29331826, 29331827, 29331828, 264906, 264907, 264908, 68712502, 264828, 56182435, 55812038, 265010, 265017, 265018, 265019, 264768, 264689, 21908765, 55811957, 265020, 265022, 264692, 33657023, 264693, 33657109, 18108370, 264839, 56182323, 264509, 264907, 264908, 264592, 264758, 264631
2608	81734786 (5215, 5216)	Novel Protein sim. GBank gl2226005 (U49873) - ORF2: function unknown [Homo sapiens]		Contains protein domain (PF00850) - Histone deacetylase family	284488, 65274572, 35696286, 22278997, 22278999, 60432049, 264259, 56182181, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264905, 264907, 60433356, 60433438, 55812038, 265011, 87168559, 265017, 265018, 264448, 264765, 264288, 264766, 264689, 21908765, 21908767, 21908769, 265020, 265021, 264691, 264692, 33657109, 27486261, 18108370, 65274791, 264636, 264556, 56182323, 18108385, 56526486
2609	94843781 (5217, 5218)	Novel Protein sim. GBank gl3024889[pp P56524]Y288_HUMAN - HYPOTHETICAL PROTEIN KIAA0288 (HA6116)			18108394, 22278994, 56994075, 60432049, 264259, 29331822, 29331825, 60432289, 29331827, 264107, 264109, 264905, 56182435, 264112, 265006, 265007, 265008, 265009, 60433356, 60433438, 265011, 87168559, 265017, 264448, 264682, 264764, 264288, 265021, 33657023, 263967, 33657182, 27486261, 18108374, 263976, 55811576, 264638, 87168518, 60432113
2610	86177654 (5219, 5220)	Novel Protein sim. GBank gl4336855[gb AAD17989] - (AF108473) leucine-rich-domain inter-acting protein 1; LEAP1 [Mus musculus]		transcript factor	22278999, 265017, 264684, 21906768, 22279000
2611	87428890 (5221, 5222)	Novel Protein sim. GBank gl3876761[emb CAA92894] - (Z88780) predicted using Genefinder; Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]		Contains protein domain (PF00254) - FKBP-type peptidyl-prolyl cis-trans isomerases	265009, 264910, 264759, 265017, 21906767, 18108365, 18108388, 60432113
2612	87771198 (5223, 5224)	Novel Protein sim. GBank gl5679136[gb AAD46874.1]AF16093 - (AF160934) BcDNA.LD14189 [Drosophila melanogaster]		transport	264685
2613	79481486 (5225, 5226)	Novel Protein sim. GBank gl5533081[gb AAD45009.1]AF16118 - (AF161181) P55T protein [Mus musculus]		UNCLASSIFIED	22278998, 22278999, 29331825, 264508, 264906, 21906754, 264602, 264766, 264769, 52644229, 21906765, 33657109, 27486284, 18108370, 263972, 264555, 60432113
2614	87643948 (5227, 5228)			UNCLASSIFIED	264768, 18108394, 264692, 264683, 264508, 284509, 264907, 264628, 264908, 264909, 18108377, 264511, 264512, 264910, 264635, 264595, 265010, 264404, 264563, 264764, 264885, 264768
2615	87361986 (5229, 5230)				

2616	87428895 (5231, 5232)	Novel Protein sim. GBank gij3876761[emb CAA92894] - (Z68760) predicted using GeneFinder. Similarity to Mouse FK506-binding protein (SW:FKB3_MOUSE) [Caenorhabditis elegans]	Contains protein domain (PF00254) - isomerase FKBP-type peptidyl-prolyl cis-trans isomerases	22278995, 22278997, 22278998, 60432048, 60432289, 264828, 60433356, 264594, 60433438, 33109954, 87168474, 265011, 265017, 265019, 264288, 264766, 21908765, 21908767, 265020, 265021, 18108376, 18108377, 18108387, 87168518, 264482, 264567
2617	86976888 (5233, 5234)	Novel Protein sim. GBank gij728831[sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII]	kinase	265010, 265019, 264369, 264693, 55811576, 22279002
2618	91231662 (5235, 5236)	Novel Protein sim. GBank gij3319282 (AF049103) - Huntingtin Interacting protein [Homo sapiens]	Contains protein domain (PF00397) - UNCLASSIFIED WW domain	264489, 22278996, 264490, 264259, 29331822, 264102, 264509, 264908, 264907, 68712502, 29331830, 265008, 264910, 265009, 60433356, 60433438, 264758, 21908754, 265011, 87168559, 265017, 265018, 264369, 264288, 264766, 264768, 264889, 21908765, 21908766, 21908767, 35695917, 265020, 265022, 33657023, 264892, 33657109, 264628, 18108374, 35695855, 18108381, 83373044, 18108365, 18108388, 55526486, 264563
2619	87684000 (5237, 5238)	Novel Protein sim. GBank gij2431772 (U68411) - putative type III alcohol dehydrogenase [Drosophila melanogaster]	Contains protein domain (PF00455) - dehydrogenase Iron-containing alcohol dehydrogenases	264259, 60432289, 60433438, 21906754, 264369, 60432113, 264566
2620	95314841 (5239, 5240)	Novel Protein sim. GBank gij4322567[gb AAD16097] - (AF090436) dachshund variant 1 [Mus musculus]	Contains protein domain (PF00628) - UNCLASSIFIED PHD-finger	52644507, 52645156, 52646842, 65274572, 22278995, 56994075, 35686286, 22278999, 60432049, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331828, 35698052, 264907, 68712502, 265008, 60433356, 33657402, 52646317, 21906754, 87168474, 265010, 265017, 265018, 264448, 264369, 264288, 264687, 264768, 52644229, 264688, 264689, 21908765, 21908768, 35695917, 52644150, 264692, 33657109, 35695763, 35696423, 264556, 52644332, 18108382, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 22279002, 264594, 264638
2621	80263495 (5241, 5242)	Novel Protein sim. GBank gij4557341[ref NP_001174.1 pATP6 - ATPase, H+ transporting, lysosomal subunit 1; vacuolar proton pump; H-ATPase subunit]		264488, 264908, 264807, 264908, 264512, 265007, 264756, 35695917, 264634, 264636, 264563, 264482
2622	81780390 (5243, 5244)	Novel Protein sim. GBank gij3880355[emb CAB05289] - (Z82285) predicted using GeneFinder [Caenorhabditis elegans]	UNCLASSIFIED	29331824, 35696052, 265007, 265010, 264288, 29148829
2623	91639306 (5245, 5246)			

2624	91639308 (5247, 5248)	Novel Protein sim. GBank gl 3880355 emb CA805299 - (Z62285) predicted using GeneFinder [Caenorhabditis elegans]		UNCLASSIFIED	56181686, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 56182181, 29331825, 60432289, 29331828, 35696052, 29146499, 68712502, 52644045, 285007, 265008, 60433356, 33109954, 21908754, 265010, 265011, 265018, 264448, 264286, 21908765, 21908766, 21908767, 29148629, 35695917, 265021, 265022, 27486265, 18108370, 60431528, 55811576, 35695855, 58182323, 18108385, 87168518, 22279002, 18108391, 264091, 264511, 263981
2625	88452068 (5249, 5250)	Novel Protein sim. GBank gl 2887429 db BAA24857 - (AB007887) KIAA0427 [Homo sapiens]		UNCLASSIFIED	22278996, 265007, 265009, 264448, 21908767, 265021, 264558, 87168518
2626	16533797 (5251, 5252)	Novel Protein sim. GBank gl 487416 (L20302) - actin filament protein [Gallus gallus]		struct	265008
2627	87636823 (5253, 5254)	Novel Protein sim. GBank gl 89462 pr J27307 - proline-rich phosphoprotein (gene PRH1, Db allele) - human		UNCLASSIFIED	22278997, 22278999, 264259, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 264907, 264909, 265008, 264591, 60433356, 60433438, 265010, 265017, 265018, 264369, 264288, 18108357, 21908765, 21908766, 265022, 65274791, 264638, 18108387, 87168518, 22279002
2628	94848254 (5255, 5256)	Novel Protein sim. GBank gl 3123552 emb CAA18609 - (AL022578) dJ393P12.2 (hypothetical Proline-rich protein KIAA0269 LIKE) [Homo sapiens]		UNCLASSIFIED	29331825, 29331826, 264102, 265008, 264766, 35695917, 264691, 33657023, 263972, 18108374, 22279000
2629	87376480 (5257, 5258)	Novel Protein sim. GBank gl 4929595 gb AAD34058.1 AF15182 - (AF151821) CGI-63 protein [Homo sapiens]		synthase	284636, 18108385
2630	78180364 (5259, 5260)			UNCLASSIFIED	52644507, 52645156, 52646385, 52646842, 22278994, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 52645080, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33656970, 264905, 264509, 264907, 264908, 264511, 264512, 265007, 265008, 264910, 52646317, 33657084, 52644296, 265010, 87168559, 265017, 265018, 265019, 264760, 264762, 264448, 264288, 264369, 264768, 264768, 52644229, 21906764, 21906765, 21906766, 21906767, 21906769, 35695917, 265020, 52644150, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 35696423, 85274791, 35695855, 264634, 264637, 52644332, 58182323, 60432113, 264566, 264486, 264685
2631	94845908 (5261, 5262)	Novel Protein sim. GBank gl 321605 pr JQ1161 - Gag protein - Visna virus (strain EV1)	Contains protein domain (PF00098) - Zinc finger, CCHC class	dna_ma_bind	
2632	38730414 (5263, 5264)				

2633	95011617 (5265, 5266)	Novel Protein sim. GBank gij1139548jBAA10889] - (D64009) seizure-related gene product 6 type 2 precursor [Mus musculus]	Contains protein domain (PF000084) - Sushi domain (SCR repeat)	22278995, 22278997, 22278998, 264259, 29331822, 29331824, 29331825, 29331827, 264508, 264908, 265008, 265007, 265008, 265009, 55812038, 33657084, 55811388, 265010, 265011, 87188559, 265018, 265019, 264683, 264288, 264886, 29148829, 33657023, 264693, 33657182, 35895763, 55811578, 264638, 56182323, 83373044, 18108385, 56526488, 87168518, 22279000, 22279002, 264565
2634	87330921 (5287, 5288)	Novel Protein sim. GBank gij5441611jemb[CAB48854.1] - (AJ388555) hypothetical protein [Canis familiaris]	UNCLASSIFIED	22278997, 264259, 29331824, 56714117, 29331827, 29331828, 264907, 33657084, 265017, 265018, 264448, 264288, 21906766, 21906767, 21906768, 29148829, 18108376, 55811578, 35695855, 87168518, 22279000, 264569, 29331822, 29331828, 265008, 60170831, 264681, 264765, 264685, 29148827, 21906769, 29148784, 265022, 60170815, 264635, 18108385, 56526488, 22279002, 264567
2635	86823144 (5268, 5270)	Novel Protein sim. GBank gij4680863jgbjAAD27721.1jAF132946) CGI-12 protein [Homo sapiens]		
2636	87260534 (5271, 5272)	Novel Protein sim. GBank gij3878148jemb[CAB07846] - (Z93386) Similarly to Yeast hypothetical 52.9 KD protein (SW:P43618); cDNA EST EMBL:M89432 comes from this gene; cDNA EST EMBL:D71008 comes from this gene; cDNA EST EMBL:D73578 comes from this gene; cDNA EST EMBL:D89025 comes ...	Contains protein domain (PF01546) - Peptidase family M20/M25/M40	
2637	95011298 (5273, 5274)	Novel Protein sim. GBank gij4758208jrefjNP_004081.1lpDUSP - dual specificity phosphatase 3 (vaccinia virus phosphatase VH1-related)	Contains protein domain (PF00782) - Dual specificity phosphatase, catalytic domain	264488, 264489, 52644507, 264887, 52646365, 52646842, 22278994, 22278996, 22278999, 20281171, 264259, 29331822, 52645080, 66714117, 29331825, 29331826, 29331827, 35696052, 29331828, 29146488, 264508, 264905, 264908, 264907, 264908, 264909, 264511, 264512, 264910, 264591, 264592, 60432229, 264593, 264594, 33657402, 60433356, 264757, 60433438, 264596, 264758, 52646317, 21906754, 52644296, 265010, 264600, 264602, 264603, 264605, 264761, 264762, 264681, 264448, 264764, 264765, 264288, 264766, 264686, 264768, 264887, 264769, 21906765, 21906768, 21906767, 21906768, 21906769, 35895917, 265021, 60170815, 264681, 33657023, 264692, 264693, 65274620, 27486264, 18108370, 264628, 264629, 18108374, 35696423, 35695855, 264632, 264634, 264635, 264637, 264638, 52644332, 264639, 264558, 83373044, 60432113, 264564, 264565, 264566, 264488, 264567

2638	84326733 (5275, 5278)	Novel Protein sim. GBank glj492989gb/AAD34105.1(AF15186 - (AF15186)) CGI-110 protein [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	60424179, 52644507, 52646842, 18108398, 58182575, 22278995, 22278998, 35698286, 22278997, 22278999, 264259, 60432048, 29331822, 60424268, 29331826, 35698052, 29146498, 284905, 52644045, 58182435, 60433356, 33657402, 55812038, 55811386, 265019, 264288, 264769, 52844229, 58181562, 29148627, 29148629, 55811957, 29148784, 35695917, 265021, 52644150, 33657023, 65274620, 33857109, 35695763, 18108374, 55810784, 35698423, 55811576, 35695855, 60431850, 56182323, 60432113, 264404
2639	95361346 (5277, 5278)	Novel Protein sim. GBank glj2190007(dbjBAA20355) - (AB004109) phosphatidylserine synthase II [Citellus griseus]		synthase	264488, 29331825, 35696052, 264508, 264509, 284909, 264512, 33657402, 60433438, 264758, 85658542, 264600, 265020, 265021, 33857109, 264628, 35698423, 264555, 264639, 264563, 264564, 264565, 264566, 284488
2640	87781330 (5279, 5280)	Novel Protein sim. GBank glj3158516 (AF067617) - contains similarity to chromo (chromatin organization modifier) domains (Pfam: chromo.hmm, score: 17.76 and 27.94) and to helicases conserved C-terminal domain (Pfam: helicase_C.hmm, score: 87.00) [Caenorhabditis elegans]	Contains protein domain (PF00271) - Helicases conserved C-terminal domain	helicase	29331822, 29331826, 264906, 33109954, 265017, 265019, 21906768, 35695763, 264636, 264637, 18108387
2641	11868834 (5281, 5282)	Novel Protein sim. GBank glj2564955 (AF030001) - unknown [Mus musculus]		UNCLASSIFIED	264828
2642	87412575 (5283, 5284)	Novel Protein sim. GBank glj4490304(lamb)CAB38785.1 - (AL035878) putative protein [Arabidopsis thaliana]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	UNCLASSIFIED	264259, 29331822, 33657402, 265019, 264369, 264691, 264634, 56526488, 22279002
2643	87643981 (5285, 5286)	Novel Protein sim. GBank glj3789797(gbjAAC67502.1) - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	helicase	22278997, 264259, 29146499, 56182435, 264910, 265010, 18108351, 264682, 264683, 264369, 264684, 264685, 264686, 29148627, 264680, 33657109, 18108370, 263973, 18108374, 264634, 264557, 264558, 18108385, 264482
2644	98177671 (5287, 5288)	Novel Protein sim. GBank glj3789797(gbjAAC67502.1) - (AF059569) actin binding protein MAYVEN [Homo sapiens]	Contains protein domain (PF00651) - BTB/POZ domain	nucl. recpt	264107, 264687
2645	17277228 (5289, 5290)	Novel Protein sim. GBank glj1706722(isp)P49749(EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2))		UNCLASSIFIED	265007
2646	94148542 (5291, 5292)	Novel Protein sim. GBank glj1706722(isp)P49749(EVX2_MOUSE - HOMEBOX EVEN SKIPPED HOMOLOG PROTEIN 2 (EVX-2))		UNCLASSIFIED	264909, 264687, 264632, 83373044

2847	91212878 (5283, 5294)		UNCLASSIFIED	56182575, 22278996, 35696286, 22278998, 284259, 29331822, 56182181, 29331825, 60424269, 60432228, 35696052, 66712502, 284908, 285007, 55812038, 33109954, 21908754, 33857084, 265018, 264448, 264288, 56181562, 21908765, 21908766, 21908768, 21908769, 35695917, 285020, 285021, 52644150, 264693, 33657109, 33657349, 60431528, 18108374, 55810784, 35696423, 56182323, 60432113, 22279002, 264584
2848	87600587 (5295, 5298)			29148498, 56182435, 33109954, 265011, 264682, 55811957, 35695917, 264690, 263978, 18108377, 35696423, 60432113
2849	84128783 (5287, 5298)	Novel Protein sim. GBank gij3041852 (AC004539) - unknown function; similar to Y09105 (PID:g1668171) (Homo sapiens)	UNCLASSIFIED	56182575, 35696286, 22278998, 29331824, 29331826, 60432228, 66712502, 56182435, 60170831, 60432229, 33857402, 33109954, 21908754, 265017, 264686, 264688, 21908765, 21908768, 60170815, 264693, 263987, 18108370, 263976, 60170394, 60432113, 22279002, 264563, 264685
2850	87297533 (5299, 5300)	Novel Protein sim. GBank gij5360271 (dbj BAA81908.1) - (AB029335) HRPET-3 (Halocynthia roretzi)		
2851	88088745 (5301, 5302)	Novel Protein sim. GBank gij4240225 (dbj BAA74891.1) - (AB020875) KIAA0868 protein (Homo sapiens)	Contains protein domain (PF00054) - Lamitin G domain	29331824, 29331826, 29331827, 265007, 55812038, 21908754, 18108366, 18108384, 22279002, 264587
2852	10343125 (5303, 5304)	Novel Protein sim. GBank gij4483956 (emb CAB11123.2) - (Z98551) predicted using hexExon; MAL3P6.28 (PFC0845c). Hypothetical protein, len: 167 aa: Similarity to model organism hypothetical proteins (C.elegans, D.melanogaster, S.cerevisiae & S.pombe). C.elegans protein ZK287.5 (TR....	UNCLASSIFIED	264682
2853	87798735 (5305, 5306)		UNCLASSIFIED	285018, 18108370, 18108387, 264566
2854	95103240 (5307, 5308)			60424179, 65274572, 56182575, 264259, 56182181, 264908, 56182435, 55811957, 35695917, 285021, 263976, 55810784, 65274791, 56182323, 83373044, 65274727
2855	91228018 (5309, 5310)	Novel Protein sim. GBank gij3875272 (emb CAB02861) - (Z81051) predicted using GeneFinder; similar to Zinc finger, C3HC4 type (RING finger); cDNA EST yk443h5.3 comes from this gene; cDNA EST yk443h5.5 comes from this gene (Caenorhabditis elegans)	transcription factor Zinc finger, C3HC4 type (RING finger)	56182575, 56181686, 264092, 264259, 56182181, 60432228, 264907, 33857402, 55812038, 21908754, 87168559, 265017, 264448, 264389, 264288, 21908765, 21908766, 21908767, 21908768, 33657109, 18108370, 264628, 55811576, 264556, 264639, 83373044, 56526486, 264404, 60432113
2856	84562801 (5311, 5312)	Novel Protein sim. GBank gij3043718 (dbj BAA25523) - (AB011189) KIAA0587 protein (Homo sapiens)		264693

2857	52561728 (5313, 5314)	Novel Protein sim. GBank gi 5689509 dbj BAA83038.1 - (AB029009) KIAA1086 protein [Homo sapiens]		dna_rna_bind	284693
2858	80602454 (5315, 5316)	Novel Protein sim. GBank gi 3688089 (AC005757) - R3281.1_1 [Homo sapiens]	Contains protein domain (PF00560) - Leucine Rich Repeat	nucleaseinhib	35696286, 264259, 29331822, 29331824, 29331826, 29331828, 265019, 264683, 21908788, 35695917, 284693, 35695855, 284637, 87168518, 264486, 264567
2859	87600765 (5317, 5318)	Novel Protein sim. GBank gi 5420387 emb CAB46879.1 - (AJ243459) proteophosphoglycan [Leishmania major]	Contains protein domain (PF01426) - BAH domain	UNCLASSIFIED	284909, 264910, 265018, 264369, 264769, 21908789, 284693, 263972, 18108388
2860	91718472 (5319, 5320)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7 - HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	Contains protein domain (PF00038) - EF hand	kinase	284488, 65274572, 35696286, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331826, 35696052, 264908, 56182435, 265008, 265009, 60433356, 264594, 265010, 265018, 55811150, 18108351, 264682, 264684, 264369, 264288, 264687, 21908765, 29148784, 35695917, 60170615, 52644150, 33657023, 33657109, 35696423, 35695855, 264556, 60170394, 18108385, 22278000, 22278002
2861	95342817 (5321, 5322)	Novel Protein sim. GBank gi 4758048 ref NP_004739.1 pCPR8 - cell cycle progression 8 protein		glycoprotein	60432049, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 284905, 264909, 264593, 33109954, 265010, 265017, 265018, 265019, 284760, 264448, 264369, 264288, 21908765, 21906768, 265022, 284691, 33657023, 27486282, 60431528, 18108374, 35695855, 18108388, 264482
2862	80228739 (5323, 5324)	Novel Protein sim. GBank gi 3874714 emb CAA91263 - (Z68494) similar to choline dehydrogenase, cDNA EST yk346d5.5 comes from this gene; cDNA EST yk346d5.3 comes from this gene [Caenorhabditis elegans]		dehydrogenase	264555, 264556, 264558, 264486
2863	87780823 (5325, 5326)	Novel Protein sim. GBank gi 5106958 gb A039908.1 AF113615 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]	Contains protein domain (PF00008) - EGF-like domain		284908, 264909, 264757, 264758, 264767, 284691, 33657023, 264638
2864	85518329 (5327, 5328)	Novel Protein sim. GBank gi 1369670 (U58977) - Notch homolog Scalloped wings [Lucilia cuprina]		oncogene	35696286, 264509, 264595, 264288, 264685, 264686
2865	67770662 (5328, 5330)	Novel Protein sim. GBank gi 4884408 emb CAB43311.1 - (AL050190) hypothetical protein [Homo sapiens]		UNCLASSIFIED	284906, 264907, 264908, 264510, 264511, 284512, 264593, 60433438, 265019, 284681, 21908765, 21908766, 21908767, 21908768, 265020, 265022, 35696423, 35695855, 22279002, 264482, 264488
2866	87828472 (5331, 5332)	Novel Protein sim. GBank gi 5106958 gb A039908.1 AF113615 - (AF113615) FH1/FH2 domain-containing protein FHOS [Homo sapiens]		UNCLASSIFIED	29331825, 265007, 264910, 60432229, 265019, 264288, 21906767, 264558, 22279002
2867	87422720 (5333, 5334)	Novel Protein sim. GBank gi 2500570 sp Q17533 RNPH_CAEEL - RIBONUCLEASE PH-LIKE PROTEIN B0584.1	Contains protein domain (PF01138) - 3' exoribonuclease family	nuclease	284907, 29331830, 264681, 264683, 264288, 35695855, 264632, 264556, 264557, 264558, 264559, 264563, 264565, 264567

2668	91216716 (5335, 5336)	Novel Protein sim. GBank gi15454186 ref NP_006327.1 pZYG - ZYG homolog	UNCLASSIFIED	56181686, 35696286, 22278998, 22278999, 56182181, 29331824, 60424299, 29331825, 35696052, 29331828, 68712502, 56182435, 60433356, 284758, 21906754, 55811386, 265011, 87168559, 265017, 265019, 55811150, 284448, 284369, 284288, 21906765, 21906768, 21906768, 55811957, 35695917, 265020, 265021, 33657023, 284682, 33657109, 35695763, 60431528, 18106374, 35698423, 55811578, 264634, 60431850, 83373044, 18108385, 87168518, 22278000, 284563, 264564
2669	95415721 (5337, 5338)	Novel Protein sim. GBank gi12147012 pir JC4899 - proline rich protein - rat		284489, 264688, 21906767, 65274572, 56182575, 21906768, 29148827, 21906769, 29148829, 35696286, 35695917, 22278998, 22278998, 265021, 265022, 60170815, 52644150, 60432049, 264259, 264691, 33657023, 284682, 29331822, 29331824, 29331825, 60432289, 33657109, 29331828, 29331827, 35696052, 29331828, 29146488, 29146499, 284905, 284908, 52644045, 284909, 58182435, 35698423, 65274781, 35695855, 265006, 284910, 264635, 60432229, 264592, 264638, 56182323, 60433356, 60170394, 60433438, 264559, 264595, 55812038, 33109954, 87168559, 60432113, 265019, 264448, 264369, 264684, 264288
2670	87613234 (5339, 5340)	Novel Protein sim. GBank gi1723523 sp Q10362 YDDB_SCHPO - HYPOTHETICAL 84.9 KD PROTEIN C2E12.11C IN CHROMOSOME 1		18108370, 263974
2671	91214936 (5341, 5342)	Novel Protein sim. GBank gi14768277 gb AAD29444.1 AF064255 - (AF064255) very long-chain acyl-CoA synthetase homolog 2; VLCS-H2 [Homo sapiens]	transport	52646842, 56994075, 264259, 29331822, 29331824, 29331825, 29331827, 33656970, 264509, 265006, 33109954, 21906754, 264682, 284288, 265021, 33657023, 33657109, 33657182, 27486281, 27486282, 27486285, 18108378, 18108385
2672	87399123 (5343, 5344)	Novel Protein sim. GBank gi14966348 gb AAD34677.1 AC00634 - (AC00634) Contains two PF01344 Kelch motif domains. [Arabidopsis thaliana]	UNCLASSIFIED	284767

2873	87430748 (5345, 5346)	Novel Protein sim. GBank gi 5457337 emb CAB41505.2 - (AJ236876) poly(ADP-ribose) polymerase-2 [Homo sapiens]	Contains protein domain (PF00644) - polymerase Poly(ADP-ribose) polymerase catalytic region.	22278995, 22278996, 22278997, 22278999, 29331822, 29331824, 29331828, 35696052, 60433438, 87168474, 87168559, 265017, 265018, 265019, 264448, 21908768, 21908769, 265020, 265021, 33657109, 27486262, 35695763, 60431850, 60170394, 87168518, 264563
2874	94847721 (5347, 5348)	Novel Protein sim. GBank gi 4768824 ref NP_004280.1 pNRF3 - nuclear factor (erythroid-derived 2)-like 3	Contains protein domain (PF00170) - bZIP transcription factor	264468, 22278996, 35696286, 264091, 264239, 29331824, 29331826, 35696052, 264511, 55812038, 85658542, 264766, 21906765, 35695917, 264629, 35696423, 18108383, 87168518
2875	79563835 (5349, 5350)		UNCLASSIFIED	264691
2876	78628983 (5351, 5352)		UNCLASSIFIED	264906, 265008
2877	94329600 (5353, 5354)	Novel Protein sim. GBank gi 1079042 pir S52154 - acetyl-CoA synthetase - fruit fly (Drosophila melanogaster)	Contains protein domain (PF00501) - AMP-binding enzyme synthase	18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278996, 35696286, 22278997, 22278999, 264480, 264259, 52645080, 29331824, 29331825, 60432289, 29331827, 29331828, 35696052, 29146499, 29331830, 264908, 52644045, 265008, 265007, 265008, 265009, 60432229, 60433356, 60433438, 55812038, 265010, 265011, 87168559, 265017, 265019, 18108351, 264682, 264448, 264683, 264288, 21906765, 21906766, 21906767, 21906768, 21908769, 55811957, 265020, 265021, 60170615, 52644150, 264691, 33657023, 263967, 33657109, 27486264, 27486265, 33657349, 35695763, 18108370, 18108374, 18108377, 55811578, 35698423, 35695855, 83373044, 18108387, 22279000, 22278002, 264564

2678	95001694 (5355, 5356)	Novel Protein sim. GBank gi 86780 pir A0485 - alanine transaminase (EC 2.6.1.2), cytosolic - human		UNCLASSIFIED	264488, 263994, 264489, 18108394, 52846842, 35696286, 22278999, 264259, 29331825, 35696052, 284508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264511, 265008, 264512, 265007, 265008, 264910, 265009, 264593, 264594, 264596, 264758, 33109954, 52646317, 21906754, 265010, 265011, 87188559, 264600, 264601, 264602, 264603, 265017, 265019, 264605, 264760, 264762, 18108351, 264763, 264882, 264683, 264784, 264288, 264766, 264687, 264768, 264769, 264689, 21906765, 21906767, 35695917, 265020, 265021, 52644150, 264691, 33657023, 264693, 18108364, 18108365, 33657109, 33657349, 264628, 18108374, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264555, 264636, 264637, 264638, 264639, 18108385, 264563, 264564, 264565, 264566, 264486, 264567
2679	95361544 (5357, 5358)	Novel Protein sim. GBank gi 1709233 sp P07514 NCSSR_BOVIN - NADH-CYTOCHROME B5 REDUCTASE	Contains protein domain (PF00970) - FAD/NAD-binding Cytochrome reductase	reductase	264488, 22278996, 35696286, 264259, 29331826, 29331827, 29331828, 264909, 56182435, 264113, 264511, 265008, 60433438, 264758, 85658542, 87168474, 265011, 265017, 265019, 264288, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 264690, 33657023, 55810764, 35696423, 55811576, 264631, 18108381, 60170394, 83373044, 87168518, 264568, 264259, 264102, 264905, 264908, 265007, 265008, 33109954, 265011, 18108351, 264768, 33657023, 20281149, 263972, 264630, 264635, 264638
2680	87800356 (5359, 5360)	Novel Protein sim. GBank gi 4586604 db BAA76824.1 - (AB023187) KIAA0980 protein (Homo sapiens)	Contains protein domain (PF00036) - EF hand	struct	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264784, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2681	90933644 (5361, 5362)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		kinase	264489, 22278995, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 265008, 264512, 264910, 264594, 60433438, 264758, 264603, 264604, 265019, 264605, 264760, 264784, 264687, 264768, 264769, 21906769, 35695917, 265020, 33657023, 264631, 264635, 264637, 264638, 264639, 264486
2682	94138934 (5363, 5364)	Novel Protein sim. GBank gi 423468 pir JQ1974 - HTF9-C protein - mouse	Contains protein domain (PF00076) - RNA recognition motif, (a.k.a. RRM, RBD, or RNP domain)	UNCLASSIFIED	35696286, 264908, 55811386, 265017, 55811150, 55811957, 35695917, 60431528, 55810764, 55811576, 35696423, 65274791, 58528486
2683	87774405 (5365, 5366)	Novel Protein sim. GBank gi 5114351 gb AAD40286.1 - (AF156271) RING finger protein terf [Homo sapiens]	Contains protein domain (PF00622) - SPRY domain	interleukinrecept	264909, 264769, 264035, 264638

2684	85787151 (5367, 5368)	Novel Protein sim. GBank gl 4886489 emb CAB43385.1 - (AL050284) hypothetical protein [Homo sapiens]			264593
2685	68054289 (5369, 5370)	Novel Protein sim. GBank gl 3342728 (AC005331) - R31341_2 [Homo sapiens]	UNCLASSIFIED		
2686	67626690 (5371, 5372)	Novel Protein sim. GBank gl 4650844 gb BAA77027.1 - (AB026190) Kelch motif containing protein [Homo sapiens]	Contains protein domain (PF01344) - struct Kelch motif		264259, 29331822, 60432289, 29331827, 29331830, 284909, 284512, 284596, 264769, 284534, 264555, 264556, 264557, 264558, 60170394, 284559, 284488
2687	87988183 (5373, 5374)	Novel Protein sim. GBank gl 5281314 gb AAD41475.1 AF133123 - transcription factor IIC102 [Homo sapiens]	Contains protein domain (PF00515) - TPR Domain	transcriptfactor	18108394, 18108398, 22278996, 35696286, 22278997, 29331826, 29331828, 68712502, 21906754, 265011, 264760, 284761, 264763, 284689, 21906765, 35696423, 264559, 18108385, 284563
2688	79859584 (5375, 5376)	Novel Protein sim. GBank gl 3880023 emb CAA97339 - (Z73088) Similarity to yeast hypothetical protein (Swiss Prot accession number Q08685); cDNA EST EMBL:D72982 comes from this gene; cDNA EST EMBL:D75947 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00560) - Leucine Rich Repeat		264908, 264760
2689	94122440 (5377, 5378)	Novel Protein sim. GBank gl 2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	22278997, 22278998, 22278999, 29331824, 35696052, 264908, 284908, 56182435, 284512, 284910, 285009, 60433438, 21906754, 18108351, 284682, 284683, 284767, 21906765, 21906766, 21906768, 33657023, 33657102, 27486262, 27486264, 33657349, 18108370, 18108372, 18108374, 35696423, 35695855, 18108385, 22279002
2690	88003055 (5379, 5380)	Novel Protein sim. GBank gl 2477513 (AC002398) - F25965_3 [Homo sapiens]	Contains protein domain (PF00620) - RhoGAP domain	struct	
2691	91219241 (5381, 5382)	Novel Protein sim. GBank gl 4107276 emb CAA67130 - (X8506) acyl-CoA synthetase [Solanum tuberosum]		synthase	65274572, 56182575, 264259, 29331822, 29331824, 29331826, 29331828, 264112, 265009, 55812038, 264596, 33109954, 265017, 264448, 264288, 264369, 264684, 21906769, 60170615, 60431528, 55810764, 264634, 264636, 264556, 264637, 22279002, 264584, 264568
2692	94111914 (5383, 5384)	Novel Protein sim. GBank gl 3513303 (AC005594) - R26984_1 [Homo sapiens]	Contains protein domain (PF00326) - Prolyl oligopeptidase family	peptidase	
2693	20438607 (5385, 5386)	Novel Protein sim. GBank gl 3122400 sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN	UNCLASSIFIED		264592 264559
2694	94111918 (5387, 5388)	Novel Protein sim. GBank gl 3122400 sp Q35682 MUG_MOUSE - MYELOID UPREGULATED PROTEIN			
2695	95345513 (5389, 5390)	Novel Protein sim. GBank gl 4972740 gb AAD34765.1 - (AF132177) unknown [Drosophila melanogaster]		collagen	35696288, 56994075, 22278999, 264259, 35696052, 29331830, 265011, 264288, 56181562, 264690, 264692, 33657023, 27486262, 263976, 18108376, 35696423, 35695855, 60170394, 83373044, 56526486, 22279000, 22279002, 264568
2696	87674040 (5391, 5392)	Novel Protein sim. GBank gl 728831 sp P39186 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		synthase	264594, 21906768, 18108370, 18108372

2697	91838472 (5393, 5394)	Novel Protein sim. GBank glj5689473dbj BAA03020.1 - (AB028991) KIAA1068 protein [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 265006, 265007, 264512, 265009, 60170831, 60433356, 264595, 264758, 87188474, 265010, 265011, 87188559, 264601, 265017, 265018, 265019, 264761, 18108351, 264448, 264288, 264766, 264688, 264689, 21906765, 21908768, 265020, 265021, 60170615, 33657109, 18108376, 35696423, 35695855, 264555, 264558, 60170394, 264559, 18108387, 56526486, 87188518, 22279002, 264583, 264482
2698	94325891 (5395, 5396)	Novel Protein sim. GBank glj841318 (U22818) - mutant sterol regulatory element binding protein-2 [Orctetulus griseus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	22278995, 35696286, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 33656970, 264906, 29331830, 264909, 52644045, 264910, 60433356, 33657402, 33109954, 265017, 265018, 285019, 264288, 21906765, 21906766, 21906767, 21906769, 29148629, 35695917, 265021, 265022, 52644150, 33657023, 33657182, 27486261, 35696423, 65274791, 264638, 60432113, 22279000
2699	87706650 (5397, 5398)	Novel Protein sim. GBank		UNCLASSIFIED	264768, 18108357, 264690, 264691
2700	94139836 (5399, 5400)	glj5174395 ref NP_006006.1 pB120 - Brain protein 120		UNCLASSIFIED	60424269, 56182435, 60432229, 60433438, 55811386, 265017, 55811150, 264448, 56181582, 55811957, 264693, 33657109, 60431528, 264629, 55810764, 55811576, 65274791, 60431850, 60432113
2701	94148584 (5401, 5402)	Novel Protein sim. GBank glj1572801 (U70854) - F38A5.1 gene product [Caenorhabditis elegans]			18108394, 52645156, 35696286, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35696052, 29331828, 29148499, 265006, 60433356, 33657402, 60433438, 264585, 33657084, 18108351, 264288, 264769, 18108359, 21906768, 35695917, 33657023, 27486261, 18108374, 18108379, 35696423, 18108382, 83373044, 18108394, 18108398, 60432113, 22279000
2702	57295368 (5403, 5404)	Novel Protein sim. GBank glj2605867 (AF030027) - 24 [Equine herpesvirus 4]		UNCLASSIFIED	29331828, 264512, 264555, 264558, 264557, 264558, 264559
2703	87649514 (5405, 5406)	Novel Protein sim. GBank glj5689399 dbj BAA02893.1 - (AB028954) KIAA1031 protein [Homo sapiens]	Contains protein domain (PF00642) - Zinc finger C-x8-C-x5-C-x3-H type (and similar)		80432289, 265007, 21906765, 21906768, 265021, 264563

2704	87649515 (5407, 5408)	Novel Protein sim. GBank gij4335894[gb]AA863284] - (AF008554) Implantation-associated protein [Rattus norvegicus]			264488, 22278995, 22278998, 29331828, 29148499, 264805, 264908, 264907, 52844045, 264511, 33857402, 264600, 264602, 265017, 264605, 264761, 18108351, 264764, 264887, 264789, 265021, 264691, 264692, 18108382, 264693, 18108370, 18108374, 264634, 264835
2705	87771745 (5408, 5410)				264489, 264508, 264511, 264512, 264910, 264593, 87168474, 264604, 264288, 264687, 264769, 264638, 264586, 264486
2706	94328789 (5411, 5412)	Novel Protein sim. GBank gij3255852[emb]CAA18621.1] - (AL021728) /prediction=(method); /match=(desc: [Drosophila melanogaster])	UNCLASSIFIED		264488, 52646842, 65274572, 22278994, 50894075, 22278997, 264259, 29331824, 29331825, 29331826, 29331828, 33856970, 264907, 264908, 264809, 52844045, 56182435, 265008, 265007, 60433438, 55812038, 21908754, 52844298, 285010, 264601, 265017, 265019, 264681, 264448, 284682, 264288, 264686, 264687, 264688, 21908766, 21908769, 55811957, 35695917, 265020, 265021, 60170615, 264690, 264691, 33857023, 264692, 264693, 65274620, 27486264, 263972, 18108374, 18108377, 264635, 264636, 264556, 60170394, 83373044, 65274727, 87168518, 22279000
2707	88089839 (5413, 5414)	Novel Protein sim. GBank gij3417284 (AC004381) - Unknown gene product [Homo sapiens]			22278996, 22278998, 56182435, 21906754, 87168559, 265017, 264448, 52845129
2708	91011351 (5415, 5416)	Novel Protein sim. GBank gij545790[bbas]147178 - DARPP-32=dopamine and cAMP-regulated phosphoprotein [human, brain, Peptide, 204 aa]	UNCLASSIFIED		65274572, 264259, 29331822, 29331825, 60432289, 29331826, 29331827, 29331828, 264909, 264510, 265007, 264910, 60433356, 60433438, 33109954, 265010, 265011, 264389, 264288, 264765, 264693, 264565
2709	94853988 (5417, 5418)	Novel Protein sim. GBank gij3169705 (AC004780) - F17127.1 [Homo sapiens]	UNCLASSIFIED		29331822, 18108370, 18108374, 83373044
2710	87627879 (5419, 5420)	Novel Protein sim. GBank gij4468311[emb]CAB37992] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]			29331824, 264759, 264693, 18108382, 18108388

2711	94111920 (5421, 5422)	Novel Protein sim. GBank gij3122400j p O358a2 J MUG_MOUSE - MYELOID UPREGULATED PROTEIN		UNCLASSIFIED	264488, 264687, 52645156, 264769, 21908784, 21908765, 21908767, 21908768, 21908769, 55811957, 56994075, 22278997, 22278998, 265020, 265021, 264690, 264259, 264691, 264692, 33657023, 29331822, 29331824, 60424269, 29331826, 33657182, 29331827, 27486262, 33657349, 284508, 264905, 264907, 60431528, 264908, 264909, 55810764, 35696423, 65274791, 35695855, 265007, 264910, 60431850, 60432229, 264557, 264558, 55812038, 33109954, 18108385, 21906754, 33657084, 87188518, 87168474, 87168559, 60432113, 265017, 22279000, 265018, 265019, 22279002, 264760, 55811150, 264681, 18108351, 264565, 264784, 264568, 264288, 264766 264488, 35696288, 22278998, 264259, 29331824, 60432289, 35696052, 264508, 264908, 66712502, 52644045, 265006, 60432229, 33657402, 60433358, 265010, 265019, 18108351, 264681, 264288, 264685, 21906765, 21906766, 21906768, 21906769, 55811957, 35695917, 265020, 265021, 60170615, 264891, 264892, 33657023, 33657109, 33657182, 33657349, 18108370, 18108374, 35696423, 35695855, 264555, 52644332, 56182323, 87188518, 60432113 66714117, 264908, 264563
2712	94312071 (5423, 5424)	Novel Protein sim. GBank gij5081315 gb AAD39343.1 AF076607 prediabetic NOD sera-reactive autoantigen [Mus musculus]	Contains protein domain (PF00515) - TPR Domain	transferase	
2713	86003084 (5425, 5428)	Novel Protein sim. GBank gij2477513 (AC002398) - F25985_3 [Homo sapiens]		UNCLASSIFIED	
2714	13528218 (5427, 5429)			UNCLASSIFIED	264636
2715	94122454 (5428, 5430)	Novel Protein sim. GBank gij4321988 gb AAD15897 - (AF067430) Smarcat1-related protein [Mus musculus]		UNCLASSIFIED	264508, 264905, 264907, 264908, 264909, 264910, 264758, 265011, 264760, 264764, 264288, 264766, 264768, 264638
2716	86003088 (5431, 5432)	Novel Protein sim. GBank gij2477513 (AC002398) - F25985_3 [Homo sapiens]		glycoprotein	264091, 264259, 29331822, 66714117,
2717	80077481 (5433, 5434)	Novel Protein sim. GBank gij3327046 gb BAA31591 - (AB014516) KIAA0818 protein [Homo sapiens]			264908, 264369, 264693, 264556, 264563 264593, 264558
2718	79604082 (5435, 5436)				264693
2719	86180423 (5437, 5438)	Novel Protein sim. GBank gij748495 (U23515) - weakly similar to gastrula zinc finger protein [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 87188559, 265019, 265021, 52644150, 264691

2720	95086242 (5439, 5440)	Novel Protein sim. GBank gi 1335873 (U46880) - ATP-dependent RNA helicase [Mus musculus]	Contains protein domain (PF00270) - DEAD/DEAH box helicase	helicase	18108374, 60424179, 264489, 56182435, 21908765, 21908766, 35698423, 22278997, 265020, 265022, 265005, 265008, 264092, 264636, 60432229, 264691, 264692, 33657023, 264693, 33657402, 83373044, 29331824, 18108366, 60424269, 29331826, 18108385, 52845129, 21906754, 35696052, 29331828, 87168474, 264100, 265010, 265011, 265019, 22278002, 264905, 264482, 264563, 264906, 18108351, 264681, 18108370, 29331830, 264908, 66712502, 32844045, 264909, 264828, 18108354
2721	95345523 (5441, 5442)	Novel Protein sim. GBank gi 4928663 gb AAD34092.1 AF15185 - (AF151855) CGI-97 protein [Homo sapiens]	Contains protein domain (PF01172) - Uncharacterized protein family UPF0023		22278995, 35698286, 264259, 29331822, 29331824, 66714117, 29331826, 264906, 60433438, 265017, 18108351, 264448, 264288, 264769, 21908766, 265021, 33657109, 263969, 60431528, 264629, 55811576, 65274791, 35695855, 264631, 264637, 60170394, 58182323, 22278000
2722	91638607 (5443, 5444)	Novel Protein sim. GBank gi 3212997 gb AAC23434.1 - (AC004987) match to ESTs AA667999 (NID:g2826700), AA165465 (NID:g1741481), Z45871 (NID:g575105), and T84026 (NID:g712314); similar to various tre-like proteins including: AF040854 (PID:g2746883), D13644 (PID:g2104571), AL02114...	Contains protein domain (PF00566) - oncogene TBC domain	oncogene	35696286, 22278999, 21906754, 265017, 264762, 264288, 21908765, 21906767, 21906768, 35695917, 18108362, 27486262, 35695855, 264558, 264559
2723	87387732 (5445, 5446)			UNCLASSIFIED	264508, 264509, 264906, 264909, 264910, 55812038, 264768, 264687, 264629, 264636, 264488
2724	87639563 (5447, 5448)	Novel Protein sim. GBank gi 4880681 gb AAD27730.1 AF13295 - (AF132955) CGI-21 protein [Homo sapiens]		ubiquitin	18108396, 22278999, 20281099, 29331824, 29331826, 60432289, 29331828, 60170831, 60432229, 60433438, 18108351, 264682, 21906766, 21908767, 21906769, 35695917, 33657023, 33657109, 18108372, 18108374, 35695855, 22279000, 22279002
2725	94853991 (5449, 5450)	Novel Protein sim. GBank gi 3169705 (AC004780) - F17127_1 [Homo sapiens]		UNCLASSIFIED	264488, 52644507, 264259, 29331827, 21908754, 285011, 18108351, 264448, 264288, 264685, 264689, 35695917, 265020, 33657182, 27486261, 18108370, 18108374, 35698423, 18108385, 22279000
2726	86880599 (5451, 5452)	Novel Protein sim. GBank gi 3342738 (AC005328) - R26860_1, partial CDS [Homo sapiens]		MHC	264488, 264828, 264685

2727	91010470 (5453, 5454)	Novel Protein sim. GBank gi 731267 sp P39219 RLUA_ECOLI - RIBOSOMAL LARGE SUBUNIT PSEUDOURIDINE SYNTHASE A (PSEUDOURIDYLATE SYNTHASE) (URACIL HYDROLYASE)	Contains protein domain (PF00849) - synthase RNA pseudouridylate synthase	65274572, 56182575, 22278994, 56994075, 22278996, 22278997, 22278999, 60432049, 29331822, 29331824, 66714117, 29331826, 29331827, 35696032, 29331828, 35696970, 264509, 66712502, 264910, 33657402, 60433438, 264758, 55812038, 21906754, 33657084, 55811388, 265018, 265019, 264767, 21906765, 21906767, 21906769, 55811957, 35695917, 52644150, 33657023, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 55811576, 35696423, 35695855, 264630, 60431850, 264638, 56182333, 87168518, 60432113, 22278000, 264564, 264565
2728	94126022 (5455, 5456)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED Mitochondrial carrier proteins	18108394, 56182435, 21906767, 55811957, 35695855, 265021, 264690, 264556, 264259, 264557, 29331822, 264559, 264448, 264288
2729	94126024 (5457, 5458)	Novel Protein sim. GBank gi 2408095 emb CAB16300 - (Z99168) putative RNA splicing protein [Schizosaccharomyces pombe]	UNCLASSIFIED Mitochondrial carrier proteins	65274572, 264259, 60432289, 66712502, 56182435, 264448, 264288, 264369, 55811957, 265021, 264557, 60432113
2730	94126026 (5459, 5460)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	transport Mitochondrial carrier proteins	264887, 29331824, 29331826, 35696032, 264107, 56182435, 265008, 265009, 264592, 60431735, 265011, 264601, 265017, 18108351, 264288, 29148627, 55811957, 265021, 264690, 18108388, 18108374, 264557, 264558, 264559, 18108387, 56526488, 264566, 264488
2731	87723022 (5461, 5462)	Novel Protein sim. GBank gi 1723239 sp Q10166 YAUB_SCHPO - HYPOTHETICAL 35.7 KD PROTEIN C26A3.1.1 IN CHROMOSOME I	Contains protein domain (PF00795) - Carbon-nitrogen hydrolase	264259, 35696032, 265006, 264758, 264762, 264448, 264288, 29148627, 21906769, 87168518, 22279002
2732	94126028 (5463, 5464)	Novel Protein sim. GBank gi 3880433 emb CAA91399 - (Z68521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL:CO9217 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED Mitochondrial carrier proteins	264687, 264489, 18108358, 56182435, 264689, 35696423, 55811957, 265021, 265006, 265008, 264910, 265009, 264690, 264555, 264259, 264556, 264557, 264558, 264559, 18108383, 33657109, 87168518, 265010, 264601, 60432113, 265017, 264905, 264448, 263972, 264389, 264567 29331825, 264509, 264809
2733	87363060 (5465, 5466)	Novel Protein sim. GBank gi 451962 db BAA75670.1 - (AB017614) OASIS protein [Mus musculus]	UNCLASSIFIED transcription factor	60424179, 52644507, 56182575, 264259, 29331828, 264907, 264510, 264910, 60433356, 265019, 55811150, 264681, 264763, 264687, 33657182, 18108370, 60431528, 60431850, 56182323, 83373044

2735	87712336 (5469, 5470)	Novel Protein sim. GBank glij3850589 (AC005278) - ESTs gbjT21276, gbjT45403, and gbjAA586113 come from this gene. [Arabidopsis thaliana]		glycoprotein	22278998, 60432289, 29331827, 29146498, 264108, 264909, 264112, 33657402, 87168474, 265017, 264762, 264448, 264764, 264684, 21906765, 264693, 33657109, 263976, 264636, 264638, 264557, 22279000, 22279002, 264567
2736	80247655 (5471, 5472)			UNCLASSIFIED	264905, 264628, 264629, 263978, 264632, 264564
2737	87604526 (5473, 5474)				264690
2738	85731808 (5475, 5476)	Novel Protein sim. GBank glij2558501[gbjBAA22896] - [D83850] hepaloma-derived growth factor. [Mus musculus]			264488, 265009, 264768, 264691
2739	94319834 (5477, 5478)	Novel Protein sim. GBank glij5420387[embjCAB46679.1] - [AJ243459] proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264684, 83373044, 264566
2740	94148762 (5479, 5480)	Novel Protein sim. GBank glij3417386[embjCAA75495] - (Y15197) microtubule-associated protein, MAP-115 [Mus musculus]		UNCLASSIFIED	264488, 56182575, 22278995, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 29146498, 29331830, 265006, 265007, 265009, 80432228, 33657402, 55812038, 87168474, 265010, 265011, 265017, 265018, 265019, 264605, 264681, 264288, 264369, 52644229, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 265022, 264691, 264692, 33657108, 18108370, 18108374, 55810764, 35695855, 264634, 80431850, 264639, 58182323, 18108382, 18108385, 65274727, 22279002, 264584
2741	98047518 (5481, 5482)	Novel Protein sim. GBank glij3242764 (AC005154) - similar to protein U28928 (PID:g881308) [Homo sapiens]		UNCLASSIFIED	22278998, 52644045, 52644229, 21906768, 21906769, 265020, 60170815, 264691
2742	87648644 (5483, 5484)	Novel Protein sim. GBank glij4758412[refjNP_004472.1]pGALN - UDP-N-acetyl-alpha-D-galactosamine:polypeptide N-acetyltransferase 2 (GALNAc-T2)	Contains protein domain (PF00652) - Similarity to lectin domain of ricin beta-chain, 3 copies.	transferase	264259, 264805, 264758, 55812038, 264369, 29148627
2743	87827991 (5485, 5486)	Novel Protein sim. GBank glij4468311[embjCAB37892] - (AL031432) dJ465N24.2.1 (PUTATIVE novel protein) (isoform 1) [Homo sapiens]		UNCLASSIFIED	35696286, 264259, 264908, 264908, 265006, 80433438, 265017, 18108351, 264448, 264764, 264288, 21906765, 21906767, 264690, 264691, 264693, 263969, 263971, 35695855, 264637, 264558, 18108382, 80432113
2744	94126030 (5487, 5488)	Novel Protein sim. GBank glij3880433[embjCAA91399] - (Z86521) similar to mitochondrial RNA splicing MSR4 like protein; cDNA EST EMBL.C09217 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00153) - Mitochondrial carrier proteins	kinase	18108374, 264488, 56182435, 21906765, 35696423, 35695917, 35695855, 265020, 265021, 264511, 265009, 264490, 264556, 264259, 264557, 56182323, 264558, 264559, 18108383, 29331824, 18108385, 33657109, 29331828, 21906754, 29331827, 29331828, 33657349, 87168518, 265018, 264905, 284482, 264448, 264486, 264369, 264288

2745	87740125 (5489, 5490)	Novel Protein sim. GBank gi 4405795 gb AAD19826 - (AF038863) RNA helicase [Homo sapiens]	Contains protein domain (PF00271) - helicase domain Helicases conserved C-terminal domain	35698286, 284509, 284905, 284807, 284908, 284909, 284510, 284512, 265008, 264758, 284801, 285017, 284604, 284783, 264288, 264886, 284769, 284693, 35698423, 35695855, 284634, 284636, 284563, 284564, 284565
2746	95418601 (5491, 5492)	Novel Protein sim. GBank gi 4758738 ref NP_004680.1 pMTA1 - metastasis associated 1	Contains protein domain (PF00320) - GATA zinc finger	22278996, 22278998, 22278999, 29331822, 29331826, 29331827, 35696052, 29331828, 264905, 284908, 284807, 284908, 284909, 52644045, 265008, 60170831, 264596, 55812036, 265018, 284683, 264288, 21908765, 21906767, 21906768, 21906769, 285020, 284690, 33657023, 284693, 33857109, 18108368, 18108374, 264558, 18108385, 22278000, 264563
2747	94112877 (5493, 5494)	Novel Protein sim. GBank gi 4557803 ref NP_000262.1 pNPC1 - Niemann-Pick disease, type C1	glycoprotein	284569, 52644507, 18108394, 22278995, 35696286, 22278997, 22278999, 52645080, 29331824, 56182181, 29331826, 29331827, 35696052, 264907, 284908, 284909, 265009, 33109954, 55811386, 87188474, 265010, 87188559, 264603, 265019, 264760, 264686, 264768, 21908789, 35695917, 60170615, 264692, 33657023, 52645129, 27486264, 60431528, 18108374, 35698423, 35695855, 264556, 58182323, 18108385, 264482
2748	91214983 (5495, 5496)	Novel Protein sim. GBank gi 4191272 emb CAA09984 - (AJ012295) apaG protein [Rhizobium etli]	Contains protein domain (PF00646) - F-box domain.	65274572, 29331828, 284112, 284511, 285019, 284760, 264767, 264768, 264789, 21906768, 21906769, 285020, 27486262, 56526486, 87188518, 22278000
2749	97346307 (5497, 5498)			264239, 284908, 284510, 265008, 285009, 264760, 264369, 264768, 264563
2750	87336344 (5499, 5500)	Novel Protein sim. GBank gi 1872498 U74297 - PIUS [Oryctolagus cuniculus]	UNCLASSIFIED	264488, 52644507, 18108396, 56994075, 264259, 29331825, 29331826, 29331827, 29331828, 264508, 265009, 264910, 264591, 284595, 33657084, 265011, 285019, 18108351, 264288, 284686, 264769, 264689, 55811957, 284693, 27486264, 18108370, 18108374, 284558, 18108385, 264482, 264563
2751	87057465 (5501, 5502)		UNCLASSIFIED	29331822, 29331824, 265017, 33657023
2752	88062675 (5503, 5504)	Novel Protein sim. GBank gi 3041859 AC004534 - OG-2 homeodomain protein-like; similar to U65067 (PID:gi1575526) [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	

2753	941138972 (5505, 5508)	Novel Protein sim. GBank gij3851648 (AF098301) - neural F-box protein NFB42 [Rattus norvegicus]	Contains protein domain (PF00646) - F-box domain.	UNCLASSIFIED	58182575, 58994075, 22278998, 29331822, 29331824, 29331825, 29331826, 265007, 264593, 55812038, 33109954, 18108351, 284288, 58181562, 21908767, 21908788, 265021, 264693, 18108374, 65274791, 284632, 58182323, 22278002, 264583, 264587
2754	94115513 (5507, 5508)	Novel Protein sim. GBank gij53428 (U13736) - calmodulin-like protein [Plum salinum]	Contains protein domain (PF00036) - EF hand	struct	22278999, 66714117, 29331827, 35886052, 29331828, 264808, 264908, 264909, 285011, 265017, 265018, 265019, 264288, 21908765, 21908767, 285022, 33657023, 264693, 58182323, 18108382, 22278000
2755	88001472 (5508, 5510)	Novel Protein sim. GBank gij2998653 (AC004510) - R30385_2 [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcriptfactor	
2756	11465808 (5511, 5512)			UNCLASSIFIED	264594
2757	85381590 (5513, 5514)	Novel Protein sim. GBank gij1173538 (U30473) - putative src-like adapter protein; non-catalytic src-like adapter protein containing SH3 and SH2 domains; homolog of mouse SLAP; Method: conceptual translation supplied by author [Homo sapiens]	Contains protein domain (PF00017) - Src homology domain 2	eph	85658542, 264693
2758	79637846 (5515, 5516)	Novel Protein sim. GBank gij3608372 (AF053786) - brain specific cortactin-binding protein CBP90 [Rattus norvegicus]		struct	264693
2759	81005312 (5517, 5518)	Novel Protein sim. GBank gij2072200 (U84863) - p40 [Borna disease virus]			65274572, 35696286, 66714117, 29331828, 284508, 58182435, 21908754, 55811957, 284628, 264636, 58182323, 22279002
2760	79824798 (5519, 5520)			UNCLASSIFIED	264908
2761	87639597 (5521, 5522)	Novel Protein sim. GBank gij4814573 (emb) CAB-3885.1 - (AL050390) hypothetical protein [Homo sapiens]	Contains protein domain (PF00023) - Ank repeat	nuclease	22278998, 29331822, 29331830, 265010, 285019, 264288, 21908765, 21908768, 21908769, 265020, 58182323, 22279002, 264563
2762	87582698 (5523, 5524)	Novel Protein sim. GBank gij3136150 (AF050182) - PERIOD 3 [Mus musculus]	Contains protein domain (PF00989) - PAS domain	struct	18108394, 22278998, 264806, 264809, 285008, 285007, 284757, 265010, 285011, 265017, 265018, 18108351, 264448, 264683, 284686, 264768, 265020, 265021, 265022, 264691, 18108362, 264693, 18108385, 33657109, 18108388, 18108370, 18108381, 18108382, 18108384, 18108388, 87168518, 264369, 35696423
2763	87539888 (5525, 5526)	Novel Protein sim. GBank gij3511122 (AF060503) - zinc finger protein [Homo sapiens]	Contains protein domain (PF01352) - KRAB box	transcriptfactor	
2764	94305140 (5527, 5528)	Novel Protein sim. GBank gij2905843 (AF045244) - ribitol kinase [Klebsiella pneumoniae]	Contains protein domain (PF00370) - FOGY family of carbohydrate kinases		52648842, 264259, 29331822, 29331825, 29331826, 29331828, 33658970, 284905, 284907, 29331830, 285006, 265009, 21908754, 265019, 264448, 21908769, 27486282, 58182323, 58526486, 87168518, 264487

2765	94315105 (5529, 5530)	Novel Protein sim. GBank gl 4698672 emb CAA17688.2 - (AL022016) /prediction=(method:; /prediction=(method:; /match=(desc: [Drosophila melanogaster])			264488, 65274572, 22278995, 35698286, 22278998, 22278999, 264259, 29331822, 29331824, 35698052, 264508, 264509, 264905, 264908, 264907, 264908, 264909, 264512, 264910, 265009, 264592, 264595, 264798, 55912038, 33109954, 265010, 87168558, 264600, 265018, 264760, 264761, 264762, 264763, 264448, 264764, 264288, 264766, 264767, 264768, 56181562, 21908764, 21908765, 21908768, 35698917, 285021, 264681, 264682, 33657023, 33657109, 264628, 18108370, 264629, 18108374, 55811576, 35698423, 35698555, 264631, 264634, 264635, 264636, 264637, 264638, 264558, 264839, 83373044, 87168518, 22279000, 22279002, 264563, 264482
2766	94315109 (5531, 5532)	Novel Protein sim. GBank gl 5441611 emb CAB46854.1 - (AJ388555) hypothetical protein [Canis familiaris]	Contains protein domain (PF00076) - RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)	dna_ma_bind	264488, 65274572, 60432289, 264907, 264909, 264511, 264512, 60433356, 264288, 264885, 264688, 35698917, 265022, 264693, 264628, 65274791, 264635, 264555, 264558, 264557, 264638, 264558, 264559, 83373044, 60432113
2767	80204297 (5533, 5534)	Novel Protein sim. GBank gl 1079451 pir A55463 - tropomodulin, skeletal muscle - chicken		struct	264112, 263974, 264558
2768	94322238 (5535, 5538)	Novel Protein sim. GBank gl 5441322 emb CAB4672.1 - (AL031427) dJ167A19.1 (novel protein) [Homo sapiens]		UNCLASSIFIED	264488, 263994, 264489, 35698286, 22278998, 22278999, 264259, 29331822, 60432289, 29331826, 35698052, 264508, 264509, 264905, 264908, 264907, 29331830, 264908, 264909, 264510, 264511, 264512, 265008, 264810, 265009, 264591, 264592, 264593, 33657402, 264594, 264595, 264757, 264596, 265011, 264604, 265018, 264760, 264681, 18108351, 264764, 264288, 264766, 264688, 264768, 18108357, 264769, 264689, 21908768, 21908769, 21908769, 35698917, 265021, 265022, 33657023, 33657109, 264628, 264629, 18108374, 35698423, 35698555, 264630, 264631, 264632, 264634, 264635, 264636, 264555, 264638, 264639, 83373044, 264563, 264564, 264565, 264566, 264489, 264567

2769	95311088 (5537, 5538)	Novel Protein sim. GBank gl 5419859 emb CAB46375.1 - (AL088725) hypothetical protein [Homo sapiens]		Iubulin	264488, 56182575, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 264908, 29331830, 56182435, 264592, 33657402, 264448, 264369, 264288, 60170615, 264891, 33657023, 264692, 33657109, 18108374, 55811576, 264834, 264836, 56182323, 83373044, 60432113, 18108398, 22278995, 22278996, 22278999, 264105, 265006, 265019, 18108351, 264687, 21908765, 18108364, 264629, 18108374, 264631, 18108385, 18108388
2770	87730182 (5539, 5540)	Novel Protein sim. GBank gl 5701865 emb CAB52157.1 - (AL108736) WD repeat protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	264259, 29331822, 29331824, 29331825, 264389
2771	98084071 (5541, 5542)	Novel Protein sim. GBank gl 3093433 (AC004125) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 29331824, 66714117, 60432289, 29331827, 264905, 265009, 264592, 55812038, 65274444, 264768, 21908769, 33657109, 263978, 264555, 264638, 264557, 83373044, 264563, 264564, 264486
2772	95357309 (5543, 5544)	Novel Protein sim. GBank gl 4885531 ref NP_005465.1 p NY C - histone deacetylase 5	Contains protein domain (PF00850) - Histone deacetylase family	histone	18108374, 264686, 264687, 263976, 56182435, 264889, 55810764, 21906766, 35696423, 55811576, 65274791, 56181886, 55811957, 35695855, 264110, 265021, 264112, 265022, 265008, 265008, 264092, 264094, 60431850, 264637, 264691, 264259, 264692, 263981, 264594, 60433356, 56182323, 264693, 264757, 56182181, 55812038, 29331825, 60424269, 18108385, 29331826, 29331827, 27466261, 29331828, 35696052, 55811386, 264107, 60432113, 265017, 55811150, 18108351, 264681, 264908, 18108370, 264484, 264682, 20281069, 264448, 66712502, 264683, 264764, 264288, 264684, 264768, 263974, 22278995, 35696286, 22278996, 22278999, 264259, 29331826, 60432289, 35696052, 264112, 33657402, 21908754, 87168559, 265017, 265018, 264288, 21906768, 21908767, 21906769, 35695917, 265020, 265021, 33657023, 33657109, 18108370, 263976, 35696423, 35695855, 87168518, 22278999, 264482
2773	94138994 (5545, 5546)	Novel Protein sim. GBank gl 3288888 (AC005253) - R28445_1 [Homo sapiens]		UNCLASSIFIED	
2774	87618908 (5547, 5548)	Novel Protein sim. GBank gl 465852 sp P34388 YLS3_CAEEL - HYPOTHETICAL 70.7 KD PROTEIN F09G8.3 IN CHROMOSOME III	Contains protein domain (PF00380) - Ribosomal protein S9/S16	ribosomalprot	

2775	95307987 (5549, 5550)	Novel Protein sim. GBank gi 4688132 gb AAD27775.1 AF07704.2 30S ribosomal protein S7 homolog [Homo sapiens]	Contains protein domain (PF00177) - ribosomal prot Ribosomal protein S7p/S5e	264488, 22278985, 56994075, 22278986, 35699286, 22278998, 22278999, 264258, 29331822, 29331824, 29331825, 60432289, 29331827, 29331828, 35698052, 265007, 21908754, 265017, 265019, 264448, 264682, 264389, 264288, 18108354, 52644228, 264689, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 60170615, 264691, 18108370, 35696423, 65274791, 35695855, 264634, 60431850, 60170394, 56182323, 264558, 18108388, 22279000, 264563, 264565, 264486, 264567
2776	87701557 (5551, 5552)			56182575, 22278998, 22278999, 264259, 29331822, 29331824, 264908, 29331830, 264510, 33657402, 21908754, 55811386, 265017, 265019, 264448, 264288, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 265022, 60170615, 55810764, 55811578, 264555, 56526486, 22279000
2777	79818729 (5553, 5554)		UNCLASSIFIED	264907, 264766
2778	82112411 (5555, 5556)		UNCLASSIFIED	264907, 264593, 264760, 264628
2779	87649729 (5557, 5558)	Novel Protein sim. GBank gi 4680711 gb AAD27745.1 AF13297 - (AF13297) CGI-36 protein [Homo sapiens]	UNCLASSIFIED	2278997, 264259, 29331824, 66714117, 35698052, 265006, 264512, 264448, 264288, 29148827, 18108364, 20281149, 18108370, 264629
2780	94878397 (5559, 5560)	Novel Protein sim. GBank gi 4758524 ref NP_004825.1 pHGX - HPK/GCK-like kinase	Contains protein domain (PF00780) - Kinase GNH domain	29146499, 65274791, 264634, 264639
2781	91220057 (5561, 5562)	Novel Protein sim. GBank gi 4469352 gb AAD21222 - (AF089502) ubiquitin specific protease UBP43 [Mus musculus]	Contains protein domain (PF00443) - Ubiquitin carboxyl-terminal hydrolase family 2	60424178, 29331824, 60424269, 66714117, 29331826, 56182435, 87168474, 265017, 264764, 58181562, 21908765, 21908768, 21908768, 35695917, 265020, 33657023, 35695855, 56182323, 87168518
2782	94233146 (5563, 5564)	Novel Protein sim. GBank gi 4505013 ref NP_002310.1 pLRN - leucine-rich neuronal protein	Contains protein domain (PF00560) - struct Leucine Rich Repeat	55274572, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331826, 60432289, 29331828, 264905, 264907, 264908, 264909, 52644045, 265009, 265017, 265018, 264604, 265019, 264780, 264683, 264288, 264766, 264685, 264686, 264768, 52644229, 264689, 21908768, 265020, 265021, 264691, 18108362, 264692, 33657023, 264693, 33657109, 33657349, 18108370, 264628, 263978, 35695855, 264557, 56182323, 83373044, 18108385

2783	80016829 (5565, 5568)	Novel Protein sim. GBank gij728831[sp]P39188[ALU1_III J WARNING ENTRY IIII		tm7	264809, 264628, 263978, 263981
2784	87614360 (5567, 5568)				264259, 29331822, 29331824, 29331825, 264482
2785	88071930 (5569, 5570)	Novel Protein sim. GBank gij2134933[pri]S58890 - collapsin response mediator protein - human		UNCLASSIFIED	22278999, 264908, 264758, 265018, 264769, 21906765, 21906768, 21906769, 265020, 264564
2786	87408542 (5571, 5572)	Novel Protein sim. GBank gij2073564 (U80223) - eukaryotic initiation factor eIF-2 alpha kinase; DGCN2 [Drosophila melanogaster]	Contains protein domain (PF00089) - Eukaryotic protein kinase domain	kinase	264905, 265017
2787	87901268 (5573, 5574)	Novel Protein sim. GBank gij5174507[re]NP_006020.1[pMA1] - paraneoplastic neuronal antigen		UNCLASSIFIED	264768, 21906765, 21906768, 55811957, 22278999, 264093, 60170815, 264259, 29331822, 18108365, 29331824, 33657109, 29331827, 35696052, 264100, 264105, 264908, 263977, 55811576, 264635, 264637, 60433438, 60432113, 265017, 265019, 22279002, 55811150, 264369, 264288
2788	88080844 (5575, 5576)	Novel Protein sim. GBank gij3252826 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
2789	85491275 (5577, 5578)	Novel Protein sim. GBank gij2495729[sp]Q92556[Y281_HUMAN - HYPOTHETICAL PROTEIN KIAA0281 (HA6725)]		UNCLASSIFIED	264103, 21906769, 264693
2790	87602784 (5579, 5580)	Novel Protein sim. GBank gij510172[emb]CAB45135.1] - (AJ242978) p821 [Homo sapiens]		struct	264488, 264769, 264910, 264631, 264636, 264690, 264691, 264258, 264638, 29331824, 264508, 264509, 264905, 264563, 264906, 264628, 18108370, 264907, 264784, 264908, 264288, 264909
2791	88083195 (5581, 5582)	Novel Protein sim. GBank gij2911266 (AC002550) - Unknown gene product [Homo sapiens]			21906764, 18108368
2792	85083783 (5583, 5584)	Novel Protein sim. GBank gij2654163[gb]AAC02581.1] - (AF045642) No definition line found [Caenorhabditis elegans]			22278996, 22278997, 264259, 29331822, 29331824, 29331825, 66714117, 29331826, 60432289, 29331827, 35696052, 264906, 66712502, 29331830, 264909, 60432229, 60433356, 60433438, 33109954, 265010, 265011, 265017, 265018, 265019, 264682, 264448, 264288, 264369, 264768, 52644229, 21906765, 21906768, 265020, 265021, 33657023, 263974, 18108374, 65274781, 35695855, 264638, 264556, 264558, 56182323, 83373044, 18108385, 56526488, 60432113, 22279000, 264567
2793	87425476 (5585, 5586)			UNCLASSIFIED	264259, 60432289, 66712502, 265009, 264636
2794	85794830 (5587, 5588)			UNCLASSIFIED	264699, 265022, 264691, 18108388, 264567

2785	85334888 (5588, 5590)	Novel Protein sim. GBank gi 5454148 ref NP_006348.1 pUBE2 - ubiquitin-conjugating enzyme E2E 3 (homologous to yeast UBC4/5)	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	65274572, 56182575, 35698288, 22278998, 22278999, 60432049, 264259, 29331822, 29331825, 66714117, 60432289, 29331828, 29331827, 35698052, 29331828, 264907, 66712502, 56182435, 264511, 265007, 264512, 264910, 60432229, 60433356, 60433438, 33109954, 85658542, 265018, 265019, 264288, 264886, 21908764, 21908765, 21908768, 21908768, 21908769, 55811957, 265020, 265021, 265022, 52644150, 33657023, 264693, 65274620, 33657109, 35696423, 55811576, 65274791, 56182323, 56526486, 60432113, 22279002, 264482, 264563, 264484, 264567
2786	94848857 (5591, 5592)	Novel Protein sim. GBank gi 4680651 gb AAD27715.1 AF132940 - (AF132940) CGI-06 protein [Homo sapiens]		UNCLASSIFIED	18108394, 65274572, 56182575, 56994075, 22278999, 264480, 60432049, 264259, 29331822, 29331824, 29331826, 35696052, 264509, 264908, 264907, 264908, 66712502, 56182435, 264510, 265006, 264512, 265007, 265008, 264910, 265009, 264591, 264592, 60433358, 264594, 264595, 55812038, 264598, 21908754, 60174639, 87168474, 265010, 265011, 265017, 265018, 265019, 55811150, 264782, 18108351, 264448, 264682, 264369, 264288, 264685, 264766, 264687, 56181562, 264769, 264689, 21908765, 21908768, 21908767, 21908768, 21908769, 55811957, 35695917, 265020, 265021, 60170615, 52644150, 264692, 33657023, 18108362, 264693, 65274620, 33657109, 33657182, 27486265, 33657349, 18108374, 35696423, 65274781, 35695855, 264556, 264557, 56182323, 264558, 60170394, 83373044, 65274727, 87168518, 22279000, 264563, 264564, 264565, 264566, 264567
2787	95110780 (5593, 5594)	Novel Protein sim. GBank gi 4838557 gb AAD31040.1 - (AF143859) potassium channel modulatory factor DEBT-91 [Mus musculus]	Contains protein domain (PF00569) - Zinc finger present in dystrophin, CBP/p300	UNCLASSIFIED	56182575, 22278995, 22278996, 22278997, 29331827, 26146499, 264509, 264508, 56182435, 264757, 21908754, 265010, 265017, 265019, 264681, 264682, 264683, 264688, 21908765, 21908767, 21908768, 21908769, 26146829, 265020, 52644150, 264690, 33657182, 264629, 18108376, 56182323, 22279002, 264563
2788	88198005 (5595, 5596)	Novel Protein sim. GBank gi 2852645 (AF007160) - unknown [Homo sapiens]		UNCLASSIFIED	264486, 264490, 264259, 264448, 20281149, 20281152, 264556, 264557, 264558, 264559, 264483, 264489, 264567

2799	88090851 (5597, 5598)	Novel Protein sim. GBank gi 3252825 (AC004382) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	22278996, 22278997, 22278998, 22278999, 60432048, 264259, 29331828, 35696052, 29331828, 264909, 60433356, 33657402, 33108954, 87168474, 264448, 52844229, 21908766, 21908767, 21908768, 35695917, 265020, 265021, 265022, 52644150, 35695855, 284634, 60432113, 22279000, 284488, 56994075, 264259, 20281099, 29331825, 29331827, 264905, 56182435, 265006, 265011, 87168558, 265017, 265019, 264448, 264288, 264766, 264686, 60170815, 264691, 264692, 27486285, 264628, 264629, 264636, 264557, 264558, 264559, 87168518, 264564, 264566, 264567, 265007, 264687
2800	88316481 (5599, 5600)	Novel Protein sim. GBank gi 4240301 dbj BAA74829.1 - (AB020713) KIAA0806 protein [Homo sapiens]		glycoprotein	
2801	86068814 (5601, 5602)		Contains protein domain (PF00627) - UBA domain		
2802	88082477 (5603, 5604)	Novel Protein sim. GBank gi 2337865 (AC002464) - organic cation transporter; 50% similarity to JC4884 (PID:g2143892) [Homo sapiens]	Contains protein domain (PF00083) - transport Sugar (and other) transporter		
2803	79577446 (5605, 5606)	Novel Protein sim. GBank gi 4559368 gb AAD23029.1 AC00658 - (AC006585) hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF01585) - G-patch domain	264639 264566	
2805	87398486 (5609, 5610)			264092, 264259, 29331822, 29331824, 29331827, 29331828, 264508, 265007, 265009, 21906754, 264369, 264288, 264632, 60170394, 264563, 264482	
2806	8788851 (5611, 5612)	Novel Protein sim. GBank gi 1168973 sp P44403 CLPB_HAEIN - CLPB PROTEIN		UNCLASSIFIED	22278995, 22278996, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29146498, 265008, 265009, 60433438, 265017, 265018, 265019, 264448, 264288, 21906765, 21906767, 21906769, 29148629, 265022, 52644150, 56182323

2807	91720702 (5813, 5814)	Novel Protein sim. GBank gl 468310 emb CAB37891.1 - (AL031432) dJ468N24.1 (PUTATIVE novel protein similar to Predicted yeast and worm proteins) [Homo sapiens]	UNCLASSIFIED	52644507, 52645156, 52846842, 18108398, 56182575, 22278994, 22278995, 22278996, 56994075, 35698286, 22278997, 22278998, 22278999, 264259, 52845080, 29331822, 29331824, 29331825, 29331826, 35698032, 29331828, 33656970, 264100, 264105, 264907, 52644045, 60433358, 264594, 60433438, 52846317, 21908754, 33109954, 33657084, 52844298, 87168474, 265011, 87188559, 265017, 265018, 265019, 18108351, 264448, 264763, 264687, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265021, 265022, 52644150, 33657023, 52645128, 33657109, 33657182, 27486261, 27486262, 27486284, 27486285, 35695763, 18108370, 18108372, 18108374, 18108376, 263977, 18108377, 35696423, 35695855, 52644332, 83373044, 18108385, 18108387, 87188518, 60432113
2808	95359111 (5615, 5616)	Novel Protein sim. GBank gl 5541863 emb CAB51071.1 - (AL096857) hypothetical protein [Homo sapiens]	MHC	60432289, 264510, 265010, 265017, 265018, 264881, 264886, 265021, 264690, 22279000, 264586
2809	88083530 (5617, 5618)	Novel Protein sim. GBank gl 2772561 - similar to ciliary dynein beta heavy chain; 78% Similarity to P23098 (PID:g118865) [Homo sapiens]	ATPase-associated	18108351
2810	87259032 (5619, 5620)			
2811	91235845 (5621, 5622)		UNCLASSIFIED	264589, 22278996, 264091, 284259, 29331828, 29146489, 29146629, 29148784, 264693
2812	88093334 (5623, 5624)	Novel Protein sim. GBank gl 3264583 (AC005189) - match to ESTs H87758 (NID:g118843) and AA085546 (NID:g182873) [Homo sapiens]	UNCLASSIFIED	22278999, 264259, 66712502, 264693
2813	91218755 (5625, 5626)	Novel Protein sim. GBank gl 4240273 db BAA74815.1 - (AB020699) KIAA0892 protein [Homo sapiens]	UNCLASSIFIED	264106
2814	90980808 (5627, 5628)	Novel Protein sim. GBank gl 3548791 (AC005620) - R33590.1 [Homo sapiens]	UNCLASSIFIED	56182575, 29331828, 264906, 66712502, 55811386, 265017, 265018, 265019, 264683, 265020, 87188518, 60432113
2815	78774521 (5629, 5630)		transcription factor	85274572
2816	85368228 (5631, 5632)	Novel Protein sim. GBank gl 5420389 emb CAB46680.1 - (AJ243460) proteophosphoglycan [Leishmania major]	UNCLASSIFIED	264907, 264909
			UNCLASSIFIED	264486, 35696286, 29331825, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 264511, 264910, 265011, 264760, 264681, 264766, 264769, 264689, 21908765, 264693, 264628, 18108370, 264629, 264631, 264634, 264563, 264564, 264566, 264486

2817	87749542 (5633, 5634)	Novel Protein sim. GBank gl 1203846 (U56966) - coded for by C. elegans cDNA yk30b3.5; coded for by C. elegans cDNA yk30b3.3 [Caenorhabditis elegans]			264259, 29331822, 29331827, 264508, 264509, 264905, 264907, 264908, 264909, 56182435, 264510, 265006, 264511, 264512, 264593, 264758, 265010, 264760, 264761, 264764, 264288, 264687, 264769, 55811957, 35695917, 33657109, 263878, 264634, 264636, 264639, 264584, 264565, 264566, 264488, 264597
2818	88073579 (5635, 5636)	Novel Protein sim. GBank gl 549986 (U13149) - possible apoptosis-associated protein [Pennisetum dillare]	Contains protein domain (PF00023) - Ank repeat	UNCLASSIFIED	66712502
2819	87783527 (5637, 5638)	Novel Protein sim. GBank gl 4929773 (gb AAD34147.1) AF15209 - (AF152097) CGI-05 protein [Homo sapiens]	Contains protein domain (PF00919) - Uncharacterized protein family UPF0004	UNCLASSIFIED	264909, 264511
2820	87785744 (5639, 5640)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	UNCLASSIFIED	16108394, 52646365, 52644045, 264112, 265009, 21906754, 265017, 18108351, 264683, 264369, 264686, 264769, 21906769, 33657023, 33657109, 18108370, 18108374, 18108377, 18108385
2821	95320511 (5641, 5642)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264638
2822	94260221 (5643, 5644)	Novel Protein sim. GBank gl 2224671 (db BAA20820) - (AB002363) KIAA0365 [Homo sapiens]		UNCLASSIFIED	264259, 29331822, 60432289, 264905, 60433356, 33657402, 265011, 264760, 21908765, 60170815, 264638
2823	95320513 (5645, 5646)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	264766
2824	95320515 (5647, 5648)	Novel Protein sim. GBank gl 399144 (sp P02747) C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR		UNCLASSIFIED	264907
2825	19742170 (5649, 5650)	Novel Protein sim. GBank gl 3559683 (emb CAA22020) - (AL033503) conserved hypothetical protein [Candida albicans]			264760
2826	94311805 (5651, 5652)				52645156, 22278994, 35696286, 22278997, 22278998, 52645080, 29331822, 29331824, 29331825, 29331827, 35696052, 29331828, 33656970, 52644045, 52646317, 33657084, 52644296, 265017, 265018, 265019, 264288, 21906764, 21906765, 21906766, 21906767, 21906768, 35695917, 52644150, 33657109, 33657182, 27486261, 27486262, 33657349, 27486265, 35695763, 35698423, 35695855, 52644332, 18108385, 87168518, 264484

2827	95320518 (5653, 5654)	Novel Protein sim. GBank gi398144 sp P02747 C1QC_HUMAN - COMPLEMENT C1Q SUBCOMPONENT, C CHAIN PRECURSOR	Contains protein domain (PF00386) - C1q domain	complement	284488, 263994, 264489, 65274572, 29331822, 68714117, 29331827, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 265008, 264511, 265007, 264512, 265008, 264910, 264591, 60432229, 264592, 264593, 264595, 264596, 21908754, 285011, 264600, 264601, 264602, 265017, 264604, 264605, 264288, 264766, 264767, 264689, 55811957, 264534, 264890, 264691, 264692, 264693, 263972, 264629, 35895855, 264631, 264634, 264635, 284555, 264636, 264637, 264556, 264638, 264558, 83373044, 18108385, 60432113, 22279002, 264583, 264584, 264585, 264586, 264587, 264488, 18108391
2828	91228615 (5655, 5656)	Novel Protein sim. GBank gi3598974 (AF077000) - protein tyrosine phosphatase TD14 [Rattus norvegicus]	Contains protein domain (PF00102) - Protein-tyrosine phosphatase	phosphatase	29331822, 35896052, 264104, 264908, 265007, 264591, 265010, 265011, 265019, 264768, 264686, 55811957, 18108370, 18108374, 55810784, 35898423, 55811578, 56182323, 83373044, 87168518, 22278996, 22278997, 264091, 264093, 60432049, 264259, 29331822, 29331825, 29331827, 29331828, 264905, 264509, 68712502, 264510, 264511, 264593, 60433438, 21908754, 265011, 264603, 18108351, 264288, 21908765, 21908768, 21908769, 29148629, 52644150, 264693, 33657109, 18108374, 264634, 18108385, 60432113, 22279000, 264585, 264488, 265008, 265019, 264639, 22279002
2829	87651244 (5657, 5658)	Novel Protein sim. GBank gi4680689 sp A027734.1 AF13295 - (AF132959) CGI-25 protein [Homo sapiens]			
2830	86087109 (5659, 5660)	Novel Protein sim. GBank gi2498667 sp Q61200 NPH1_MOUSE - NEUREXOPHILIN 1			
2831	87614717 (5661, 5662)			UNCLASSIFIED	265017
2832	87631809 (5663, 5664)			UNCLASSIFIED	22278997, 22278999, 52646317, 264288, 264688, 21908767, 60431528, 264638, 22279000
2833	87612938 (5665, 5666)	Novel Protein sim. GBank gi5262615 emb CAB45747.1 - (AL080158) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264555, 264556, 264558
2834	86974703 (5667, 5668)	Novel Protein sim. GBank gi2224567 dbj BAA20772 - (AB002311) KIAA0313 [Homo sapiens]			263972
2835	87775712 (5669, 5670)	Novel Protein sim. GBank gi4589532 dbj BAA76788.1 - (AB023161) KIAA0944 protein [Homo sapiens]		ATPase-associated	60432289, 29331828, 265008, 265010, 265017, 264448, 55811957, 265020, 18108370
2836	85724748 (5671, 5672)	Novel Protein sim. GBank gi2351588 (U76618) - N-RAP [Mus musculus]	Contains protein domain (PF00412) - LIM domain containing proteins	transcript factor	284259, 264112, 265010, 264762, 264764, 263974, 264555, 264558, 264559

2837	87766482 (5673, 5674)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243458) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	18108394, 22278997, 22278998, 29331822, 284907, 284909, 265006, 265007, 265018, 265019, 264682, 264288, 21906766, 21906787, 55811957, 35695917, 18108374, 56182323, 22279000, 22279002
2838	87775382 (5675, 5676)	Novel Protein sim. GBank gij973378 (U31263) - core protein [Hepatitis C virus]		UNCLASSIFIED	18108394, 18108397, 264259, 29331826, 265007, 265019, 264448, 18108368, 20281149, 264565, 264567
2839	85799317 (5677, 5678)	Novel Protein sim. GBank gij1575515 (U84899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]		UNCLASSIFIED	284555
2840	87774663 (5678, 5680)	Novel Protein sim. GBank gij1575515 (U84899) - thrombospondin-related anonymous protein [Plasmodium gallinaceum]			284509, 264511, 265011, 264288, 264769, 265020, 264634, 264638, 264556
2841	86982568 (5681, 5682)	Novel Protein sim. GBank gij2224605[dbj]BA20780] - (AB002330) KIAA0332 [Homo sapiens]	Contains protein domain (PF00076) - RNA recognition motif (a.k.a. RRM, RBD, or RNP domain)	dna_rna_bind	56182575, 35696052, 264907, 264908, 284909, 284910, 264593, 264595, 264766, 265022, 264691, 33637182, 35695763, 18108370, 35695855, 264631, 284559, 264563, 264567
2842	80080086 (5683, 5684)	Novel Protein sim. GBank gij578957[emb]CAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264600
2843	91012494 (5685, 5686)	Novel Protein sim. GBank gij578957[emb]CAB51350.1] - (AL050306) dJ475B7.1 (novel KIAA0615 and KIAA0323 LIKE protein) [Homo sapiens]		UNCLASSIFIED	264906, 264907, 264908, 264909, 264910, 284784, 35695855, 83373044, 18108385
2844	56731154 (5687, 5688)	Novel Protein sim. GBank gij585123[sp]Q08879[FBL, MOUSE - FIBULIN-1, ISOFORM C PRECURSOR BASEMENT-MEMBRANE PROTEIN 90] (BM-90)	Contains protein domain (PF00008) - EGF-like domain		264685
2845	84321718 (5689, 5690)	Novel Protein sim. GBank gij5420387[emb]CAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		homeobox	29148498, 87168474, 264686, 35696423, 83373044, 264564
2846	88318613 (5691, 5692)	Novel Protein sim. GBank gij5308263[gb]A041995.1[AC00623] - (AC006233) unknown protein [Arabidopsis thaliana]		UNCLASSIFIED	29331830, 264909, 265008, 265011, 87168559, 264629, 264556
2847	81811757 (5693, 5694)	Novel Protein sim. GBank gij339676 (AC005390) - R31180.1 [Homo sapiens]		UNCLASSIFIED	264908, 264766, 264769, 264629, 264637, 264568
2848	87612843 (5695, 5696)	Novel Protein sim. GBank gij5262615[emb]CAB45747.1] - (AL080156) hypothetical protein [Homo sapiens]		UNCLASSIFIED	264450, 264259, 264508, 264905, 264907, 264510, 265007, 265008, 264591, 264592, 264593, 264594, 264595, 55812038, 265010, 265011, 264604, 264783, 264764, 264765, 264786, 264688, 264628, 264629, 264555, 264638, 264556, 264557, 264638, 264558, 264559, 264563, 264566, 264567
2849	86084203 (5697, 5698)	Novel Protein sim. GBank gij3342218 (AC004131) - Unknown gene product [Homo sapiens]			29331822, 35696052, 264509, 264906, 265007, 264594, 265018, 264288, 263972, 35696423, 18108384, 56526486, 18108390
2850	87623636 (5699, 5700)			UNCLASSIFIED	35696286, 265008, 265009, 265018, 264288, 35695917, 264693, 18108374, 35695855, 22279000

2851	87820548 (5701, 5702)	Novel Protein sim. GBank gij4321819[gb]AAD15788.1] - (AF051088) seven transmembrane domain orphan receptor [Mus musculus]		UNCLASSIFIED	264906, 264907, 56182435, 264758, 55811386, 265010, 18108351, 264448, 264369, 21906765, 264691, 264692, 264693, 35895855, 264556, 18108385, 264567, 264591
2852	86987023 (5703, 5704)	Novel Protein sim. GBank gij1825729 (U88308) - similar to drosophila membrane protein PATCHED SP:P18502 (PID:g128645) [Caenorhabditis elegans]		UNCLASSIFIED	
2853	87784630 (5705, 5706)	Novel Protein sim. GBank gij2702347 (AF027503) - putative membrane-associated guanylate kinase 1 [Mus musculus]	Contains protein domain (PF00397) - Kinase WW domain		56182575, 55811150, 264690, 27486262, 27486265, 264632, 56182323, 56526486, 22279002
2854	88083557 (5707, 5708)	Novel Protein sim. GBank gij2795825 (AC004021) - kelch protein; ring canal component involved in cytoplasmic bridges; 77% Similarity to A45773 (PID:g1079086) [Homo sapiens]	Contains protein domain (PF01344) - dna_ma_bind Kelch motif		35686286, 29331824, 29331826, 29331828, 264908, 264768, 264693, 22279002, 264482
2855	94723858 (5709, 5710)	Novel Protein sim. GBank gij1504040[gb]BAA13218] - (D86983) similar to D.melanogaster peroxidase(U11052) [Homo sapiens]	Contains protein domain (PF00580) - glycoprotein Leucine Rich Repeat		22278994, 29331822, 29331824, 29331825, 264908, 264908, 265009, 33109954, 265018, 265019, 264448, 21906765, 265020, 264690, 27486265, 83373044, 22279000, 22279002, 264482
2856	88083358 (5711, 5712)	Novel Protein sim. GBank gij3264583 (AC005189) - match to ESTs H97758 (NID:g1118643) and AA085548 (NID:g1628773) [Homo sapiens]			21906766, 22278997, 265022, 29331822, 29331826, 27486262, 265007, 265009, 265017, 264482, 264563, 18108351
2857	95348288 (5713, 5714)	Novel Protein sim. GBank gij3041855 (AC004537) - similar to tumor suppressor p33ING1; similar to AF044078 (PID:g2829208) [Homo sapiens]	Contains protein domain (PF00628) - struct PHD-finger		22278995, 35696286, 29331824, 29331825, 35696052, 264103, 264108, 56182435, 21906765, 21906769, 265020, 18108368, 35695783, 22279002, 264583
2858	87434748 (5715, 5716)	Novel Protein sim. GBank gij462585[sp]P35227[ME18_HUMAN - DNA-BINDING PROTEIN MEL-18 (ZINC FINGER PROTEIN 144)]	Contains protein domain (PF00087) - zinc finger, C3HC4 type (RING finger)		264569, 264887, 22278995, 22278996, 22278997, 22278999, 264259, 29331826, 29331827, 29331828, 264509, 264905, 264908, 29331830, 264908, 52644045, 264909, 264511, 264512, 265007, 265008, 264910, 265009, 264593, 60433356, 264595, 264758, 21906754, 265010, 265011, 264604, 265018, 264760, 18108351, 264763, 264682, 264764, 264765, 264288, 264369, 264685, 264766, 264768, 18108357, 264769
2859	90937875 (5717, 5718)	Novel Protein sim. GBank gij4325320[gb]AAD17331.1] - (AF124427) claudin-15 [Mus musculus]		UNCLASSIFIED	21906768, 21906767, 265021, 264534, 60170615, 264691, 264692, 18108370, 264829, 18108374, 264631, 264636, 263981, 18108381, 264558, 18108385, 22279002, 264594, 264586, 264486, 264567, 60424179, 65274572, 29331828, 264905, 264511, 264758, 265011, 21906767, 21906769, 55811957, 265021, 56182323

2880	87532589 (5719, 5720)	Novel Protein sim. GBank g 4469188 emb CAB38414.1 - (AL031588) dJ1163J1.2.1 (novel protein similar to C. elegans B0035.16 and bacterial tRNA (5'-Methylaminomethyl-2-thiouridylate)-Methyltransferases) (isoform 1) [Homo sapiens]		UNCLASSIFIED	284259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 284510, 284511, 33109954, 18108351, 284683, 284765, 284389, 284686, 21908765, 284691, 284692, 284693, 18108388, 22279002, 284482
2881	86688507 (5721, 5722)	Novel Protein sim. GBank g 3941730 (AF108083) - BS4 [Homo sapiens]			284389, 284692
2882	87568585 (5723, 5724)	Novel Protein sim. GBank g 4505013 ref NP_002310.1 p RN - leucine-rich neuronal protein		UNCLASSIFIED	284691, 284638
2883	91220421 (5725, 5726)	Novel Protein sim. GBank g 3249088 (AC004473) - Contains similarity to goliath protein gb M97204 from D. melanogaster. [Arabidopsis thaliana]	Contains protein domain (PF00096) - struct Zinc finger, C2H2 type		56994075, 35696286, 22278998, 29331822, 29331824, 35696052, 29331828, 284106, 284511, 55812038, 33657084, 55811388, 265018, 265019, 21906765, 21906768, 21906769, 35695917, 265020, 265022, 33657023, 33657109, 33657349, 284629, 18108378, 60431850, 56182323, 18108385, 18108387, 87168518, 22279002
2884	87420030 (5727, 5728)	Novel Protein sim. GBank g 1078451 p J A55463 - tropomodulin, skeletal muscle - chicken	struct		284259, 284910
2885	95312191 (5729, 5730)	Novel Protein sim. GBank g 438840 (L19048) - MSA-2 [Plasmodium falciparum]			22278995, 21906764, 284482
2886	95105480 (5731, 5732)	Novel Protein sim. GBank g 585703 sp Q07066 PMP2_RAT - 22 KD PEROXISOMAL MEMBRANE PROTEIN	glycoprotein		65274572, 22278998, 22278999, 284259, 29331824, 29331827, 29331828, 60433438, 21906754, 265018, 284448, 284764, 52844150, 83373044
2887	86808001 (5733, 5734)	Novel Protein sim. GBank g 4580987 gb AAD24571.1 AF12108 - (AF121081) cAMP inducible 2 protein [Mus musculus]	UNCLASSIFIED		284488, 284768, 21906798, 22278998, 285022, 284259, 284508, 284805, 284907, 284511, 284910, 284635, 284636, 284637, 265011, 265017, 265018, 285019, 284583, 264088, 284566, 284764, 284389, 284587, 284486, 284288, 284768

2868	95303283 (5735, 5738)	Novel Protein sim. GBank gl 1292869 emb CAA63923 - (X94232) t-Cell activation protein [Homo sapiens]		18108392, 264488, 22278994, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 35896052, 29331828, 264508, 52644045, 264828, 265006, 265007, 268008, 265009, 264591, 60432229, 264593, 60433356, 264595, 21906754, 265017, 285019, 264682, 264369, 21906765, 21906766, 21906767, 21906768, 285021, 265022, 264691, 33657182, 18108368, 27486261, 27486262, 27486264, 27486265, 18108370, 18108374, 35896423, 35895855, 284632, 56182323, 87168518, 264404, 22279000, 22279002, 264482, 264563, 264564, 264567, 264487
2869	88094412 (5737, 5738)		UNCLASSIFIED	264369
2870	84404574 (5739, 5740)		UNCLASSIFIED	264905, 264908, 264764, 21906769, 264634
2871	88318621 (5741, 5742)	Novel Protein sim. GBank gl 5306283 gb AAD41995.1 AC00623 - (AC006233) unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	264259, 29331822, 60432289, 29331827, 264907, 265008, 265017, 265018, 264682, 264764, 18108354, 265021, 27486265, 264629, 18108387, 264567, 263981
2872	95312187 (5743, 5744)	Novel Protein sim. GBank gl 112205 pir B39066 - proline-rich protein 15 - rat	kinase	
2873	88094252 (5745, 5746)		UNCLASSIFIED	264488, 18108374, 264768, 264687, 264688, 264689, 35696423, 35696286, 35695917, 264510, 264511, 265007, 264512, 265008, 264910, 264534, 264634, 264635, 264555, 264592, 264259, 264558, 60433438, 60432289, 35696052, 265011, 264600, 264601, 60432113, 264508, 264563, 264482, 264509, 264905, 264908, 264564, 18108351, 264763, 18108370, 264907, 264566, 264908, 264764, 264288, 264567, 264909, 264486, 264766, 18108391

2874	94313548 (5747, 5748)	Novel Protein sim. GBank gij3212854 (AC004005) - unknown protein [Arabidopsis thaliana]	UNCLASSIFIED	52644507, 52645158, 52646385, 56182575, 22278994, 22278995, 56994075, 35696286, 60432049, 264259, 52645080, 29331822, 56182181, 29331824, 60424266, 29331825, 68714117, 29331826, 29331827, 35696052, 29331828, 33656970, 66712502, 52644045, 285007, 265009, 60433358, 264758, 55812038, 18108348, 52646317, 33109954, 33657084, 265017, 264604, 285018, 265019, 264692, 264369, 264288, 264888, 52644229, 21906766, 21906767, 21906768, 55811957, 265020, 265021, 265022, 52644150, 33657023, 52645129, 18108374, 18108376, 35696423, 56182323, 18108387, 87168518, 60432113, 22278000, 22279002, 264563, 264565
2875	88083726 (5748, 5750)	Novel Protein sim. GBank gij2781386 (AC004010) - similar to Leucine-rich transmembrane proteins; 44% similarity to U42767 (PID:g1736918) [Homo sapiens]	glycoprotein	22278996, 22278997, 22278998, 29331826, 29331828, 29146489, 66712502, 265008, 265017, 18108351, 264883, 264689, 21906767, 18108376, 18108377, 55811576, 60170394, 22279000, 284487
2876	88080854 (5751, 5752)	Novel Protein sim. GBank gij2979530 (AC004449) - R33683_2 [Homo sapiens]	Ig	
2877	84747029 (5753, 5754)	Novel Protein sim. GBank gij4704208 [emb]CAB41846.1] - (AL035419) dJ1100H13.1 (putative novel protein) [Homo sapiens]	Fibroblast growth factor	52646385, 65274572, 56182575, 22278997, 22278998, 22278999, 60432048, 52645080, 60424289, 60432289, 29331827, 35696052, 29331828, 66712502, 52644045, 56182435, 60433356, 33657402, 33857084, 265018, 55811150, 264448, 264369, 21908766, 21908768, 21908769, 265020, 33657023, 33657109, 33657182, 27486262, 264629, 60431528, 55811576, 52644332, 56182323, 264658, 83373044, 18108385, 56526486, 60432113, 22279000, 22279002, 264563
2878	88085309 (5755, 5756)	Novel Protein sim. GBank gij3876775 [emb]CAB03067] - (Z81077) predicted using GeneFinder; Similarity to Yeast protein 8248 (TR:G587531) [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264259, 29331822, 29331826, 264905, 264509, 264907, 264809, 264510, 265006, 264511, 264512, 33657402, 264758, 21906754, 18108351, 264681, 264682, 264288, 264684, 264685, 264768, 264689, 21906769, 264690, 33657023, 264693, 18108364, 33657109, 264629, 18108374, 264630, 264632, 264556, 264637, 264639, 264558, 18108385, 18108387, 264563, 264564, 264565, 264566, 264486, 264567

2879	87688122 (5757, 5768)	Novel Protein sim. GBank gll4895145[gb AAD32762.1] - (AF127374) unknown [Streptomyces lavendulae]	Contains protein domain (PF00315) - UNCLASSIFIED	18108359, 264259, 264905, 18108370, 264629, 264908, 264909, 18108374, 18108377, 265006, 264910, 264637, 60170394, 264559, 285017, 264564, 264565, 264567, 264684, 264369
2880	94851438 (5759, 5760)	Novel Protein sim. GBank gll4880703[gb AAD27741.1]AF132968 - (AF132968) CGI-32 protein [Homo sapiens]		264488, 52646365, 52646842, 22278994, 35986286, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 29331828, 29331827, 35986052, 29331828, 264107, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 52644045, 264510, 265006, 264511, 265007, 264512, 265009, 264910, 264594, 21906754, 52646317, 52644286, 87186559, 264600, 264604, 264605, 264760, 264764, 264288, 264766, 264768, 264687, 264769, 21906768, 21906769, 35959517, 265021, 264690, 264692, 33657023, 52645129, 33657109, 33657182, 27486262, 33657349, 264629, 18108374, 35959585, 264634, 264635, 264636, 264637, 264638, 264557, 52644332, 264558, 264559, 83373044, 264404, 22279000, 264563, 264483, 264587, 264486
2881	87650538 (5761, 5762)	Novel Protein sim. GBank gll733571 (U23452) - No definition line found [Caenorhabditis elegans]	UNCLASSIFIED	22278998, 29331822, 52644045, 21906765, 264639, 60432113
2882	87714367 (5763, 5764)	Novel Protein sim. GBank gll118112 (U41559) - No definition line found [Caenorhabditis elegans]		264488, 22278996, 22278999, 29331822, 29331826, 264908, 60170831, 60433356, 55812038, 264881, 264882, 264886, 264887, 264888, 21906768, 21906769, 264693, 263987, 18108374, 55811576, 56182323, 22279002, 264568
2883	95362875 (5765, 5766)	Novel Protein sim. GBank gll4868008[gb AAD31087.1]AF106934 - (AF106934) vitamin D receptor-interacting protein [Homo sapiens]	Contains protein domain (PF00400) - UNCLASSIFIED	WD domain, G-beta repeat
2884	87784643 (5767, 5768)	Novel Protein sim. GBank gll2224697[dbj BAA20832] - (AB002376) KIAA0378 [Homo sapiens]	UNCLASSIFIED	265018, 264634
2885	83006308 (5769, 5770)	Novel Protein sim. GBank gll1255889 (U53344) - T07H8.5 gene product [Caenorhabditis elegans]	complementrecept	264686, 264693
2886	91237823 (5771, 5772)	Novel Protein sim. GBank gll9882323[dbj BAA34521.1] - (AB018344) KIAA0801 protein [Homo sapiens]	Contains protein domain (PF00084) - UNCLASSIFIED	60432048, 264259, 29331828, 264908, 264511, 264595, 60433438, 264596, 265017, 264805, 263969, 263972, 264555, 83373044, 87186518, 264566
2887	91227860 (5773, 5774)	Novel Protein sim. GBank gll4508015[ref NP_003447.1]pZNF2 - zinc finger protein 205	transcriptfactor	18108351, 264686, 264629, 264631, 264639, 83373044, 264482
2888	95105816 (5775, 5776)	Novel Protein sim. GBank gll4508015[ref NP_003447.1]pZNF2 - zinc finger protein 205	Contains protein domain (PF00086) - UNCLASSIFIED	264488, 264259, 29331828, 264508, 264906, 264593, 264758, 264766, 264769, 18108374, 83373044, 264486

2889	87806562 (5777, 5778)				UNCLASSIFIED	58994075, 29331824, 265009, 264760, 18108354, 264288
2890	78703853 (5779, 5780)	Novel Protein sim. GBank gl 854085 emb CAA58337 - (X83413) U88 [Human herpesvirus 6]			UNCLASSIFIED	264591, 264768
2891	38084428 (5781, 5782)	Novel Protein sim. GBank gl 3877750 emb CA801509 - (Z78064) predicted using GeneFinder; similar to collagen; cDNA EST EMBL:D65885 comes from this gene; cDNA EST EMBL:D89451 comes from this gene; cDNA EST EMBL:D68028 comes from this gene; cDNA EST EMBL:D89658 comes from this gene...			UNCLASSIFIED	264591, 264595, 264369, 264685, 264693, 264628, 264563, 264566
2892	95418745 (5783, 5784)	Novel Protein sim. GBank gl 4929759 gb AAD34140.1 AF15190 - (AF151903) CGI-145 protein [Homo sapiens]			UNCLASSIFIED	56274572, 35698286, 29331828, 264110, 265009, 60433438, 265018, 265019, 18108351, 264288, 21906765, 21906766, 21906769, 55811957, 264690, 65274620, 263987, 35695855
2893	87798014 (5785, 5786)				UNCLASSIFIED	264259, 265010, 264682, 18108370, 264555, 264556
2894	87755885 (5787, 5788)	Novel Protein sim. GBank gl 5669015 gb AAD46135.1 - (AF080171) zinc finger protein ZNF232 [Homo sapiens]	Contains protein domain (PF000096) - Zinc finger, C2H2 type		transcript factor	264259, 265008, 60433438, 52644286, 265011, 264369, 35695917, 18108381, 18108382, 18108388
2895	86938778 (5789, 5790)	Novel Protein sim. GBank gl 3924708 emb CAA84646 - (Z35597) Weak similarity with sea squirt nidogen precursor protein (blastp score 71); cDNA EST EMBL:T02069 comes from this gene; cDNA EST EMBL:D78135 comes from this gene; cDNA EST EMBL:D73147 comes from this gene; cDNA EST EMB...	Contains protein domain (PF01437) - Plexin repeat			29331824, 265007, 264762, 264636, 264563
2896	87752122 (5791, 5792)	Novel Protein sim. GBank gl 4885549 ref NP_005456.1 pPKBG - protein kinase B gamma	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain			18108392, 18108394, 18108398, 22278998, 264259, 29331822, 29331824, 29148499, 264908, 264908, 265007, 265009, 265018, 265019, 264388, 264685, 264689, 21906786, 265021, 264693, 33657182, 264639, 18108384, 18108388, 264567
2897	95413057 (5793, 5794)	Novel Protein sim. GBank gl 4502877 ref NP_001296.1 pCLDN - Clostridium perfringens enterotoxin receptor 1			UNCLASSIFIED	60424179, 56182575, 22278998, 35698286, 22278997, 22278999, 60432049, 264259, 29331824, 29331825, 60424269, 60432289, 29331826, 29331828, 35698052, 264908, 56182435, 265009, 264910, 60170831, 60431735, 60433358, 60433438, 65274444, 55811386, 265018, 18108351, 264448, 264288, 264687, 21906765, 21906766, 21906767, 21906769, 55811957, 35695917, 264534, 33657023, 33657109, 35695763, 264628, 264629, 80431528, 18108374, 55810764, 55811576, 35698423, 35695855, 264555, 56182323, 18108385, 264404, 22279000, 22279002, 264566
2898	87750340 (5795, 5796)				UNCLASSIFIED	22278995, 264604, 18108385, 264566

2899	80357670 (5787, 5788)					264764, 21906764, 264692
2900	94233338 (5789, 5800)	Novel Protein sim. GBank gl 4581470 emb CAB40137.1 - (Y18483) SLC7A8 protein [Homo sapiens]		UNCLASSIFIED	glycoprotein	85274572, 56182575, 35696286, 60432049, 264259, 29331824, 66714117, 29331826, 35696052, 29331828, 66712502, 56182435, 265006, 265007, 265008, 265009, 60433356, 264758, 265018, 264764, 264765, 264288, 264768, 21906764, 21906768, 21906769, 265020, 264692, 264693, 32833986, 264631, 83373044, 60432113
2901	87444731 (5801, 5802)	Novel Protein sim. GBank gl 4759272 ref NP_004614.1 pTTC4 - tetrairicopeptide repeat domain 4		phosphatase		22278995, 22278997, 22278999, 60432049, 29331822, 29331824, 29331825, 29331827, 35696052, 33656970, 264910, 265009, 21906754, 33657084, 87168474, 265010, 265018, 21906764, 21906765, 21906768, 21906767, 21906769, 33657023, 264693, 33657109, 33657349, 35696423, 35695855, 283981, 56182323, 22279002
2902	85745271 (5803, 5804)	Novel Protein sim. GBank gl 2414615 emb CAB16384 - (Z99259) hypothetical protein [Schizosaccharomyces pombe]				284683, 264691
2903	87606733 (5805, 5806)	Novel Protein sim. GBank gl 1078318 pir S52241 - XLCL2 protein - African clawed frog				264887, 22278994, 264259, 29331826, 29331828, 264905, 52644045, 56182435, 264511, 265017, 265018, 18108351, 264448, 264883, 264769, 264869, 35695917, 52644150, 87168518, 60432113, 22279002
2904	86458072 (5807, 5808)	Novel Protein sim. GBank gl 5639823 gb AAD4585.1 AF14367 - (AF143676) multispinning nuclear envelope membrane protein nutilm [Homo sapiens]		UNCLASSIFIED		52646385, 22278999, 264259, 35696052, 265011, 265017, 264683, 264769, 35695917, 285020, 263967, 18108374, 35695855, 284637, 284952, 18108385, 18108387
2905	84449826 (5809, 5810)	Novel Protein sim. GBank gl 728937 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		oncogene		265009, 264681, 264682
2906	85341051 (5811, 5812)	Novel Protein sim. GBank gl 4889259 gb AAD27831.1 AF12185 - (AF121858) sorting nexin 8 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	UNCLASSIFIED		22278996, 35696286, 22278998, 264259, 60432289, 29331828, 29331830, 66712502, 265009, 60170831, 33109954, 264448, 264683, 264288, 264689, 21906766, 21906767, 21906768, 55811957, 35695817, 265022, 52644150, 264691, 33657023, 264692, 264693, 35695855, 60432113, 264588

2907	81211383 (5813, 5814)	Novel Protein sim. GBank gi 1707079 (U80451) - contains strong similarity to a DNA-J-like domain (PS:PS00636) [Caenorhabditis elegans]	Contains protein domain (PF00226) - eph - DnaJ domain	52644507, 56182575, 56181686, 22278995, 56994075, 35696286, 60432049, 56182181, 35696052, 60431735, 264595, 55812038, 21906754, 55811386, 265019, 264682, 264389, 56181562, 21906766, 55811957, 35695917, 265020, 265021, 33657023, 33657109, 60431528, 55811576, 35696423, 35695855, 264638, 22279000
2908	80414246 (5815, 5816)	Novel Protein sim. GBank gi 2673917 (AC002561) - putative ATP-dependent RNA helicase [Arabidopsis thaliana]	helicase	265009, 33109954, 18108351, 264766, 265021, 264691, 264692, 18108374, 264556, 264638, 264557, 264558
2909	87420225 (5817, 5818)		eph	264239, 87168474, 265018, 18108365, 264628
2910	86601075 (5819, 5820)	Novel Protein sim. GBank gi 45393335 emb CA837483.1 - (AL035539) putative protein [Arabidopsis thaliana]		22278995, 264509, 264512, 265007, 33657402, 265017, 264369, 265022, 18108365, 264628
2911	94216615 (5821, 5822)	Novel Protein sim. GBank gi 4469187 emb CA838415.1 - (AL031588) dJ1163J1.3 (novel protein similar to mouse B98) [Homo sapiens]	glucoamylase	52646365, 18108397, 22278995, 22278997, 22278998, 22278999, 29331824, 29331825, 52644045, 265008, 265018, 264448, 21906765, 21906766, 21906767, 21906768, 21906769, 55811957, 265021, 18108370, 18108372, 18108374, 22279000
2912	87731803 (5823, 5824)	Novel Protein sim. GBank gi 4929637 gb AAD34079.1 AF15184 - (AF15184) CGI-84 protein [Homo sapiens]	Contains protein domain (PF00904) - Involucrin repeat	52645156, 264092, 60432049, 264259, 52645080, 29331824, 29331825, 66712502, 33109954, 264780, 264683, 264288, 264686, 265021, 264693, 18108388, 263976, 264404
2913	87713823 (5825, 5826)	Novel Protein sim. GBank gi 854065 emb CAA58337 - (X03413) U88 [Human herpesvirus 6]	Contains protein domain (PF00096) - UNCLASSIFIED Zinc finger, C2H2 type	52644507, 52645156, 52646842, 56182575, 35696286, 22278997, 264259, 52645080, 29331827, 35696052, 29331828, 264828, 52644045, 56182435, 55812038, 52646317, 21906754, 52644296, 87168474, 265017, 265018, 265019, 18108351, 264682, 264686, 264689, 21906765, 21906766, 21906767, 21906768, 35695917, 265020, 52644150, 27486261, 27486262, 27486265, 35695763, 55811576, 35695855, 52644332, 22279000, 22279002, 264563
2914	87797300 (5827, 5828)			264557

2915	88081972 (5829, 5830)	Novel Protein sim. GBank gi 5174485 ref NP_008030.1 pKIAA - endocytic receptor (macrophage mannose receptor family)	Contains protein domain Lectin C-type domain	eph	264569, 264488, 264687, 264768, 21906768, 52846842, 21906767, 21906768, 56182575, 29148629, 35695917, 22278996, 22278997, 22278998, 285021, 22278999, 52644150, 264691, 264259, 60432048, 264692, 52845129, 33657109, 33657182, 29331827, 27486261, 35696052, 29331828, 27486282, 27486264, 27486285, 33657349, 29146498, 29146499, 264908, 264907, 18108370, 264908, 18108372, 52644045, 18108374, 56182435, 35695855, 264112, 264510, 265008, 60432229, 264593, 60433358, 56182323, 18108382, 55812038, 18108385, 33108954, 21908784, 33657084, 87168518, 265010, 265011, 60432113, 265017, 265018, 22279000, 285019, 55811150, 264681, 18108351, 264763, 264448, 264683, 264566, 18108354, 264389, 264288, 264768
2918	95337780 (5831, 5832)	Novel Protein sim. GBank gi 5104851 dbj BA80165.1 - (AP000061) 303aa long hypothetical dTDP-4- dehydroharmose reductase [Aeropyrum pernix]		dehydrogenase	52845156, 65274572, 22278994, 22278995, 35696288, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331825, 66714117, 60432289, 29331826, 29331827, 29331828, 33656970, 264509, 264908, 29331830, 52644045, 264909, 56182435, 60170831, 264592, 264593, 33657402, 60433386, 52646317, 21906754, 33108954, 33657084, 52644296, 85658542, 265011, 265017, 265018, 265019, 18108351, 264448, 264288, 52644229, 21906765, 21906768, 21906767, 21906768, 21906769, 55811957, 35695917, 265021, 265022, 52644150, 33657023, 33657109, 33657182, 27486261, 27486282, 27486284, 35695763, 18108376, 55811578, 35698423, 65274791, 35695855, 52644332, 264557, 264638, 56182323, 18108387, 87168518, 22279002, 264482
2917	87454546 (5833, 5834)	Novel Protein sim. GBank gi 3169065 emb CAA19260.1 - (AL023704) putative translocation elongation factor-Tu fa mily [Schizosaccharomyces pombe]		UNCLASSIFIED	60433438, 264602, 264682, 87168518, 60432113
2918	85690528 (5835, 5836)	Novel Protein sim. GBank gi 559218 pir S38038 - hypothetical protein YKL201c - yeast (Saccharomyces cerevisiae)			264638
2919	87641497 (5837, 5838)	Novel Protein sim. GBank gi 2564955 (AF030001) - unknown [Mus musculus]			66714117, 66712502, 263981

2920	87789523 (5839, 5840)				35696286, 22278997, 264259, 52645080, 29331824, 29331826, 29331827, 264828, 264909, 56182435, 264511, 264758, 33109954, 21906754, 52644296, 265010, 285011, 264601, 265017, 265019, 264681, 264687, 21906767, 265021, 52644150, 264690, 264691, 264692, 264693, 33657109, 33657182, 27486262, 27486284, 27486285, 35696423, 35696555, 264632, 264636, 264637, 264638, 56182323, 60170394, 18108385, 87168518, 60432113, 35696286, 22278997, 264091, 264092, 264094, 264259, 29331822, 29331824, 29331826, 29331827, 35696052, 29146498, 264104, 264105, 264107, 264509, 264110, 264112, 264512, 60433356, 21906754, 87168474, 265017, 18108351, 264288, 21906765, 21906766, 21906767, 21906769, 35695917, 265021, 263974, 18108374, 263976, 263977, 18108376, 264555, 263981, 56528488, 87168518, 22278900, 22279002, 264906, 264909, 264511, 265008, 265008, 264593, 33657402, 60174639, 18108351, 264763, 21906765, 29146627, 35695917, 264692, 264629, 263978, 55811576, 35695855, 264555, 264558, 56182323, 60170394, 22279000, 264486, 264488, 18108397, 22278995, 22278996, 22278997, 22278998, 22278999, 29331825, 29331826, 29331827, 29331830, 264511, 265009, 33657402, 265011, 265017, 265018, 264683, 18108354, 21906765, 21906767, 21906768, 21906769, 52644150, 264691, 264692, 33657109, 263974, 18108376, 264631, 264636, 18108385, 18108387, 22278900, 264563, 264568, 265017, 264628, 20281152, 264556
2921	91639982 (5841, 5842)	Novel Protein sim. GBank gij4580013jpb/AAD24202.1 U83194_ - (U83194) TRAF4-associated factor 2 [Homo sapiens]	Contains protein domain (PF00787) - PX domain		
2922	87748762 (5843, 5844)	Novel Protein sim. GBank gij4569514 dbj BAA76779.1 - (AB023152) KIAA0935 protein [Homo sapiens]	Contains protein domain (PF01074) - Glycosyl hydrolases family 38	kinase	
2923	95337799 (5845, 5846)	Novel Protein sim. GBank gij483526 emb CAB42898.2 - (Z83844) dJ37E16.4 (similar to mouse p116Rip protein) [Homo sapiens]	Contains protein domain (PF00169) - PH domain	struct	
2924	87781967 (5847, 5848)	Novel Protein sim. GBank gij2133095 pir S72254 - ribosomal protein L36, mitochondrial - yeast (Saccharomyces cerevisiae)	Contains protein domain (PF00444) - Ribosomal protein L36	ribosomal prot	
2925	95090120 (5849, 5850)	Novel Protein sim. GBank gij238898 emb CAB11718 - (Z89880) actin associated protein [Schizosaccharomyces pombe]		UNCLASSIFIED	56182575, 35696286, 264259, 60432289, 29331827, 264508, 52644045, 264910, 264591, 60432229, 55812038, 21906754, 264681, 264448, 264683, 264288, 264685, 52644229, 264689, 21906765, 21906766, 21906768, 21906769, 265021, 285022, 60170615, 264692, 33657023, 264693, 33657109, 35696423, 65274791, 56182323

2926	95343003 (5851, 5852)	Novel Protein sim. GBank gl 283032 pir j S22456 - hydroxyproline-rich glycoprotein - perennial leucisite			29331828, 265011, 264768, 264689, 264764, 264288, 264630, 264637
2927	80408018 (5853, 5854)				
2928	20452178 (5855, 5856)			UNCLASSIFIED	264559
2929	81622920 (5857, 5858)	Novel Protein sim. GBank gl 3413320 emb CAA06915 - (AJ006215) CMP-N-acetylneuraminic acid synthetase [Mus musculus]		UNCLASSIFIED	264569, 264489, 22278994, 35696286, 22278996, 22278998, 22278999, 264094, 264259, 52845080, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35696052, 33656970, 264109, 29331830, 52844045, 265009, 33109954, 52844286, 87168539, 264780, 264762, 264448, 264764, 264288, 264766, 264768, 21906765, 21906768, 21906769, 35695917, 264691, 33657023, 264693, 33657109, 18108374, 263976, 35696423, 35695855, 263981, 22279000, 22279002, 264567, 264486
2930	95302755 (5859, 5860)			UNCLASSIFIED	56182575, 56181686, 35696286, 22278996, 22278998, 22278999, 264259, 29331825, 60432289, 29331828, 264905, 52844045, 56182435, 285008, 60170831, 264592, 60432229, 60433356, 87168474, 265010, 265011, 265017, 285018, 265019, 264762, 264448, 264683, 264288, 264766, 21906765, 21906769, 35695917, 60170815, 33657023, 33657109, 264628, 18108370, 18108372, 35696423, 35695855, 264556, 56182323, 60432113, 264597
2931	84312693 (5881, 5882)	Novel Protein sim. GBank gl 3786433 (AF098505) - similar to Arabidopsis thaliana male sterility protein 2 (SW/Q08891) [Caenorhabditis elegans]	Contains protein domain (PF00471) - Ribosomal protein L33	UNCLASSIFIED	52845156, 22278997, 22278998, 29331822, 52845080, 29331824, 60432289, 33656970, 60433356, 60433438, 33109954, 21906765, 21906768, 21906769, 21906770, 21906778, 265020, 52844150, 33657023, 33657109, 33657182, 27486265, 35696423, 35695855, 264555, 87168518, 60432113, 264568
2932	79632623 (5883, 5884)				264906, 264907
2933	91720776 (5885, 5886)	Novel Protein sim. GBank gl 3378056 (AF017777) - helicase [Drosophila melanogaster]	helicase		264488, 18108392, 56182575, 22278999, 264091, 264259, 29331825, 60432289, 29331827, 264508, 52844045, 56182435, 265007, 285009, 264592, 60433356, 60433438, 21906754, 265017, 264682, 264288, 52844229, 21906765, 21906768, 21906769, 265022, 52844150, 33657023, 33657109, 27486265, 264635, 264636, 60170394, 56182323, 18108385, 60432113, 264565, 264566, 264567

2934	86576025 (5867, 5868)				22278997, 22278999, 29331824, 33657402, 264691, 27486282, 264628, 87168518, 22279000
2935	86410579 (5869, 5870)			UNCLASSIFIED	56182575, 22278995, 60433356, 33657402, 264758, 33109954, 21908754, 265018, 265019, 264448, 264788, 21908784, 21908765, 265021, 264692, 33657023, 33657109, 33657349, 55810764, 22279000
2936	87605863 (5871, 5872)	Novel Protein sim. GBank gl 4153862 (AC005065) - determined by GENSCAN prediction and spliced EST; match to EST R84329 (NID:842735) [Homo sapiens]	Contains protein domain (PF00856) - SET domain	nuclease	22278997, 29331827, 29331828, 265009, 265017, 264605, 265020, 55811578, 18108387, 60432113, 264563
2937	94853098 (5873, 5874)	Novel Protein sim. GBank gl 5174409 (ref NP_006101.1 pCD2B - CD2 antigen (cytoplasmic tail)-binding protein 2		UNCLASSIFIED	56994075, 22278999, 264259, 60432049, 29331822, 56182181, 29331827, 29331828, 264908, 264908, 264909, 56182435, 265006, 264512, 264910, 60170831, 60433356, 265011, 265018, 18108351, 264448, 264288, 264786, 52844228, 21908765, 29148784, 65274791, 264556, 56182323, 60170394, 264558, 60432113, 264585, 264486, 264567
2938	95418773 (5875, 5876)	Novel Protein sim. GBank gl 3319890 (emb CAA76720) - (Y17267) ubiquitin-conjugating enzyme [Mus musculus]	Contains protein domain (PF00179) - Ubiquitin-conjugating enzyme	ubiquitin	264488, 56182575, 22278996, 35696286, 22278997, 22278998, 22278999, 264490, 264259, 29331822, 29331824, 66714117, 29331827, 35696052, 264107, 264905, 66712502, 52644045, 56182435, 264511, 265008, 265009, 60432228, 33657402, 60433438, 55812038, 21908754, 65658542, 285010, 285011, 87168559, 265017, 265018, 265019, 264681, 264288, 264689, 21908765, 21908767, 21908768, 55811957, 35695917, 265020, 60170615, 264690, 264691, 264692, 33657023, 264693, 65274620, 33657109, 18108370, 18108374, 263978, 35696423, 35693855, 264555, 264556, 18108381, 56182323, 60170394, 83373044, 18108385, 56528486, 60432113, 22279002
2939	87786622 (5877, 5878)	Novel Protein sim. GBank gl 3978900 (emb CAA99809) - (Z75547) similar to WD domain, G-beta repeat: cDNA EST yk371b7.5 comes from this gene; cDNA EST yk312h1.5 comes from this gene; cDNA EST yk465d5.5 comes from this gene; cDNA EST yk472c4.5 comes from this gene; cDNA EST yk292f8....	Contains protein domain (PF00400) - WD domain, G-beta repeat	ATPase-associated	264907, 265018, 264681, 264685, 264686

2940	95011103 (5878, 5880)			UNCLASSIFIED	22278986, 29331822, 29331824, 66714117, 29331826, 29331828, 264905, 264908, 66712502, 29331830, 265011, 265017, 264784, 264389, 21906766, 21906767, 33657023, 33657109, 32833986, 18108374, 18108377, 264634, 83373044, 18108385, 18108387, 264568 264557
2941	21423370 (5881, 5882)	Novel Protein sim. GBank gij3413872jdbjBAA32300j - (AB007824) KIAA0455 protein [Homo sapiens]		UNCLASSIFIED	264910, 265010, 264768
2942	87430203 (5883, 5884)	Novel Protein sim. GBank gij1172845jlpj46629jRB25_RABIT - RAS-RELATED PROTEIN RAB-25		glycoprotein	
2943	95314504 (5885, 5886)	Novel Protein sim. GBank gij4829653jgbjAAD34087.1jAF15185 - (AF15185) CGI-92 protein [Homo sapiens]		collagen	60432049, 264259, 60432289, 29331827, 29146498, 265008, 264593, 80433396, 60433438, 265010, 265011, 265017, 265018, 264683, 264766, 18108381, 65274727, 60432113, 264587
2944	95081063 (5887, 5888)	Novel Protein sim. GBank gij4878282jembjCAB41190.1j - (AL049680) 1-acylcerol-3-phosphate acyltransferase-like protein [Arabidopsis thaliana]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	58994075, 22278998, 60432049, 264259, 29331822, 29331824, 60424289, 60432289, 29331826, 29331828, 264905, 264907, 52844045, 264909, 264511, 265006, 265009, 264594, 21906754, 87168559, 264603, 265017, 265018, 18108351, 264682, 264766, 264687, 264689, 21908765, 21906766, 21908767, 21906768, 21906769, 265021, 60170615, 52844150, 264690, 264691, 33657023, 264692, 264693, 33657109, 33657182, 33657349, 18108370, 18108374, 18108377, 55811576, 35696423, 35695855, 264635, 264555, 264556, 56182323, 264635, 264555, 264556, 56182323, 60170394, 264558, 264559, 83373044, 58525486, 87168518, 60432113, 22279002, 264482, 264583, 264484, 264567
2945	94233560 (5889, 5890)	Novel Protein sim. GBank gij72883jlpjP39188jALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII	Contains protein domain (PF00096) - Zinc finger, C2H2 type	UNCLASSIFIED	60424179, 22278995, 22278996, 22278998, 22278999, 264259, 56182181, 29331824, 60424289, 60432289, 35696052, 264908, 285006, 60433356, 55812038, 264759, 55811386, 265018, 264681, 18108351, 264448, 264683, 264389, 264288, 264687, 56181562, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 264693, 80431528, 55810764, 35696423, 35695855, 264630, 60170394, 83373044, 22279000, 264568, 264587

2946	94317315 (5891, 5892)	Novel Protein sim. GBank gi 5441952 gb AAD43195.1 AF07286 - (AF072864) peroxisomal membrane protein PMP 24 [Homo sapiens]		UNCLASSIFIED	264488, 264259, 264508, 264509, 264806, 264907, 264909, 264510, 264511, 265007, 264512, 264910, 264591, 264593, 18108351, 264764, 264288, 264684, 264769, 265021, 264692, 33657109, 264628, 264629, 18108374, 264631, 264634, 264636, 264637, 18108380, 264638, 264639, 83373044, 264555, 264588, 264496, 264567
2947	87362952 (5893, 5894)	Novel Protein sim. GBank gi 3540281 gb AAC34383.1 - (AF056116) Ali-1 related protein [Fugu rubripes]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 29146498, 264508, 29331830, 265007, 265008, 265009, 60432229, 21906754, 265010, 265017, 265019, 264766, 264685, 21906765, 21906766, 21906767, 21906768, 21906769, 265020, 264628, 18108370, 264629, 264630, 18108387, 60432113
2948	87626527 (5895, 5896)	Novel Protein sim. GBank gi 5566614 gb AAB65654.2 - (AF001533) mitogen-induced [Mus musculus]			52846842, 22278995, 264259, 29331824, 29331825, 29331827, 29331830, 264909, 265007, 265009, 265019, 264763, 264684, 264288, 264685, 264686, 21906767, 264691, 264692, 264693, 18108374, 55811576, 18108385, 22279002, 264563, 264567
2949	88175545 (5897, 5898)	Novel Protein sim. GBank gi 2132923 pir S67133 - probable membrane protein YOR240w - yeast (Saccharomyces cerevisiae)		UNCLASSIFIED	22278996, 22278997, 60432229, 29331826, 29331827, 29331828, 35696052, 29146499, 264104, 264107, 264905, 66712502, 264908, 60433356, 60433438, 87168559, 264764, 52844229, 56181562, 21906767, 21906768, 21906769, 265022, 60170815, 33857023, 35696423, 263981, 264558, 60432113, 22279002
2950	95086870 (5899, 5900)	Novel Protein sim. GBank gi 468102 sp P34629 Y0J8_CAEEL - PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III	Contains protein domain (PF00883) - Cytosol aminopeptidase family	peptidase	264488, 35696286, 264259, 35696052, 264907, 265007, 264910, 265017, 265018, 264288, 264768, 35695917, 265020, 18108362, 18108370, 18108379, 35696423, 65274791, 35695955, 264556, 58526486, 264486
2951	87392357 (5901, 5902)	Novel Protein sim. GBank gi 4688902 emb CAB41450.1 - (AJ238248) centaurin beta2 [Homo sapiens]			264693

2952	95329852 (5903, 5904)	Novel Protein sim. GBank gl 5596893 emb CAB51405.1 - (AL098881) hypothetical protein [Homo sapiens]	Contains protein domain (PF00650) - transcript factor CRL/TRIO domain.	264687, 52645156, 21908766, 21906769, 22278996, 265020, 284890, 60432049, 264259, 264693, 29331822, 18108365, 29331825, 60432289, 33657109, 18108368, 29331827, 35696052, 27486262, 264508, 264905, 20281149, 264908, 264907, 29331830, 284908, 264909, 35695855, 264511, 265008, 265009, 264910, 264635, 264636, 60432229, 264638, 60433358, 264639, 264758, 87168518, 265017, 22279000, 22279002, 264760, 264563, 264482, 18108351, 264448, 264288
2953	88093575 (5905, 5906)	Novel Protein sim. GBank gl 119522 sp P10658 ISRC_RABIT - PROBABLE PHOSPHOSERINE AMINOTRANSFERASE (PSAT) (ENDOMETRIAL PROGESTERONE-INDUCED PROTEIN) (EPIP)	Contains protein domain (PF00286) - UNCLASSIFIED Aminotransferases class-V	18108396, 56994075, 22278996, 26331822, 29331824, 29331825, 29331827, 35696052, 264508, 264905, 264908, 264907, 264510, 264591, 264594, 33657402, 264595, 264596, 264758, 52848317, 21908754, 33657084, 52844296, 87168559, 264600, 264760, 264681, 18108351, 264784, 264369, 264288, 264687, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 33657023, 18108364, 52845129, 33657109, 33657349, 18108374, 263978, 35695855, 264637, 264638, 87168518, 264482, 264563, 264565, 29331822
2954	88088288 (5907, 5908)	Novel Protein sim. GBank gl 4885281 ref NP_005251.1 pGDF9 - growth differentiation factor 9	Contains protein domain (PF00019) - Igf domain	
2955	87698428 (5909, 5910)	Novel Protein sim. GBank gl 3452473 (AF084205) - serine/threonine protein kinase TAO1 [Rattus norvegicus]	Contains protein domain (PF00069) - kinase Eukaryotic protein kinase domain	264259, 29331822, 29331824, 29331825, 29331826, 35696052, 284908, 52844045, 264512, 60432228, 265018, 265019, 55811150, 264789, 21906787, 21906768, 21908769, 265021, 60170815, 55810764, 264567
2956	85788745 (5911, 5912)	Novel Protein sim. GBank gl 4889254 gb AAD27830.1 AF12185 - (AF121857) sorting nexin 7 [Homo sapiens]	Contains protein domain (PF00787) - PX domain	22278996, 264259, 29331827, 264908, 21906768
2957	90333301 (5913, 5914)	Novel Protein sim. GBank gl 4503023 ref NP_000089.1 pCPT2 - carnitine palmitoyltransferase II precursor	cadherin	22278999, 264259, 29331824, 29331827, 265008, 264595, 264758, 265010, 265011, 284448, 264763, 264683, 264288, 264685, 18108357, 29148828, 264690, 18108362, 264693, 18108370, 60431528, 18108374, 264634, 18108381, 58182323, 18108382, 18108385, 18108388, 58526486, 87168518, 264482, 264487
2958	87440014 (5915, 5916)	Novel Protein sim. GBank gl 4240257 dbj BAA74907.1 - (AB020891) KIAA0884 protein [Homo sapiens]		264595, 264596, 264681, 264369, 264629, 264631, 264587

2959	95109420 (5917, 5918)	Novel Protein sim. GBank gij988221 (U33005) - Tbet1 [Mus musculus]	Contains protein domain (PF00566) - oncogene TBC domain	263994, 2227897, 264259, 60432049, 29331828, 29331828, 35696032, 29331830, 68712502, 56182435, 265008, 264512, 265008, 265009, 60433356, 60433438, 264596, 265017, 265018, 264683, 264288, 264766, 264769, 21906766, 21906787, 21906789, 265020, 60170815, 264692, 27486265, 18108374, 65274791, 35696855, 83373044, 56328486, 60432113
2960	87420081 (5918, 5920)		UNCLASSIFIED	35696286, 56182435, 87168474, 265010, 60170615, 35696423, 56182323, 18108383, 87168518, 264483
2961	85413416 (5921, 5922)	Novel Protein sim. GBank gij5596846 (emb)(CA805177.2) - (Z82266) predicted using Genefinder; similar to WD domain, G-beta repeats [Caenorhabditis elegans]	Contains protein domain (PF00400) - transcript factor WD domain, G-beta repeat	22278997, 22278998, 264259, 29331822, 29331824, 29331826, 29331828, 264907, 264908, 52644045, 265008, 33657402, 21906754, 87168474, 265011, 87168559, 265017, 21906789, 265020, 60170815, 264692, 33657023, 35695763, 18108370, 18108374, 35696423, 264632, 264636, 18108385, 87168518, 22279002, 264564, 264567
2962	87812700 (5923, 5924)		UNCLASSIFIED	35696286, 22278997, 264092, 264094, 264259, 29331824, 66714117, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 264905, 264509, 264907, 264908, 264909, 264510, 264512, 264593, 264594, 60433438, 264758, 52646317, 264602, 264603, 264605, 264760, 264762, 264764, 264288, 264766, 264686, 264768, 264769, 35695917, 265020, 264691, 264634, 264636, 264637, 264638, 264639, 18108385, 264583, 264585, 264586, 264587, 264486
2963	95313464 (5925, 5926)	Novel Protein sim. GBank gij424023 (dbj)(BAA74880.1) - (AB020874) KIAA0887 protein [Homo sapiens]	Contains protein domain (PF00101) - Helix-loop-helix DNA-binding domain	18108392, 56994075, 22278998, 22278999, 29331822, 29331825, 29331826, 29331827, 29331828, 265007, 265008, 264592, 264594, 21906754, 265018, 264760, 264687, 264689, 65274620, 33657182, 27486281, 264629, 55810764, 35696423, 264555, 264636, 264637, 264557, 264558, 264563
2964	94324617 (5927, 5928)		UNCLASSIFIED	264259, 29331828, 33657402, 265017, 265018, 264692, 18108368, 35696423, 83373044, 18108388

2865	80384782 (5929, 5930)	Novel Protein sim. GBank gi14885447 re NP_005452.1 pKRM1 - Kreiser (mouse) mal- related leucine zipper homolog		transcriptfactor	284259, 29331826, 284508, 284509, 284905, 284907, 284908, 284909, 284511, 285008, 284910, 284591, 284593, 284594, 33657402, 285011, 284760, 284762, 284764, 284288, 284685, 284766, 284692, 33657109, 284628, 284829, 35695855, 284630, 284631, 284632, 284634, 284635, 284636, 284637, 284638, 284639, 284593, 284587, 18108381 60432289, 284682, 284448
2866	91725248 (5931, 5932)	Novel Protein sim. GBank gi1526275 emb CAB45690.1 - (Xenopus laevis) [Xenopus laevis]			
2867	94658303 (5933, 5934)	Novel Protein sim. GBank gi1624225 (U19181) - Rabin3 [Rattus norvegicus]		UNCLASSIFIED	284488, 284508, 284509, 284908, 284909, 284511, 284910, 284594, 284758, 85658542, 284762, 284764, 285021, 284556, 18108381, 284584, 284486
2868	95302776 (5935, 5936)	Novel Protein sim. GBank gi14928715 gb AAD34118.1 AF15188 - (AF151881) CGI-123 protein [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C3HC4 type (RING finger)		284687, 52645156, 21906765, 52646365, 21906767, 18108398, 35696423, 22278996, 35696286, 22278997, 265020, 22278999, 265021, 265022, 284093, 284636, 284690, 52644150, 264259, 33657023, 52645080, 284693, 29331822, 56182181, 29331824, 66714117, 29331825, 33109954, 52645129, 29331826, 21906754, 33657182, 29331827, 29331828, 35696052, 27486282, 87168518, 87168474, 265010, 87168559, 265018, 22278000, 265019, 22279002, 264583, 18108351, 284908, 284907, 284448, 66712502, 284568, 284389, 284288, 52646842, 22278998, 22278999, 22278999, 60432049, 284259, 29331824, 29331825, 29331826, 29331828, 284508, 284909, 52644045, 56182435, 265009, 60433438, 55812038, 21906754, 265011, 87168559, 285018, 265019, 284448, 284288, 284389, 52644229, 21906768, 21906769, 21906769, 29148784, 285020, 265021, 52644150, 284691, 33657109, 18108374, 56182323, 60170394, 87168518, 60432113, 22278000
2869	95310957 (5937, 5938)	Novel Protein sim. GBank gi13024743 sp O24734 THSA_SULS7 - THERMOSOME, ALPHA SUBUNIT (CHAPERONIN ALPHA SUBUNIT)		eph	
2870	86088071 (5939, 5940)	Novel Protein sim. GBank gi13165407 (AC004755) - fos37502_1 [Homo sapiens]	Contains protein domain (PF00046) - Homeobox domain	homeobox	

2871	94186930 (5941, 5942)	Novel Protein sim. GBank gi1728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII		lm7	264488, 56182575, 35866286, 56994075, 29331824, 29331826, 29146499, 264508, 264905, 264907, 264112, 264910, 21908754, 87188558, 265018, 265019, 18108351, 264889, 21908765, 21908767, 21908768, 265020, 265021, 60170815, 18108364, 264828, 264629, 18108374, 264636, 264556, 264558, 83373044, 18108384, 18108385, 87188518, 264584, 264587
2872	86825943 (5943, 5944)	Novel Protein sim. GBank gi1728836 sp P39193 ALU6_HUMAN - IIII ALU SUBFAMILY SP WARNING ENTRY IIII		kinase	265017, 35695917, 265021, 33657109, 22279002, 264563
2873	91215301 (5945, 5946)	Novel Protein sim. GBank gi17246789 (AF040642) - No definition line found [Caenorhabditis elegans]		UNCLASSIFIED	29331822, 264692, 33657349, 55811576, 264563
2874	91673002 (5947, 5948)	Novel Protein sim. GBank gi1786117 (L41834) - nuclear protein [Ensis minor]		UNCLASSIFIED	18108392, 52644507, 56182575, 56181686, 22278995, 22278996, 35898286, 22276897, 22278998, 22278999, 264259, 52845080, 29331824, 29331825, 66714117, 60424269, 29331826, 29331827, 29331828, 35696052, 66712502, 264908, 52644045, 265007, 264910, 265009, 60433438, 33109954, 21908754, 55811386, 52644286, 87188474, 87188559, 265017, 265018, 265019, 18108351, 264448, 264389, 264288, 52644229, 18108359, 21908765, 21908767, 21908768, 35695917, 265020, 265021, 52644150, 264691, 264692, 33657023, 27486262, 27486264, 35695763, 18108370, 18108376, 55810784, 55811576, 35696423, 35695855, 264630, 264635, 264557, 52644332, 264558, 83373044, 18108387, 87188518, 60432113, 22279000, 264482, 264487
2875	95325213 (5949, 5950)	Novel Protein sim. GBank gi13880812 emb CAA19508 - (AL023839) similar to HECT-domain (ubiquitin-transferase); cDNA EST yk480d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00832) - HECT-domain (ubiquitin- transferase).	ubiquitin	29331824, 29331827, 29331828, 264910, 85858542, 265011, 265018, 264448, 264288, 264769, 21908767, 265020, 264691, 264559, 83373044
2876	87771202 (5951, 5952)	Novel Protein sim. GBank gi15878136 gb AAD46874.1 AF16093 - (AF160934) BcDNA LD14189 [Drosophila melanogaster]		transport	22278996, 264906, 265007, 265010, 265011, 265017, 265019, 18108351, 264685, 264689, 18108370, 264639, 18108385
2877	91725254 (5953, 5954)	Novel Protein sim. GBank gi15282751 emb CAB45890.1 - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]		UNCLASSIFIED	264509, 264288

2878	87332059 (5955, 5958)	Novel Protein sim. GBank gij746549 (U23522) - No definition line found [Caenorhabditis elegans]	Contains protein domain (PF00480) - ROK family	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 284259, 60432289, 29331827, 29146499, 56182435, 265006, 265007, 265009, 60433356, 60433438, 21908754, 285010, 285011, 265017, 265018, 265019, 284288, 284685, 284688, 21908765, 21908768, 21908767, 21908768, 21908769, 265020, 265021, 265022, 35696423, 264639, 60432113, 22279000, 22279002
2879	91725258 (5957, 5958)	Novel Protein sim. GBank gij526275 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]	complement		264488, 65274572, 56994075, 22278999, 284093, 29331822, 29331824, 264288, 55811957, 33657023, 33657109, 18108370, 55811576, 56182323, 60432113, 264482, 265009, 21908767, 263981, 22279000, 264629, 264564
2880	86298600 (5959, 5960)			UNCLASSIFIED	
2881	87376330 (5961, 5962)				
2882	95303675 (5963, 5964)	Novel Protein sim. GBank gij4928767 [gb]AAD34144.1 [AF151907] CGI-149 protein [Homo sapiens]			22278995, 56994075, 22278996, 22278997, 22278998, 22278999, 264092, 29331824, 29331827, 29331828, 264905, 264591, 264592, 264594, 264595, 264596, 33657084, 284448, 21908765, 21908768, 21908767, 21908768, 21908769, 285020, 265022, 18108365, 33657182, 33657349, 35698423, 83373044, 22279000, 22279002
2883	91725258 (5965, 5966)	Novel Protein sim. GBank gij526275 [emb]CAB45690.1] - (AJ243177) Xenopus RPA interacting protein alpha [Xenopus laevis]			60424179, 52846842, 18108398, 22278997, 264093, 60432049, 264259, 29331822, 60432289, 33656970, 264905, 52844045, 265006, 60431735, 87188474, 265018, 265019, 18108351, 264448, 21908765, 21908768, 35695917, 33657023, 52845129, 18108370, 35698423, 83373044, 56526486, 60432113, 264404, 22279002
2884	94136467 (5967, 5968)	Novel Protein sim. GBank gij2393734 (AC002542) - similar to C. elegans F11A10.5; 80% similarity to Z88297 (PID:g1130819) [Homo sapiens]	ATPase-associated		
2885	87098072 (5969, 5970)	Novel Protein sim. GBank gij103160 [pir]S22126 - finger protein unkempt - fruit fly (Drosophila melanogaster)	UNCLASSIFIED		264910, 55812038, 56181562, 55811957, 264628, 55810784, 264632, 264635, 60432113
2886	86284861 (5971, 5972)				
2887	86455934 (5973, 5974)			UNCLASSIFIED	55811957, 264566, 264369

2988	95357753 (5975, 5976)	Novel Protein sim. GBank gi 4679028 gip AAD27002.11 - (AF077207) HSPC021 [Homo sapiens]	UNCLASSIFIED	264488, 65274572, 22278995, 22278996, 22278997, 22278999, 264092, 264094, 264259, 60432049, 29331824, 29331826, 60432289, 35698052, 29331828, 264107, 264905, 264907, 264908, 66712502, 264828, 264909, 56182435, 265006, 265007, 265008, 60170831, 60432229, 264593, 60433356, 264757, 60433438, 21906754, 265010, 265011, 87168559, 265017, 265018, 264682, 264448, 264389, 264288, 264685, 52644229, 21906765, 21906767, 21906769, 35695917, 265021, 265022, 52644150, 264690, 33657023, 65274620, 263967, 33657109, 27486262, 18108370, 18108372, 18108374, 55810764, 65274791, 35695955, 264635, 264636, 264637, 263981, 264638, 56182323, 83373044, 60432113, 22279000, 264563, 264564, 264565, 264566, 264567, 22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21906765, 21906767, 21906768, 18108374
2989	91225118 (5977, 5978)	Novel Protein sim. GBank gi 113671 sp P23964 ALUF_HUMAN - IIII ALU CLASS F WARNING ENTRY IIII	kinase	264563, 264565, 264566, 264567, 22278996, 22278997, 264905, 264511, 60170831, 264593, 265019, 21906765, 21906767, 21906768, 18108374
2990	87330444 (5979, 5980)	Novel Protein sim. GBank gi 2828838 sp P97348 RHOD_MOUSE - RHO-RELATED GTP-BINDING PROTEIN RHOD	Contains protein domain (PF00071) - Ras family	265007, 264512, 18108351, 264288, 264689, 265020, 264691, 33657023, 33657109
2991	94325361 (5981, 5982)		UNCLASSIFIED	264563
2992	85425184 (5983, 5984)		UNCLASSIFIED	264259, 265019, 264889, 18108385
2993	94325363 (5985, 5986)		UNCLASSIFIED	264488, 29331822, 265017, 264761, 21906769, 65274791, 263981, 264565
2994	94136634 (5987, 5988)	Novel Protein sim. GBank gi 2496549 sp Q50658 YU02_MYCTU - HYPOTHETICAL 28.7 KD PROTEIN CY339.02	transport	22278994, 22278995, 56994075, 22278997, 22278999, 264259, 29331822, 29331824, 29331825, 29331826, 29331827, 29331828, 265008, 265009, 264910, 33109954, 87168474, 87168559, 265018, 265019, 264448, 264288, 21906766, 21906767, 21906768, 21906769, 265021, 265022, 33657023, 264693, 35695955, 83373044, 18108385, 22279000, 264565, 264586, 264905, 264907, 265019, 18108351, 264683
2995	87591070 (5989, 5990)	Novel Protein sim. GBank gi 2734081 (AF000195) - similar to oxysterol-binding proteins [Caenorhabditis elegans]		65274572, 35696286, 264259, 29331824, 35696052, 29146489, 264508, 264907, 265007, 265008, 60433438, 18108348, 265017, 264681, 264683, 264288, 264766, 264769, 264889, 35695917, 60170815, 33657023, 264692, 264634, 264555, 18108381, 18108382, 18108388, 264484
2996	91013788 (5991, 5992)	Novel Protein sim. GBank gi 2828912 (AC002291) - Similar ATP-dependent RNA Helicase [Arabidopsis thaliana]	Contains protein domain (PF00270) - helicase DEAD/DEAH box helicase	

2997	87627440 (5993, 5994)	Novel Protein sim. GBank gi 4589652 dbj BA078848.1 - (AB023221) KIAA1004 protein [Homo sapiens]	homeobox	264488, 56182575, 264258, 66714117, 29331826, 35898052, 264508, 264509, 264907, 264908, 265006, 87168474, 265019, 264448, 264682, 264685, 264766, 21906764, 21906766, 21906768, 21906769, 27488261, 18108374, 35896423, 264634, 264635, 264638, 264557, 18108385, 87188518, 52846385, 22278997, 264508, 264908, 18108351, 21908765, 21908767, 18108370, 18108374, 35896423, 264636, 264639
2998	88095361 (5995, 5996)	Novel Protein sim. GBank gi 3947569 emb CA22252 - (AL034384) cDNA EST yk255b9.3 comes from this gene; cDNA EST yk255b9.5 comes from this gene; cDNA EST EMBL:M75923 comes from this gene [Caenorhabditis elegans]	UNCLASSIFIED	56182575, 22278996, 28147620, 29331825, 29146498, 29146499, 264905, 68712502, 265006, 265009, 21906754, 85858542, 18108351, 29148627, 29148829, 60170615, 33837109, 27486262, 18108370, 18108374, 264558, 264557, 264558, 60170394, 18108385, 264563
2999	94847055 (5997, 5998)	Novel Protein sim. GBank gi 115408 sp P18835 CC19_CAEEL - CUTICLE COLLAGEN 19	UNCLASSIFIED	264887, 22278997, 22278999, 264259, 29331822, 29331824, 35898052, 28146498, 264508, 264905, 264908, 264907, 264908, 284508, 284510, 284511, 285006, 285007, 285008, 285009, 264910, 33857402, 264757, 284595, 264598, 264758, 21906754, 285011, 264600, 285017, 285018, 264605, 265019, 264760, 264761, 264762, 264681, 264682, 264764, 264288, 264685, 264766, 264686, 264768, 264769, 21906765, 21906768, 35895917, 265020, 264691, 264692, 33857023, 284693, 33857109, 33857182, 27486261, 264628, 264629, 18108374, 18108376, 35896423, 35895855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264556, 264638, 264639, 60170394, 83373044, 20788451, 22279002, 264563, 264486, 264567
3000	95089370 (5999, 6000)	Novel Protein sim. GBank gi 1163174 (U32575) - similar to yeast Sec8p. Swiss-Prot Accession Number P32844; similar to mammalian B94, Swiss-Prot Accession Number Q03169; Method: conceptual translation supplied by author [Rattus norvegicus]	UNCLASSIFIED	18108394, 52846842, 56182575, 29331824, 29331825, 29331827, 264910, 33109954, 52844286, 265017, 265019, 264288, 265020, 265021, 52844150, 264892, 35895763, 55810764, 35896423, 56182323, 18108387, 284563, 264564
3001	88078454 (6001, 6002)	Novel Protein sim. GBank gi 2078470 (AC002073) - Putative gene. Genscan predictions confirmed by EST splicing; coded for by human cDNAs AA122029 (NID:g1678046), D31562 (NID:g644442), AA158721 (NID:g1733515), R59640 (NID:g830335) and F13082 (NID:g709111) [Homo sapiens]	calthapsin	284488, 29331824, 29331825, 29331826, 264906, 284510, 285009, 21908754, 264682, 264688, 33857023, 264565
3002	87718167 (6003, 6004)	Novel Protein sim. GBank gi 3589478 (AF085185) - Myosin-IA [Acanthamoeba castellanii]	UNCLASSIFIED	

3003	86848078 (6005, 6006)	Novel Protein sim. GBank gl1754969 (U30292) - collagen type XIII alpha-1 chain [Mus musculus]	Contains protein domain (PF01391) - Collagen triple helix repeat (20 copies)	collagen	284512, 284583, 284584, 284587, 284486
3004	8806876 (6007, 6008)	Novel Protein sim. GBank gl12224629(dbj)gAA208021 - (AB002342) KIAA0344 [Homo sapiens]			29331830, 21906769, 284691, 33657109, 293972, 18108385
3005	87794843 (6008, 6010)	Novel Protein sim. GBank gl14680859(gb)AAD27719.1(A13284 - (AF132844) CGI-10 protein [Homo sapiens])	Contains protein domain (PF01360) - Monooxygenase	oxygenase	29331822, 29331824, 29331827, 60433438, 285011, 285019, 21906766, 21906787, 21906788, 265020, 33657023, 33657349, 60170394, 22279002, 284567
3008	87422224 (6011, 6012)	Novel Protein sim. GBank gl13930525 (AF064447) - sex-determination protein homolog Fem1a [Mus musculus]	Contains protein domain (PF00023) - Ank repeat	MHC	284259, 29331822, 284512, 21906754, 285018, 284687, 21906765, 284691, 264555, 284556, 284558, 18108385
3007	90936005 (6013, 6014)	Novel Protein sim. GBank gl12565052 (U80738) - CAGH1a [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	transcript factor	52844507, 52845156, 65274572, 264909, 284512, 285018, 284760, 284448, 284765, 284689, 60170615, 18108374, 20281152, 284636, 52844332
3008	80416249 (6015, 6016)	Novel Protein sim. GBank gl13127193 (AF062389) - kidney-specific protein [Rattus norvegicus]	Contains protein domain (PF00501) - AMP-binding enzyme	synthase	284905, 284593, 284766, 284636, 52846842, 58182575, 22278995, 22278996, 284259, 29331825, 29331828, 29331827, 29331828, 35698052, 264508, 264509, 284907, 58182435, 264511, 265007, 284512, 265008, 284757, 284758, 55812038, 264759, 33108954, 21906754, 285010, 265011, 284600, 265017, 265018, 265019, 284760, 18108351, 284288, 264389, 21906764, 21906765, 21906767, 55811957, 265020, 265021, 284691, 18108368, 27486262, 20281149, 18108370, 55811576, 284637, 284558, 284557, 18108381, 284558, 58182323, 264558, 18108385, 18108368, 22279002, 284486
3010	95317217 (6019, 6020)	Novel Protein sim. GBank gl14827370(gb)AAD33084.1(A160797 - (AF067972) DNA cytosine methyltransferase 3 alpha [Homo sapiens])	Contains protein domain (PF01923) - Protein of unknown function	UNCLASSIFIED	284686, 284687, 21906767, 21906769, 55811957, 22278995, 35695917, 22278996, 22278997, 265020, 265021, 60170615, 284692, 33657023, 29331822, 284693, 18108364, 29331824, 33657109, 60432289, 29331827, 27486261, 29331828, 264508, 284909, 55811576, 35695855, 265008, 284556, 60433438, 83373044, 18108387, 65274727, 60432113, 265017, 22279000, 285019, 284584, 284682, 284764
3011	94323597 (6021, 6022)	Novel Protein sim. GBank gl15052319(gb)AAD38501.1(A11883 - (AF118836) citrin; adult-onset type II citrullinemia protein [Homo sapiens])	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	35696052, 58182435, 284758, 21906754, 265018, 284760, 284762, 18108351, 284682, 284448, 21906766, 65274620, 18108374, 284482, 284564
3012	87763087 (6023, 6024)			UNCLASSIFIED	283972

3013	81238789 (6025, 6026)	Novel Protein sim. GBank gi 3702286 (AC005787) - R33374_1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	transcriptfactor	264488, 263994, 35686286, 22278997, 264259, 29331824, 60424269, 66714117, 35696052, 284905, 284908, 284907, 284908, 284909, 56182435, 284511, 284512, 284910, 284591, 284592, 264593, 264594, 33657402, 60433438, 264595, 264598, 55812038, 264758, 33109954, 21908754, 265010, 265018, 264604, 284760, 284682, 264683, 284764, 284389, 284288, 284785, 264786, 264686, 284788, 264687, 21906767, 35695917, 265020, 33657023, 264692, 284693, 33657109, 284628, 264629, 55811576, 35698423, 35695855, 264630, 284631, 284632, 284634, 284635, 264636, 284637, 264638, 284639, 83373044, 284563, 284595, 284586, 264587
3014	79877263 (6027, 6028)	Novel Protein sim. GBank gi 3878374 emb CAA93081 - (Z68879) Similarity to Yeast Chl12p protein (PIR Acc. No. S54453); cDNA EST EMBL:D27950 comes from this gene; cDNA EST EMBL:D27949 comes from this gene; cDNA EST EMBL:D33447 comes from this gene; cDNA EST EMBL:D33318 comes from...		ATPase_associated	264760
3015	8695468 (6029, 6030)				22278995, 22278996, 22278997, 264259, 29331824, 29331828, 264908, 265007, 265008, 264910, 265011, 265017, 265019, 264891, 33657109, 18108370, 35695855, 264556, 264564
3016	8775945 (6031, 6032)	Novel Protein sim. GBank gi 168818 sp P41733 CC91_YEAST - CELL DIVISION CONTROL PROTEIN 91		UNCLASSIFIED	52644507, 52646842, 56994075, 52645080, 29331822, 29331824, 35696052, 33656970, 52644045, 264596, 33657084, 265017, 265019, 52644229, 21906767, 35695917, 52644150, 33657023, 33657109, 27486261, 27486262, 27486284, 33657349, 27486265, 35695763, 35695855, 87168518
3017	95011154 (6033, 6034)	Novel Protein sim. GBank gi 4589659 dbj BAA76851.1 - (AB023224) KIAA1007 protein [Homo sapiens]			264488, 18108397, 22278996, 35696286, 22278999, 264259, 29331822, 60432289, 264908, 29331830, 264909, 56182435, 265008, 265007, 265008, 265009, 264591, 60433358, 60433438, 52646317, 21906754, 55811386, 265010, 265011, 87168559, 265017, 265018, 265019, 264288, 264687, 21908765, 21908766, 21908767, 21908769, 265020, 265022, 65274820, 52645129, 33657109, 33657182, 18108370, 283972, 18108374, 284631, 52644332, 83373044, 18108385, 18108388, 56528486, 87168518, 264404, 60432113, 22279000, 264567

3018	11073891 (6035, 6036)	Novel Protein sim. GBank glj3219332 (AC004020) - Unknown gene product [Homo sapiens]		oncogene	264558 264559, 52644507, 18108394, 65274572, 56182575, 22278994, 22278995, 56994075, 22278998, 22278999, 264259, 29331822, 29331824, 60432289, 29331827, 264908, 56182435, 265007, 265009, 60432229, 264593, 60433356, 55812038, 21906754, 87168474, 265011, 87168559, 265017, 265018, 265019, 264681, 18108351, 264448, 264682, 264683, 18108354, 264685, 264687, 264689, 21906766, 21906768, 21906769, 52644150, 264690, 264691, 33657023, 264692, 264693, 33657109, 52645129, 33657349, 264629, 65274781, 264634, 52644332, 56182323, 18108385, 87168518, 22279000, 22279002, 264563
3020	94318251 (6038, 6040)	Novel Protein sim. GBank glj3414809 (AF081529) - <i>rls</i> [Mus musculus]	Contains protein domain (PF00415) - Regulator of chromosome condensation (RCC1)	ATPase-associated	264488, 263994, 35696286, 264259, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264510, 264910, 60174639, 264600, 264603, 264760, 264762, 264682, 264763, 264764, 264288, 264369, 264766, 264687, 264688, 264769, 55811957, 35695917, 33657023, 264628, 35696423, 35695855, 264630, 264632, 264634, 264635, 264636, 264637, 264558, 264557, 264638, 264639, 83373044, 18108385, 264564, 264567, 264486
3021	80478512 (6041, 6042)	Novel Protein sim. GBank glj3880889 (emb) [CAB09005] - (Z85559) cDNA EST yk23864.5 comes from this gene; cDNA EST EMBL:C13455 comes from this gene; cDNA EST yk32996.5 comes from this gene; cDNA EST CEMSH45R comes from this gene [Caenorhabditis elegans]			264769, 264629, 264482
3022	87718500 (6043, 6044)			UNCLASSIFIED	264259, 29331826, 29331828, 264288, 264568
3023	95305484 (6045, 6046)	Novel Protein sim. GBank glj416592 (sp) P32323/JAG1_YEAST - A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR	Contains protein domain (PF00614) - Phospholipase D. Active site motif	UNCLASSIFIED	264488, 22278995, 35696286, 22278997, 29331826, 35696052, 264907, 29331830, 52644045, 56182435, 60432229, 264592, 60433356, 60433438, 264689, 21906767, 55811957, 35695917, 265021, 18108378, 263978, 264635, 264558, 22279000
3024	86675305 (6047, 6048)			UNCLASSIFIED	60432049, 264760, 21906768, 55811957, 35695917, 264690, 264555, 264559, 264593, 55811576
3025	65706629 (6049, 6050)	Novel Protein sim. GBank glj295671 (L11275) - selected as a weak suppressor of a mutant of the subunit AC40 of DNA dependant RNA polymerase I and III [Saccharomyces cerevisiae]			

3028	87643862 (8051, 8052)	Novel Protein sim. GBank gl 3024052 sp P97824 KARI_RAT - KALIRIN (PAM COOH-TERMINAL INTERACTOR PROTEIN 10) (P-CIP10)		UNCLASSIFIED	22278996, 22278997, 264490, 29331825, 264111, 265007, 60170831, 265010, 87168559, 265019, 21906765, 29148627, 263987, 20281149, 20281089, 263975, 293977, 20281071, 56526486, 22279000
3027	94844563 (8053, 8054)	Novel Protein sim. GBank gl 4929847 gb AAD34084.1 AF15184 - (AF151847) CGI-89 protein [Homo sapiens]	Contains protein domain (PF01529) - DHC zinc finger domain	UNCLASSIFIED	18108394, 22278995, 22278996, 35696286, 22278997, 22278998, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 60432289, 29331828, 29331827, 29331828, 35696052, 264905, 264907, 29331830, 264908, 264909, 264510, 265007, 265008, 265009, 264910, 33657402, 264596, 21906754, 265010, 265011, 87168559, 264600, 265018, 18108351, 264682, 264683, 264764, 264288, 264685, 264687, 264789, 264889, 21906765, 21906766, 21906767, 21906768, 21906769, 29148629, 35695917, 265020, 265021, 265022, 52844150, 264682, 33657023, 264693, 52645129, 33657109, 27486281, 18108374, 55811576, 35696423, 65274791, 264636, 264556, 264557, 264638, 60170394, 264639, 264558, 83373044, 18108385, 56528486, 22279000, 22279002
3028	94231997 (8055, 8056)	Novel Protein sim. GBank gl 308052 emb CAA18650 - (AL022589) hypothetical protein [Schizosaccharomyces pombe]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	22278995, 22278996, 22278997, 22278999, 264259, 29331824, 29331827, 35696052, 264908, 265007, 265008, 265009, 60170831, 21906754, 265011, 87168559, 265018, 264762, 264883, 264765, 264689, 21906765, 21906768, 21906769, 29148629, 35695917, 265021, 265022, 33657109, 27486285, 264628, 264629, 18108374, 35696423, 35695855, 264638, 60170394, 22279000, 22279002, 264482, 264584
3029	87619284 (8057, 8058)			UNCLASSIFIED	22278997, 22278999, 29331827, 264905, 264509, 264909, 264510, 264511, 264512, 87168474, 265019, 18108351, 21906768, 284534, 264690, 264693, 263989, 18108370, 264558, 22278000, 22279002, 264482
3030	87544928 (8059, 8060)	Novel Protein sim. GBank gl 3757728 emb CAA18782 - (AL022727) dJ8019.1 (olfactory receptor-like protein (hs8M1-1)) [Homo sapiens]	Contains protein domain (PF00001) - 7 transmembrane receptor (rhodopsin family)	Im7	
3031	91677953 (8061, 8062)	Novel Protein sim. GBank gl 4530587 gb AAD22105.1 - (AF132000) TADA1 protein [Homo sapiens]		UNCLASSIFIED	22278995, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 29331826, 29331827, 29331828, 35696052, 264908, 265018, 21906765, 21906766, 21906767, 21906768, 265021, 263974, 18108374, 264558, 56526486, 22279000, 22279002

3032	94130124 (6063, 6064)	Novel Protein sim. GBank gi 1019951 (U37429) - similar to M. musculus MERS and other AHPCTSA proteins [Caenorhabditis elegans]	Contains protein domain (PF00534) - synthase Glycosyl transferases group 1	22278996, 35696286, 264259, 29331824, 28331828, 284907, 29331830, 264758, 33109954, 87168474, 87168559, 265019, 264286, 21906769, 285021, 284693, 35696423, 35695855, 264636, 56182323, 83373044, 87168518
3033	95308321 (6065, 6066)	Novel Protein sim. GBank gi 5031573 ref NP_005712.1 pACTR - ARP3 (actin-related protein 3, yeast) homolog	Contains protein domain (PF00022) - struct Actin	35696286, 264259, 29331826, 35696052, 264508, 264905, 264906, 284907, 284908, 284909, 265008, 284591, 21908754, 265010, 265019, 264681, 264369, 264768, 21906764, 21906768, 35695917, 33657023, 264628, 35695955, 264632, 264635, 284639, 284482, 264563
3034	80415373 (6067, 6068)		UNCLASSIFIED	284908, 284907, 264510, 264592, 265010, 264762, 264766, 264637, 264638, 264486, 264636
3035	91220692 (6069, 6070)	Novel Protein sim. GBank gi 3738207 emb CAA21262 - (AL031853) conserved ATP-GTP binding protein [Schizosaccharomyces pombe]	UNCLASSIFIED	
3036	91718323 (6071, 6072)	Novel Protein sim. GBank gi 728837 sp P39194 ALU7_HUMAN - III ALU SUBFAMILY SQ WARNING ENTRY IIII	kinase	284907, 33657402, 265021
3037	95307434 (6073, 6074)	Novel Protein sim. GBank gi 4406580 gb AAD20040 - (AF131766) Similar to Ena-VASP like protein [Homo sapiens]		265017
3038	95421807 (6075, 6076)	Novel Protein sim. GBank gi 5360093 gb AAD42865.1 AF15509 - (AF155099) NY-REN 18 antigen [Homo sapiens]	Contains protein domain (PF00827) - UBA domain	22278996, 22278997, 264259, 284905, 285007, 265009, 80433356, 21906754, 285018, 285019, 18108351, 264687, 21906765, 265020, 265021, 65274620, 27486282, 264636, 56182323, 18108385, 22279000
3039	87332257 (6077, 6078)	Novel Protein sim. GBank gi 4757128 emb CAB42094.1 - (AJ238717) ZRP protein [Rattus norvegicus]	UNCLASSIFIED	35696286, 28331828, 264109, 264110, 264511, 265007, 21906754, 265011, 264681, 264683, 264687, 21906768, 284691, 18108370, 263972, 264629, 18108374, 263977, 35696423, 264584, 18108391, 284692, 264556, 18108382, 18108385, 264567
3040	90933517 (6079, 6080)	Novel Protein sim. GBank gi 4884278 emb CAB43247.1 - (AL050037) hypothetical protein [Homo sapiens]	UNCLASSIFIED	
3041	86312357 (6081, 6082)	Novel Protein sim. GBank gi 3876073 emb CAB04122.1 - (Z81505) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D28025 comes from this gene; cDNA EST EMBL:D28024 comes from this gene; cDNA EST EMBL:D33210 comes from this gene; cDNA EST EMBL:D33441 comes from this ...	UNCLASSIFIED	56994075, 22278997, 22278998, 29331827, 33656970, 33109854, 21906754, 87168559, 264600, 264683, 21906765, 21906768, 22279002
3042	85749402 (6083, 6084)	Novel Protein sim. GBank gi 790236 (U21156) - sarcolemmal associated protein-2 [Cryptotagus cuniculus]	glycoprotein	264636

3043	87773028 (6085, 6088)	Novel Protein sim. GBank gij854085[embj CAA58337] - (X83413) U88 [Human herpesvirus 6]		UNCLASSIFIED	35688286, 60424269, 35696052, 284508, 284905, 66712502, 58182435, 55811386, 52844296, 55811150, 35895917, 60170615, 33657109, 18108374, 284634, 60431850, 22278998, 22278998, 22278999, 29331824, 56182435, 284511, 265007, 60170831, 60432229, 60433356, 33109954, 18108351, 264288, 35695917, 18108388, 18108370, 60170394
3044	87646182 (6087, 6088)	Novel Protein sim. GBank gij4104922 (AF042278) - o251 homolog [Pseudomonas putida]	Contains protein domain (PF01209) - ubiquitin/COO5 methyltransferase family	glycoprotein	
3045	94127598 (6089, 6090)	Novel Protein sim. GBank gij4589880[dbj BAA76859.1] - (AB023232) KIAA1015 protein [Homo sapiens]	Contains protein domain (PF00096) - Zinc finger, C2H2 type	dna_rna_bind	264488, 264259, 35696052, 284508, 284905, 284509, 264906, 284907, 284909, 284511, 265006, 264591, 264593, 33109954, 284604, 264784, 284683, 284288, 284766, 264768, 21906765, 21906768, 55811957, 35695917, 27486262, 18108370, 264628, 18108374, 35695855, 264630, 264632, 264635, 264563, 264584, 264566
3046	88088247 (6091, 6092)			UNCLASSIFIED	22278999, 29331822, 29331824, 29331825, 29331826, 60432289, 29331827, 29331828, 264906, 52846317, 55811957, 60432113, 22279000, 22279002, 264482, 264584
3047	95088924 (6093, 6094)			UNCLASSIFIED	264488, 22278996, 22278997, 22278999, 29331824, 29331825, 56182435, 264511, 265008, 265009, 265011, 265017, 264766, 21906768, 21906769, 35695917, 52844150, 33657349, 65274791, 35695855, 264555, 60432113, 22279000, 264566
3048	87629418 (6095, 6096)	Novel Protein sim. GBank gij4588034[gb AAD25862.1]AF09287 - (AF092878) zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00087) - Zinc finger, C3HC4 type (RING finger)	UNCLASSIFIED	284102, 29148784
3049	88228655 (6097, 6098)	Novel Protein sim. GBank gij5454158[ref NP_008286.1]pVARS - valyl-IRNA synthetase 1	Contains protein domain (PF01406) - IRNA synthetases class I (C)	UNCLASSIFIED	22278997, 29331826, 284907, 264758, 87168559, 265018, 264448, 21908768, 265020, 33657109, 35695855, 60432113, 22279000
3050	87643878 (6099, 6100)	Novel Protein sim. GBank gij4589842[dbj BAA76843.1] - (AB023216) KIAA0999 protein [Homo sapiens]	Contains protein domain (PF00069) - Eukaryotic protein kinase domain	kinase	264259, 29331825, 264909, 265007, 264512, 265019, 284288, 21908768, 265020, 284693, 18108385, 56526486, 87168518, 22279002, 264566
3051	87750599 (6101, 6102)				22278997, 264595, 265019, 264288, 284693, 87168518
3052	57108030 (6103, 6104)	Novel Protein sim. GBank gij117528[sp P14755]CRYL_RABIT - LAMBDA-CRYSTALLIN	dehydrogenase		264534

3053	95350373 (6105, 6106)	Novel Protein sim. GBank gi 3947613 emb CAA19465.1 - (AL023828) cDNA EST EMBL:M89008 comes from this gene; cDNA EST yk282d3.5 comes from this gene [Caenorhabditis elegans]		UNCLASSIFIED	65274572, 56181686, 22278995, 35696286, 22278998, 264259, 60432289, 265008, 265009, 60433438, 21906754, 265010, 87168559, 264603, 265018, 265019, 264763, 264764, 264288, 21906765, 21906766, 21906768, 21906769, 35695917, 18108374, 35696423, 264638, 56182323, 22279000, 264563
3054	86843510 (6107, 6108)	Novel Protein sim. GBank gi 107621 pir S50755 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii		UNCLASSIFIED	35698286, 35696052, 28331830, 264908, 264909, 264512, 264910, 265017, 264604, 264766, 265020, 33657109, 264628, 35695855, 264636, 264564, 264566, 264486
3055	95350537 (6109, 6110)	Novel Protein sim. GBank gi 4680655 gb AAD27717.1 AF13294 - (AF132942) CGI-08 protein [Homo sapiens]		transport	60424179, 65274572, 56182575, 35696286, 22278998, 22278999, 60432049, 264259, 60424269, 60432289, 35696052, 56182435, 265008, 265009, 60170831, 60432229, 60431735, 60433356, 264594, 60433438, 21906754, 55811386, 265011, 87168559, 265019, 18108351, 264683, 264288, 264369, 264688, 21906768, 55811957, 35695917, 60170815, 33657023, 65274620, 33657109, 35695763, 60431528, 18108374, 55810764, 55811576, 35696423, 65274791, 264636, 60431850, 18108381, 56182323, 60170394, 18108385, 60432113, 264564, 264565, 264566
3056	91661636 (6111, 6112)	Novel Protein sim. GBank gi 726837 sp P39194 ALU7 SQ WARNING ENTRY IIII		glycoprotein	264488, 264569, 18108394, 52646842, 22278997, 22278998, 22278999, 264259, 66714117, 29331828, 29331827, 35696052, 264508, 264509, 264905, 264906, 264907, 264908, 264909, 265006, 264512, 265007, 265008, 265009, 264910, 33657402, 55812038, 264596, 264758, 265010, 265011, 265017, 265019, 264760, 18108351, 264762, 264763, 264764, 264288, 264766, 264687, 18108357, 264768, 264769, 264689, 21906765, 21906766, 21906767, 21906768, 21906769, 35695917, 265020, 265021, 264681, 264693, 33657109, 18108370, 264628, 264629, 18108374, 55811576, 35696423, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264638, 18108381, 83373044, 18108385, 22279000, 22279002, 264563, 264564, 264565, 264566, 264486, 264567

3057	95412748 (6113, 6114)	Novel Protein sim. GBank gij3878119[emb CAA88860] - (Z49088) similar to GTP-binding protein; cDNA EST EMBL:M89111 comes from this gene; cDNA EST EMBL:D27709 comes from this gene; cDNA EST EMBL:D27708 comes from this gene; cDNA EST EMBL:D73788 comes from this gene; cDNA EST yk353....			284508, 284905, 284907, 284908, 284909, 284510, 284512, 284910, 284592, 284594, 284767, 18108374, 284635, 284555, 284637, 284639, 284583, 284564, 284585, 284486
3058	78646228 (6115, 6116)			UNCLASSIFIED	284693
3059	87829425 (6117, 6118)	Novel Protein sim. GBank gij4588034[gb AAD25962.1 AF092878] zinc RING finger protein SAG [Homo sapiens]	Contains protein domain (PF00097) - Zinc finger, C2HC4 type (RING finger)	UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 284490, 284259, 29331824, 29331825, 29331827, 35896052, 29331828, 285007, 60433438, 285017, 285018, 285019, 284681, 284448, 284288, 284768, 21906765, 21908766, 21906767, 21906769, 29148629, 29148784, 265022, 52644150, 18108370, 284636, 18108385, 284583, 284587
3060	78346681 (6119, 6120)			UNCLASSIFIED	284567
3081	87740984 (6121, 6122)			UNCLASSIFIED	284112, 52644296, 21906768, 33657023, 283974, 18108385
3062	87619465 (6123, 6124)	Novel Protein sim. GBank gij4454690[gb AAD20863] - (AF070657) glutathione S-transferase subunit 13 homolog [Homo sapiens]		transferase	284908, 265008, 18108351, 284566
3063	80076023 (6125, 6126)	Novel Protein sim. GBank gij2246532 (U93872) - ORF 73, contains large complex repeat CR 73 [Kaposi's sarcoma-associated herpesvirus]		UNCLASSIFIED	18108359, 284558
3064	91241528 (6127, 6128)	Novel Protein sim. GBank gij4240315[gb BAA74936.1] - (AB020720) KIAA0913 protein [Homo sapiens]	Contains protein domain (PF00403) - Heavy-metal-associated domain	UNCLASSIFIED	52846365, 52846842, 65274572, 56182575, 56181686, 22278995, 22278996, 22278997, 22278998, 284259, 60432049, 29331824, 68714117, 284508, 284907, 284908, 56182435, 285009, 60432229, 60433438, 55812038, 52844286, 285018, 284682, 284288, 284686, 284768, 284887, 52844229, 284689, 21908768, 284691, 284692, 284693, 18108370, 18108377, 55811576, 284636, 56182323, 284558, 284639, 18108385, 22278990, 22278992
3065	91639201 (6129, 6130)	Novel Protein sim. GBank gij5658743[gb AAD45960.1 AC005067] Supported by Human EST H08032.1 (NID:g872854), mouse EST AA870042.1 (NID:g2965487), and gencan [Homo sapiens]		UNCLASSIFIED	22278996, 22278998, 284093, 284094, 284095, 29331824, 60424289, 68714117, 284100, 284907, 285007, 284591, 60432229, 284593, 265011, 285019, 18108351, 284766, 284767, 21906765, 21906768, 284693, 20281069, 22279000, 22279002, 284482, 284588, 284587

3066	91224437 (6131, 6132)	Novel Protein sim. GBank gi 4684268 emb CABA3245.1 - (ALO50028) hypothetical protein [Homo sapiens]		UNCLASSIFIED	18108397, 22278995, 56994075, 22278998, 264905, 68712502, 265006, 264512, 264910, 264758, 60174639, 264760, 18108351, 264764, 264683, 18108359, 264692, 18108364, 18108368, 18108370, 18108377, 18108379, 60170394, 264587, 264488, 264489, 35696286, 22278996, 56994075, 264259, 29331822, 29331825, 35696052, 29331828, 264508, 264905, 264509, 264906, 264907, 264908, 264909, 264112, 264510, 264511, 264512, 265008, 265009, 264910, 264591, 264592, 264593, 264594, 264757, 264595, 264596, 264758, 265010, 265011, 87168559, 264601, 264802, 264603, 264604, 264605, 265019, 264760, 264762, 264448, 264763, 264764, 264288, 264369, 264766, 264768, 264687, 264769, 264688, 21906765, 21906767, 21906768, 35695917, 265020, 265021, 264534, 52644150, 264691, 33657023, 264693, 264628, 60431528, 263977, 35695855, 264630, 264631, 264634, 264635, 264636, 264637, 264638, 264639, 83373044, 56526486, 87168518, 22279000, 22279002, 264563, 264483, 264564, 264565, 264566, 264587, 264486
3067	95422551 (6133, 6134)	Novel Protein sim. GBank gi 4689258 gb AAD27832.1 AF12185 - (AF12185) sorting nexin 9 [Homo sapiens]	Contains protein domain (PF00787) - struct PX domain		264112, 22278996, 56994075, 22278998, 22278999, 264259, 264107, 264905, 29331830, 52644045, 264110, 60170831, 264592, 264594, 33657402, 21906754, 33109954, 87168474, 87168559, 265017, 264448, 264764, 264683, 264766, 52644229, 21906765, 21906766, 21906768, 21906769, 60170815, 33657023, 18108370, 18108376, 264634, 264557, 80170394, 56182323, 18108385, 87168518, 22279000, 264482
3068	85360851 (6135, 6136)	Novel Protein sim. GBank gi 3878119 emb CAA88860 - (Z49068) similar to GTP-binding protein; cDNA EST	Contains protein domain (PF01928) - struct GTPase of unknown function		
3069	95412753 (6137, 6138)	EMBL:M88111 comes from this gene: cDNA EST EMBL:D27709 comes from this gene: cDNA EST EMBL:D27708 comes from this gene: cDNA EST EMBL:D73788 comes from this gene: cDNA EST yk353...			

3070	94318173 (6138, 6140)	Novel Protein sim. GBank gl 387778 emb CAB05527 - (Z83110) cDNA EST yk472b5.3 comes from this gene; cDNA EST yk474a7.3 comes from this gene; cDNA EST yk472b5.5 comes from this gene; cDNA EST yk466c10.3 comes from this gene; cDNA EST yk468c10.5 comes from this gene; cDNA EST EM...	Synthase	264488, 22278994, 22278995, 22278996, 58994075, 22278997, 22278999, 264259, 29331822, 29147620, 29331824, 66714117, 29331826, 29146498, 29146499, 66712502, 29331830, 52644045, 56182435, 264511, 265007, 264512, 264910, 60170831, 264592, 264758, 33109954, 21908754, 87168474, 265019, 18108351, 284448, 264683, 264288, 52844228, 264689, 21908765, 21908768, 21908787, 21908769, 35695917, 265020, 265021, 60170815, 52644150, 264691, 33657023, 27486261, 27486264, 264628, 18108370, 18108377, 55811576, 35695855, 284634, 264635, 18108381, 60170394, 56182323, 264558, 83373044, 18108385, 18108387, 56526486, 264404, 264563, 264566
3071	84325573 (6141, 6142)	Novel Protein sim. GBank gl 4502425 et NP_001709.1 pBMP6 - bone morphogenetic protein 6 precursor	Contains protein domain (PF00085) - Igf Thiredoxin	264488, 65274572, 18108398, 22278996, 35695288, 22278997, 22278998, 22278999, 264259, 29331822, 66714117, 29331826, 35695052, 29331828, 29146498, 29146499, 264907, 264908, 29331830, 264909, 52644045, 56182435, 265006, 265007, 264512, 265008, 265009, 60170831, 60432229, 264592, 60433358, 33657402, 60433438, 33109954, 52644298, 87168474, 265010, 265017, 264681, 264288, 264685, 284766, 264687, 264769, 284689, 21906765, 21906768, 21906787, 21906768, 21906769, 35695917, 265020, 265021, 265022, 60170815, 52644150, 264690, 264691, 264692, 33657023, 264693, 33657109, 263971, 18108374, 18108377, 35695423, 55811576, 65274791, 35695855, 264630, 264635, 264636, 264557, 60170394, 83373044, 60432113, 22279000, 22279002, 264563, 264584, 264585, 264586, 264567, 56182575, 29331822, 29331824, 29331825, 29146498, 264908, 52644045, 56182435, 265009, 60433438, 55812038, 18108351, 264683, 264369, 52644229, 52644150, 33657023, 264693, 33657109, 18108374, 55811576, 65274791, 264555, 56182323, 60432113, 264564
3072	95115892 (6143, 6144)	Novel Protein sim. GBank gl 1263289 (U47856) - fibrin-4 [Araneus diadematus]	transcriptfactor	

3073	86147248 (6145, 6146)	Novel Protein sim. GBank gi134840 sp P22328 CORB_HUMAN - CORNIFIN B (SMALL PROLINE-RICH PROTEIN IB) (SPR-IB) (14.9 KD PANCORNULIN)		UNCLASSIFIED	264769
3074	88089351 (6147, 6148)	Novel Protein sim. GBank gi13411947 (AC004932) - similar to yeast hypothetical protein ybk4; similar to P38164 (PID:g586461) [Homo sapiens]		UNCLASSIFIED	264488, 265019, 264448, 264288, 21906767, 264693, 18108368, 18108370, 18108374, 264567
3075	88085752 (6149, 6150)	Novel Protein sim. GBank gi4557349 ref NP_000456.1 pBARD - BRCA1 associated RING domain 1	Contains protein domain (PF00023) - Ank repeat	homeobox	264509, 264907, 264689, 264693, 56526486
3076	87818219 (6151, 6152)			UNCLASSIFIED	18108398, 29331822, 29331827, 60432229, 265017, 264891, 264683
3077	88734277 (6153, 6154)	Novel Protein sim. GBank gi3023956 sp Q00808 HET1_PODAN - VEGETATILE INCOMPATIBILITY PROTEIN HET-E-1	Contains protein domain (PF00400) - kinase WD domain, G-beta repeat		65274572, 35696052, 264511, 60170831, 87168474, 264369, 35695917, 33657182, 27486264, 33657349, 35695763, 35695855, 264639
3078	88089355 (6155, 6156)	Novel Protein sim. GBank gi13900850 (AC004994) - similar to KIAA0600; similar to d1026456 (PID:g3043724) [Homo sapiens]			22279002
3079	87821893 (6157, 6158)	Novel Protein sim. GBank gi13875410 emb CAB02876 - (Z81052) Similarity to Yeast ABC1P protein (SW:ABC1_YEAST); cDNA EST yk229g8.3 comes from this gene; cDNA EST yk229g8.5 comes from this gene [Caenorhabditis elegans]		transport	29331824, 29331826, 264758, 55811386, 265017, 55811150, 52644229, 21908788, 265020, 265021, 264693, 18108376, 264631, 52644332, 22279002
3080	95298274 (6159, 6160)	Novel Protein sim. GBank gi15257221 gb AAD41265.1 - (AF117887) protein arginine methyltransferase [Mus musculus]		interferon	264488, 52644507, 22278996, 22278998, 264490, 264259, 29331824, 66714117, 29331825, 29331826, 29331827, 29331828, 29146499, 264508, 264905, 264828, 52644045, 56182435, 265006, 264591, 264596, 21906754, 60174639, 265010, 264882, 264448, 264763, 264683, 264764, 264288, 264685, 264768, 264688, 264689, 21906755, 21906767, 21906769, 55811957, 35695917, 265020, 60170815, 52644150, 264682, 33657023, 264693, 65274820, 33657109, 27486261, 35695763, 264628, 18108370, 65274791, 264558, 56182323, 60170394, 264482, 264565, 264484
3081	88084864 (6161, 6162)	Novel Protein sim. GBank gi1728831 sp P39188 ALU1_HUMAN - IIII ALU SUBFAMILY J WARNING ENTRY IIII		UNCLASSIFIED	18108398, 264509, 264905, 264906, 264907, 264908, 264909, 264510, 264511, 265009, 264910, 264595, 264758, 265011, 265018, 264760, 264761, 264763, 264764, 18108354, 264685, 264766, 264628, 264629, 264630, 264631, 264632, 264634, 264635, 264555, 264638, 18108382, 18108385, 264563, 264565, 264568
3082	80310121 (6163, 6164)				264764, 55811957, 264555, 264564

3083	68085768 (6165, 6166)	Novel Protein sim. GBank gij888241 (U28488) - C56C10.3 gene product [Caenorhabditis elegans]		UNCLASSIFIED	264488, 264259, 29331824, 264106, 265008, 264591, 264592, 21906754, 264288, 264767, 21906768, 21906769, 29148784, 264691, 264632, 22278000
3084	67448568 (6167, 6168)	Novel Protein sim. GBank gij476774(pir)A37475 - probable structural component p38 - borna disease virus			22278995, 60432289, 35696052, 264905, 264906, 264907, 264908, 264909, 265006, 265007, 264910, 264593, 264595, 264758, 264369, 264288, 264768, 35695917, 265020, 18108374, 35696423, 264631, 264558, 264555, 264556, 264587, 264486, 265011, 264681
3085	67765781 (6169, 6170)	Novel Protein sim. GBank gij2565057 (U80741) - CAGH44 [Homo sapiens]		UNCLASSIFIED	
3086	67768942 (6171, 6172)	Novel Protein sim. GBank gij3894189 (AC005662) - hypothetical protein [Arabidopsis thaliana]		UNCLASSIFIED	22278998, 264092, 264259, 29331822, 29331825, 264108, 264112, 18108351, 264687, 263967, 263974, 55810784, 263981, 18108385, 264487
3087	67462888 (6173, 6174)				52646365, 56994075, 22278997, 22278998, 29331824, 29331825, 35696052, 60433438, 33109954, 21906754, 52646317, 265017, 264682, 264369, 264684, 21908767, 21906768, 265020, 264691, 33657023, 33657109, 52645129, 33657182, 27486262, 35695855, 87168518, 264591
3088	91224441 (6175, 6176)	Novel Protein sim. GBank gij3355304 (AF001549) - Unknown gene product [Homo sapiens]		UNCLASSIFIED	
3089	95361242 (6177, 6178)	Novel Protein sim. GBank gij4688146(pbl)AAD27782.1(AF07704) lambda-crystallin [Homo sapiens]	Contains protein domain (PF00725) - 3-hydroxyacyl-CoA dehydrogenase	dehydrogenase	18108397, 65274572, 56182575, 56181686, 56994075, 35696288, 22278997, 22278998, 264259, 29331824, 29331825, 29331826, 29331828, 264907, 29331830, 264909, 56182435, 264510, 265007, 60170831, 60432229, 21906754, 55811386, 265017, 265018, 265019, 264760, 55811150, 264288, 264766, 56181562, 21906765, 21906766, 21906767, 21906768, 265021, 60170815, 27486262, 18108370, 60431528, 35696423, 264558, 264559, 60432113, 264486

3090	95342371 (6179, 6180)	Novel Protein sim. GBank g 1354050 (U47024) - MEM3 [Mus musculus]		UNCLASSIFIED	50424179, 52845156, 65274572, 56182575, 56181686, 22278995, 35696286, 56994075, 22278996, 22278998, 22278999, 264259, 29331822, 56182181, 29331824, 29331825, 29331826, 29331827, 29331828, 35696052, 33659970, 264908, 264908, 52644045, 264828, 265006, 265007, 265008, 60170831, 60432229, 60433356, 33657402, 55812038, 264758, 21908754, 33109954, 52646317, 55811386, 52644296, 87168474, 265011, 87168559, 265017, 265018, 265019, 55811150, 18108351, 264681, 264448, 264288, 264369, 18108357, 264768, 52644229, 56181562, 21908764, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265022, 60170815, 264690, 52644150, 264691, 33657023, 18108365, 65274620, 33657109, 18108368, 33657182, 27486281, 27486265, 35695763, 18108374, 18108376, 55810784, 35696423, 55811576, 65274781, 35695855, 264557, 56182323, 83373044, 18108387, 18108388, 87168518, 22279000, 22279002, 264563, 264482
3091	95317424 (6181, 6182)	Novel Protein sim. GBank g 3873932(emb)(CAB01859) - (Z79598) Similarity to Bovine aspartyl beta hydroxylase (TR:G162694); cDNA EST EMBL:D27916 comes from this gene; cDNA EST EMBL:D27915 comes from this gene; cDNA EST EMBL:D64881 comes from this gene; cDNA EST EMBL:D68139 comes f...		UNCLASSIFIED	35696286, 29331822, 35696052, 264508, 264509, 264905, 264906, 264908, 264909, 264510, 264758, 265010, 265011, 264583, 264685, 264788, 264788, 264769, 264693, 264628, 35696423, 35695855, 264632, 264635, 264639, 264482, 264583, 264486

3092	95314592 (6183, 6184)	Novel Protein sim. GBank gij1710756[sp15880]RS2_HUMAN - 40S RIBOSOMAL PROTEIN S2 (S4) (LLREP3 PROTEIN)	Contains protein domain (PF00333) - Ribosomal protein S5	ribosomalprot	284488, 60424179, 18108386, 22278995, 58994075, 22278986, 35696286, 22278997, 22278998, 60432049, 284259, 29331822, 28331824, 28331825, 29331826, 29331827, 35696032, 28331828, 28146498, 28146499, 284508, 284509, 284905, 284906, 284907, 28331830, 284908, 284909, 284113, 284510, 284511, 265008, 284512, 265007, 265008, 284910, 265009, 60170831, 284591, 284592, 60431735, 284593, 284594, 60433438, 284595, 284758, 21908754, 265010, 265011, 284601, 284602, 265017, 284603, 284604, 265018, 284605, 265019, 284760, 284762, 284681, 18108351, 264763, 284682, 264448, 284784, 284683, 284288, 284369, 284765, 284786, 284688, 284787, 284687, 284788, 284789, 284688, 21908764, 284689, 21908765, 21908766, 21908767, 21908768, 21908769, 29148629, 29148784, 35895917, 265020, 285021, 284534, 60170815, 284690, 284691, 284692, 65274620, 33657109, 27486262, 284628, 284629, 18108374, 263978, 18108377, 35896423, 284630, 284631, 284632, 284634, 284635, 284555, 284636, 284637, 284556, 284638, 284557, 284558, 284639, 60170394, 18108385, 284259, 29331824, 35896052, 284905, 265006, 60432228, 60431735, 284684, 284369, 284288, 284766, 21908767, 35898423, 83373044, 18108389
3093	94318457 (6185, 6186)	Novel Protein sim. GBank gij5002567[emb]CAB44347.1] - (Y17454) LSFR1 protein [Homo sapiens]	UNCLASSIFIED		
3094	94316875 (6187, 6188)	Novel Protein sim. GBank gij400734[sp131044]PBP_RAT - PHOSPHATIDYLETHANOLAMINE-BINDING PROTEIN (23 KD MORPHINE-BINDING PROTEIN) (P23K)	Contains protein domain (PF01161) - Phosphatidylethanolamine-binding protein	collagen	18108398, 284259, 60432289, 29331827, 284511, 284763, 284288, 284787, 285022, 284691, 284693, 65274791, 56182323, 284584, 284565

3095	94848182 (6189, 6190)	Novel Protein sim. GBank gjl4877759 gb AAD31421.1 AF12444 - (AF124440) MAGE tumor antigen D1 (Homo sapiens)	Contains protein domain (PF01454) - MAGE family	UNCLASSIFIED	18108397, 56182575, 22278995, 35696286, 56994075, 22278997, 22278999, 264259, 60432049, 66714117, 29331825, 60432289, 35696052, 336566970, 29146498, 264508, 264905, 284509, 29331830, 284909, 264510, 264511, 264512, 265007, 265008, 265009, 60170831, 264758, 21906754, 85658542, 265010, 265011, 87168559, 265017, 265018, 265019, 264760, 264681, 264682, 264683, 264764, 264369, 284288, 284686, 264768, 264769, 264689, 21906765, 21906768, 21906767, 55811957, 35695917, 265020, 265021, 265022, 52644150, 264691, 264692, 33657023, 264693, 263972, 18108376, 55811576, 35696423, 284952, 60170394, 264639, 83373044, 18108385, 18108387, 65274727, 87168518, 60432113, 264482, 264563, 264564, 264566, 264487, 18108391, 22278995, 22278996, 22278997, 22278999, 29331824, 29331825, 29331826, 29331827, 33656970, 264905, 264908, 265008, 264910, 33657402, 265011, 265017, 265018, 264369, 21906766, 21906767, 21906768, 35695917, 265020, 60170615, 264691, 264692, 264693, 27486261, 27486262, 18108370, 60431528, 264634, 264636, 264639, 22279000, 264568, 264488, 29331822, 29331825, 60432289, 29331826, 35696052, 29331828, 29331830, 264594, 55812038, 33109954, 33657084, 87168474, 87168559, 52644229, 21906765, 21906767, 18108376, 35696423, 52644332, 264638, 60432113, 22279002 264634, 264637, 264565
3096	87756128 (6191, 6192)	Novel Protein sim. GBank gjl3882221 dbj BAA34470.1 - (AB018293) KIAA0750 protein (Homo sapiens)	Contains protein domain (PF00307) - Calponin homology (CH) domain	struct	
3097	88264895 (6193, 6194)	Novel Protein sim. GBank gjl4468288 emb CAB37931 - (AL022395) dJ273N12.1 (PUTATIVE protein based on EST matches) (Homo sapiens)	Contains protein domain (PF00846) - F-box domain.	UNCLASSIFIED	
3098	80258024 (6195, 6196)				
3099	91243325 (6197, 6198)	Novel Protein sim. GBank gjl303603 dbj BAA02145.1 - (D12621) cytochrome P-450L TBV (Homo sapiens)		cyto450	264488, 35696286, 29331822, 29331824, 29331825, 29331827, 265007, 265008, 265010, 265011, 265018, 265019, 18108357, 21906766, 265020, 265022, 55811576, 56182323, 22279002, 264563
3100	87602421 (6199, 6200)	Novel Protein sim. GBank gjl1083784 pir JB48013 - proline- rich proteoglycan 2 precursor, parotid - rat		UNCLASSIFIED	29331825, 60432289, 35696052, 264910, 60432229, 264592, 264288, 264693, 263967, 264635
3101	76602134 (6201, 6202)			UNCLASSIFIED	264808, 264693, 264628, 264630, 264632

3102	91220892 (6203, 6204)	Novel Protein sim. GBank gij5305708[gb]/AAD41781.1[AF12853] - (AF128536) cytoplasmic phosphoprotein PACSIN2 [Homo sapiens]	Contains protein domain (PF00018) - SH3 domain	struct	35696286, 22278998, 22278999, 29331827, 35696052, 264909, 264512, 265008, 60170831, 60433356, 33109954, 18108351, 264684, 264689, 21908767, 60170815, 264692, 33657023, 264638, 22278000, 264482, 264564 UNCLASSIFIED
3103	90938004 (6205, 6206)	Novel Protein sim. GBank gij484584[sp]/P35292[RB17_MOUSE - RAS-RELATED PROTEIN RAB-17]		UNCLASSIFIED	35895917, 264565
3104	87340633 (6207, 6208)	Novel Protein sim. GBank gij5032207[refNP_005698.1]pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	264259, 264684, 264532, 33657182, 264558
3105	94148603 (6209, 6210)				22278997, 264259, 29331824, 35696052, 29331828, 264508, 264509, 264905, 264906, 264907, 264908, 264511, 264910, 264591, 264594, 264758, 264760, 264681, 264762, 264784, 264288, 264786, 264788, 264687, 264789, 21906766, 21906768, 35695917, 33657023, 264692, 264693, 264628, 264629, 35695855, 264630, 264631, 264632, 264634, 264635, 264637, 264638, 264639, 83373044, 264404, 22279002, 264563, 264565, 264566, 264486, 264567
3106	95381416 (6211, 6212)	Novel Protein sim. GBank gij1938574 (U97190) - B0025.2 gene product [Caenorhabditis elegans]			22278996, 22278997, 22278998, 22278999, 264092, 264093, 264094, 29331822, 264906, 264907, 264908, 52844045, 56182435, 264112, 265008, 265009, 55812038, 265017, 285018, 264883, 264886, 264687, 264789, 52844228, 21906765, 21906768, 21906769, 55811957, 265020, 265022, 264690, 52844150, 264692, 264693, 18108370, 18108377, 55811576, 56182323, 18108385, 18108388, 22279000, 264563
3107	95343272 (6213, 6214)	Novel Protein sim. GBank gij3341441[emb]CAA76851] - (Y17794) winged-helix transcription factor [Gallus gallus]			22278995, 22278996, 35696286, 22278997, 22278999, 264091, 264093, 264259, 29331822, 29331825, 29331826, 60432289, 29331827, 29331828, 33656970, 264105, 264512, 265009, 60433356, 60433438, 265011, 265017, 265018, 21906765, 21906768, 21906767, 21906769, 265021, 264691, 33657109, 27486261, 27486265, 18108370, 263972, 18108374, 55811576, 18108385, 55526488, 264482, 264487, 56182435, 264288, 264690, 264564
3108	87340635 (6215, 6216)	Novel Protein sim. GBank gij5032207[refNP_005698.1]pTSSC - tumor-suppressing STF cDNA 6		UNCLASSIFIED	

3109	94318461 (6217, 6218)	Novel Protein sim. GBank gij5002587[emb]CAB44347.11 - (Y17454) LSR1 protein [Homo sapiens]	Contains protein domain (PF000096) - strud Zinc finger, C2H2 type	UNCLASSIFIED	264480, 264908, 265007, 264910, 264593, 264683, 264684, 264687, 21906767, 21906768, 264683, 18108370, 264629, 18108374, 264632, 264638, 22279000
3110	95080716 (6219, 6220)	Novel Protein sim. GBank gij1076211[pir]S50735 - hypothetical protein VSP-3 - Chlamydomonas reinhardtii			264488, 65274572, 22278985, 22278987, 60432049, 264259, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 264908, 264510, 265008, 265007, 265008, 265009, 60432228, 33657402, 60433356, 265011, 87168559, 264600, 265017, 265018, 265019, 18108351, 264288, 264369, 21906768, 21906787, 21906768, 265020, 60170815, 264693, 65274620, 18108370, 264639, 18108384, 22279000, 264583, 18108390
3111	87754512 (6221, 6222)	Novel Protein sim. GBank gij3282231 (U75454) - C2H2 type zinc finger protein [Homo sapiens]	Contains protein domain (PF000096) - strud Zinc finger, C2H2 type		264488, 18108398, 66712502, 265017, 265018, 265019, 264448, 21906787, 265020, 33657023, 18108385, 18108388, 35698423, 52644332, 18108385, 18108388
3112	88043639 (6223, 6224)	Novel Protein sim. GBank gij3900848 (AC005023) - match to EST AA361117 (NID:2013438) [Homo sapiens]	Contains protein domain (PF000046) - homeobox		
3113	88207086 (6225, 6226)	Novel Protein sim. GBank gij2459810 (AF005856) - anon2A5 [Drosophila yakuba]	Homeobox domain	im7	18108397, 22278999, 264259, 29331824, 35698052, 264907, 264757, 60433438, 87168559, 264763, 264448, 18108354, 264288, 21906787, 21906789, 35695917, 264690, 264691, 264692, 264693, 18108365, 18108381, 18108384, 18108385, 18108388, 87168518, 22278000, 22279002
3114	78643167 (6227, 6228)	Novel Protein sim. GBank gij4968270[gb]AAB52261.2] - (U97002) similar to acyl-CoA dehydrogenases and epoxide hydrolases; Pfam domain PF00441 (Acyl-CoA_dh). Score=57.4, E-value=1.7e-16, N=2; contains similarity to Pfam domain PF00702 (Hydrolase). Score=57.4, E-value=1e-13, N=1 [C...]	Contains protein domain (PF00702) - hydrolase haloacid dehalogenase-like hydrolase		264908, 66162435, 264810, 21906754
3115	94117866 (6229, 6230)	Novel Protein sim. GBank gij5032228[ref]NP_005676.1[pWBSC - Williams-Beuren syndrome chromosome region 11	transcript factor		60424176, 56182575, 264259, 29331824, 60424269, 29331826, 66712502, 264510, 265007, 60431735, 60433356, 55812036, 55811386, 265019, 264288, 264689, 21906789, 264691, 33657023, 264693, 60431528, 263974, 60431850, 56182323, 264559, 22279000, 22279002
3116	78642855 (6231, 6232)		UNCLASSIFIED		264905, 264758, 21906784, 264690
3117	87771268 (6233, 6234)		UNCLASSIFIED		264510, 265011, 18108351, 264288, 264689, 264691, 18108368, 18108372, 263981, 264558, 264584

3118	84665848 (6235, 6238)	Novel Protein sim. GBank gi 3880563 emb CAB01444.1 - (Z78018) predicted using GeneFINDER; similar to serine/threonine kinase; cDNA EST YK353d10.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF000008) - Igr EGF-like domain	52645156, 52646842, 65274572, 56182575, 22278995, 56994075, 22278996, 35696286, 22278997, 22278998, 22278999, 264259, 29331822, 29331824, 66714117, 29331826, 29331827, 35696052, 29331828, 264905, 264908, 28331830, 52644045, 56182435, 264510, 264511, 265007, 265008, 265009, 264757, 52646317, 21906754, 33657084, 52644296, 87168474, 87168559, 265017, 265018, 264605, 265019, 264762, 264448, 264882, 264884, 264288, 264766, 56181562, 21906765, 21906766, 21906768, 21906769, 265020, 265022, 264690, 52644150, 264691, 33657023, 264693, 33657109, 33657349, 264628, 18108370, 60431528, 18108374, 35696423, 65274791, 60170394, 83373044, 87168518, 22279000, 22279002, 264488, 265008, 264288
3119	85728796 (6237, 6238)		Contains protein domain (PF003328) - Histidine acid phosphatase	
3120	87344040 (6239, 6240)	Novel Protein sim. GBank gi 5019819 gb AAD37863.1 AF14315 - (AF143152) putative NADH oxidoreductase complex I subunit [Caenorhabditis elegans]	UNCLASSIFIED	264488, 264509, 264510, 264511, 264512, 264288, 264486
3121	84110735 (6241, 6242)	Novel Protein sim. GBank gi 4501877 ref NP_001088.1 pACR - acrosin		52644507, 52645156, 52646365, 52646842, 22278994, 56994075, 22278996, 22278999, 264259, 29331824, 29331827, 35696052, 52644045, 265008, 52646317, 87168474, 87168559, 21906765, 52644150, 33657023, 18108374, 264637
3122	11814528 (6243, 6244)		UNCLASSIFIED	264638
3123	86083003 (6245, 6246)	Novel Protein sim. GBank gi 2439517 (AC002563) - putative RHO/RAC effector protein; 95% similarity to P49205 (PID:G1345680) [Homo sapiens]	Contains protein domain (PF00780) - CNH domain	18108392, 29331822, 29331824, 29331825, 264905, 265007, 55812038, 265019, 18108351, 264682, 264288, 264766, 21906764, 21906765, 21906768, 21906769, 55811957, 18108365, 18108366, 27486265, 18108374, 18108381, 18108384, 22279000, 22279002, 264482
3124	87766899 (6247, 6248)		UNCLASSIFIED	264805
3125	81216607 (6249, 6250)	Novel Protein sim. GBank gi 4980828 gb AAD35412.1 AE00171 - (AE001714) oxidoreductase, short chain dehydrogenase/reductase family [Thermotoga maritima]	Contains protein domain (PF00106) - short chain dehydrogenase	56181686, 264259, 66714117, 60432289, 29331826, 29331827, 264907, 264908, 264828, 265009, 60433356, 33657402, 60433438, 264758, 18108351, 264288, 28148627, 29148628, 33657023, 33657109, 18108382, 56528488

3128	95337205 (6251, 6252)			UNCLASSIFIED	22278989, 264490, 264259, 60432049, 29331822, 60432289, 29146498, 52644045, 56182435, 265009, 60433438, 265010, 87168559, 265017, 265018, 55811150, 264783, 264683, 264389, 264685, 29148629, 33657023, 264693, 33657109, 18108374, 55811576, 18108385, 60432113, 22279002, 35696286, 22278996, 22278999, 29331826, 264908, 60433438, 87168559, 264604, 21908765, 21908769, 33657023, 33657349, 264629, 18108374, 18108377, 22279000, 22279002
3127	91639233 (6253, 6254)	Novel Protein sim. GBank gjl2628280(emb)(CAA16694.1) - (AL021687) putative protein [Arabidopsis thaliana]			
3128	87674330 (6255, 6256)	Novel Protein sim. GBank gjl3885828 (AF090133) - lin-7-A [Rattus norvegicus]	Contains protein domain (PF00595) - PDZ domain (Also known as DHR or GLGF).	misc_channel	22278996, 264259, 52644045, 265008, 21908764, 265017, 265018, 21908768, 18108376, 18108387, 22279000, 22279002
3129	87755412 (6257, 6258)	Novel Protein sim. GBank gjl3135273 (AC003058) - hypothetical protein [Arabidopsis thaliana]	Contains protein domain (PF00400) - WD domain, G-beta repeat	kinase	56182575, 264259, 29331825, 29331826, 52644045, 56182435, 60433356, 264600, 264682, 264763, 264764, 264369, 264288, 264686, 55811957, 264692, 33657023, 33657109, 60432113, 264564, 264566
3130	14983860 (6259, 6260)	Novel Protein sim. GBank gjl3329465 (AF064553) - NSD1 protein [Mus musculus]			264636
3131	95351468 (6261, 6262)	Novel Protein sim. GBank gjl1848277 (U86136) - telomerase-associated protein TP-1 [Homo sapiens]	Contains protein domain (PF00400) - WD domain, G-beta repeat	UNCLASSIFIED	56182575, 264259, 29331824, 264907, 56182435, 264594, 60433438, 55812038, 33109954, 21908754, 33657084, 87168474, 264448, 264766, 21908769, 55811957, 265020, 265021, 265022, 60170615, 33657023, 33657109, 33657182, 27486261, 33657349, 85274791, 60170394, 56182323, 83373044, 87168518, 264564

3132	95415459 (6263, 6264)	Novel Protein sim. GBank gi 4680647 gb AAD27713.1 AF13293 - (AF13293) CGI-03 protein [Homo sapiens]	Contains protein domain (PF00789) - UBX domain	ubiquitin	52844507, 52846842, 52846365, 85274572, 56182575, 22278994, 22278995, 35696286, 56994075, 22278996, 22278997, 22278998, 22278999, 60432049, 52645080, 29331822, 29331824, 29331825, 60432289, 29331826, 29331827, 29331828, 35696052, 264508, 52844045, 56182435, 284910, 60170831, 60432229, 60433356, 33657402, 55812038, 52846317, 21908754, 52844296, 85658542, 87188559, 285017, 265018, 285019, 284448, 264288, 264369, 52644229, 21908765, 21908766, 21908767, 21908768, 21908769, 35695917, 265020, 265021, 60170615, 52844150, 264692, 33657023, 52645129, 33657109, 33657182, 27486261, 27486262, 27486265, 33657349, 35695763, 18108374, 18108376, 55811576, 35695855, 18108385, 18108387, 56526466, 87168518, 60432113, 22279002
3133	67379414 (6265, 6266)	Novel Protein sim. GBank gi 4507613 ref NP_003738.1 pTNKS - TANKYRASE		polymerase	22278994, 22278998, 264905, 265008, 265007, 87168559, 264760, 21908767, 18108374, 22279000, 22279002, 264563 264595, 264369, 264665, 264628, 264566
3134	94849818 (6267, 6268)	Novel Protein sim. GBank gi 1729827 sp P54633 TALA_DICDI - FILOPODIN (TALIN HOMOLOG)			
3135	86388356 (6269, 6270)	Novel Protein sim. GBank gi 3093478 (AF012927) - fibrinogen-binding protein [Streptococcus equi]		struct	22278998, 264095, 29331826, 33657402, 18108348, 263974
3136	84845839 (6271, 6272)	Novel Protein sim. GBank gi 827101 pir S44092 - probable carrier protein c2 - Caenorhabditis elegans	Contains protein domain (PF00153) - Mitochondrial carrier proteins	transport	22278998, 264259, 264828, 265006, 265008, 60433438, 265019, 264764, 264288, 264769, 264689, 265020, 27486262, 263972, 65274791, 264557, 264558
3137	88257647 (6273, 6274)	Novel Protein sim. GBank gi 3342730 (AC005331) - R31341_1 [Homo sapiens]		UNCLASSIFIED	22278995, 22278996, 22278997, 22278998, 22278999, 264259, 29331822, 29331825, 29331826, 29331827, 29331828, 264510, 265008, 21908754, 87168474, 265011, 87168559, 285017, 285018, 285019, 18108351, 264682, 264769, 21908765, 21908766, 21908767, 21908769, 55811857, 35695917, 265020, 265021, 52844150, 18108370, 18108374, 22279000, 22279002, 264482, 264486

3138	04130188 (8275, 8278)	Novel Protein sim. GBank gij4408759[gbjAAD20070] - (AC008838) hypothetical protein [Arabidopsis thaliana]			264589, 264488, 264907, 264511, 264593, 33109954, 87188559, 264681, 264684, 264685, 264686, 264687, 264788, 264688, 264689, 264691, 264692, 264693, 33657109, 264631, 264634, 264635, 264636, 264637, 60170394, 83373044, 18108385, 18108388, 60432113, 22279000, 22279002
3139	87325503 (8277, 8278)	Novel Protein sim. GBank gij228938[prj]1814452C - Hyp-rich glycoprotein [Zea diploperennis]		UNCLASSIFIED	22278997, 22278998, 22278999, 264905, 265018, 265019, 21908765, 265020, 264636, 264557
3140	91222692 (8278, 8280)	Novel Protein sim. GBank gij832[embjCAA37773] - (X53744) 88kDa subunit of signal recognition particle [Canis familiaris]		struct	22278995, 56994075, 35696286, 264908, 264909, 80433356, 21908754, 52644296, 87168474, 87168559, 264683, 264288, 264685, 264686, 265022, 264693, 27486262, 35695855, 264630, 264555, 264568
3141	87323584 (8281, 8282)	Novel Protein sim. GBank gij3213227 (AF035209) - putative v-SNARE VIIa [Mus musculus]		UNCLASSIFIED	56182575, 35696286, 29331828, 264909, 265009, 265018, 18108351, 264369, 21908766, 29148627, 265020, 264628, 264629, 264831, 18108385
3142	95419028 (8283, 8284)	Novel Protein sim. GBank gij2498197[spjQ85245]C561_PIG - CYTOCHROME B561 (CYTOCHROME B-561)		cytochrome	52645156, 52646365, 22278995, 35696286, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 29331827, 29148499, 56182435, 265007, 80170831, 60432229, 33657402, 264595, 80433438, 264758, 21908754, 264288, 264766, 264687, 52844228, 21908765, 21908767, 21908768, 60170815, 52644150, 65274620, 33657109, 35695763, 18108370, 18108376, 65274791, 35695855, 264631, 264557, 87168518, 60432113, 22279000
3143	95351475 (8285, 8286)	Novel Protein sim. GBank gij5420387[embjCAB46679.1] - (AJ243459) proteophosphoglycan [Leishmania major]		UNCLASSIFIED	264488, 56182575, 22278996, 22278998, 22278999, 29331822, 29331824, 60432289, 35696052, 29331828, 264508, 264905, 264908, 264907, 264908, 264909, 52644045, 56182435, 264511, 264512, 265008, 264910, 60432229, 33657402, 80433356, 80433438, 55812038, 265011, 265018, 264760, 264763, 264448, 264764, 264684, 264288, 264685, 264686, 264768, 264689, 21908765, 21908766, 21908767, 21908769, 35695917, 264690, 33657023, 264693, 263967, 33657109, 264628, 264629, 18108374, 263978, 55811578, 35695855, 264630, 264631, 264632, 264634, 264635, 264636, 264637, 264558, 87188518, 60432113, 22279000, 22279002, 264563, 264566, 264488

3144	95336329 (6287, 6288)	Novel Protein sim. GBank gll4884460[emb]CAB43322.1] - (AL050225) hypothetical protein [Homo sapiens]			264488, 18108396, 22278996, 35696286, 22278997, 22278998, 29331826, 29331827, 35696052, 29331828, 264106, 265006, 265007, 265009, 33657402, 85658542, 265011, 18108351, 264448, 264369, 21908765, 21908766, 21908767, 265020, 265021, 52844150, 27486281, 18108370, 18108374, 35696423, 56182323, 83373044, 22279000, 22279002, 264567
3145	86811657 (6289, 6290)	Novel Protein sim. GBank gll3679709[emb]CAB03330] - (Z81118) Similarity to Human endosomal protein P162 (TR:Q15075); cDNA EST EMBL:Z14487 comes from this gene; cDNA EST EMBL:Z14556 comes from this gene; cDNA EST EMBL:D27011 comes from this gene; cDNA EST EMBL:D27015 comes from l...	UNCLASSIFIED		18108397, 29331824, 29146499, 20281100, 265006, 55812038, 265010, 21908766, 29148827, 21908768, 29148784, 264692, 33657023, 33657109, 35695763, 263981, 56182323, 87168518
3146	87756314 (6291, 6292)	Novel Protein sim. GBank gll2135746[pir]S69890 - mitogen Inducible gene mig-2 - human	Contains protein domain (PF00169) - PH domain	struct	264259, 29331826, 29331828, 29331830, 264510, 264511, 265007, 265009, 264600, 265017, 18108351, 264448, 264369, 21908768, 265021, 264692, 33657109, 18108374, 35696423, 35695855, 60432113, 264564
3147	94848512 (6293, 6294)	Novel Protein sim. GBank gll3674279[emb]CAB07315.1] - (Z92825) predicted using GeneFinder; cDNA EST yk315e12.3 comes from this gene; cDNA EST yk315e12.5 comes from this gene [Caenorhabditis elegans]	Contains protein domain (PF00702) - haloacid dehalogenase-like hydrolase	UNCLASSIFIED	56181866, 35696286, 60432049, 264259, 56182181, 29331825, 60432289, 35696052, 56182435, 265008, 264910, 60431735, 60433358, 60433438, 265010, 264448, 264288, 265022, 33657023, 33657109, 60431528, 65274791, 264631, 56182323, 264404, 22278002
3148	95362169 (6295, 6296)	Novel Protein sim. GBank gll5225322[gb]AAD40851.1[AF083108] siruin type 3 [Homo sapiens]	UNCLASSIFIED		35696286, 35696052, 264511, 85658542, 87168474, 264764, 35696423, 264555, 264556, 264557, 264558, 83373044, 56528488, 60432113
3149	95308548 (6297, 6298)	Novel Protein sim. GBank gll4200448 (AF102777) - FYVE finger-containing phospholipase kinase [Mus musculus]	Contains protein domain (PF01363) - FYVE zinc finger	leph	29331822, 35696052, 264109, 29148629, 18108381
3150	87655472 (6299, 6300)	Novel Protein sim. GBank gll3378454[emb]CAA76893] - (Y17850) ganglioside-induced differentiation associated protein 1 [Mus musculus]	Contains protein domain (PF00043) - Glutathione S-transferases	transferase	264259, 29331822, 29331824, 29331825, 29331827, 52646317, 264688, 35695855, 56182323, 264639
3151	87772355 (6301, 6302)	Novel Protein sim. GBank gll172591 (M63577) - SFP1 [Saccharomyces cerevisiae]	Contains protein domain (PF00096) - oncogene	oncogene	29331822, 265008
3152	85698108 (6303, 6304)		UNCLASSIFIED		21908754, 87168559, 264605, 21908768, 52844150, 27486284, 35696423, 22279000

3153	95317289 (6305, 6306)	Novel Protein sim. GBank gi4895041 gb AAD32705.1 AF143957 coronin-3 [Mus musculus]	Contains protein domain (PF00400) - struct WD domain, G-beta repeat	264488, 52645365, 35698286, 22278996, 22278997, 22278999, 60432049, 264259, 29331826, 60432289, 33656970, 264508, 264908, 33657402, 264595, 60433438, 87188474, 87188559, 264801, 265019, 264448, 264682, 264784, 264288, 264369, 264768, 21906765, 21906768, 21906767, 21908768, 21908769, 29148784, 265021, 265022, 60170615, 52644150, 264690, 264891, 33657023, 65274620, 33657109, 18108370, 35695855, 264638, 60170394, 87188518, 60432113, 22279000, 22279002, 22278998, 264259, 29331824, 66712502, 265008, 265010, 265017, 18108354, 264891, 33657023, 264683, 20281149, 18108374
3154	87718573 (6307, 6308)	Novel Protein sim. GBank gi4880661 gb AAD27720.1 AF13294 - (AF132945) CGI-11 protein [Homo sapiens]	ATPase-associated	29331828, 264509, 264805, 264908, 264510, 264511, 264512, 33657402, 264681, 264883, 33657023, 18108370, 264634, 264639, 18108385, 264583, 264486
3155	87762384 (6309, 6310)	Novel Protein sim. GBank gi728837 sp P39194 ALU7_HUMAN - IIII ALU SUBFAMILY SQ WARNING ENTRY IIII	UNCLASSIFIED	56182575, 22278996, 22278997, 22278998, 22278999, 60432049, 264259, 29331822, 29331824, 66714117, 29331825, 29331826, 29331827, 35698052, 52644045, 265007, 265009, 60170831, 60432229, 60433356, 21906754, 33109954, 87168474, 265010, 265017, 265018, 265019, 18108351, 264448, 264288, 264689, 21906766, 21906768, 21908769, 35695917, 265020, 265022, 264692, 18108370, 35698423, 56182323, 22279002
3156	87737448 (6311, 6312)	Novel Protein sim. GBank gi5630078 gb AAD45821.1 AC00601 - (AC006017) N-acetylglucosaminyltransferase, similar to Q10473 (PID:g1709559) [Homo sapiens]	transferase Contains protein domain (PF00652) - struct Similarity to lectin domain of ricin beta-chain, 3 copies.	18108396, 264259, 29331826, 35696052, 29146498, 87168559, 265017, 264448, 264288, 264691, 18108386, 52645129, 35698423, 52644332
3157	88259577 (6313, 6314)		Contains protein domain (PF00023) - kinase Ank repeat	264488, 263974
3158	80034118 (6315, 6316)	Novel Protein sim. GBank gi5306064 gb AAD41895.1 AF15677 - (AF156776) ASB-3 protein [Homo sapiens]	UNCLASSIFIED	56182575, 22278998, 29331824, 264106, 60433356, 264758, 265011, 87168559, 264448, 18108354, 264768, 21908768, 265020, 264691, 264692, 33657109, 18108374, 35698423, 264555, 60170394, 22279000
3159	94124114 (6317, 6318)	Novel Protein sim. GBank gi5531272 emb CAB50887.1 - (A243800) WSC4 homologue [Kluyveromyces fragilis]	UNCLASSIFIED	18108351, 264555, 264556, 264557, 264558, 264559
3160	80221068 (6319, 6320)	Novel Protein sim. GBank gi3930525 (AF084447) - sex-determination protein homolog Fam1a [Mus musculus]	Contains protein domain (PF00023) - struct Ank repeat	

3161	88074111 (8321, 8322)				284488, 22278995, 22278997, 22278998, 284259, 29331822, 60432289, 29331828, 52844045, 285017, 285018, 284448, 284288, 21808764, 21808767, 285020, 18108374, 284638, 284566
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Table 2

Tissue ID	Tissue Name	Tissue Information	Disease Association
20281069	192xN	Protein-protein Interactions	Any
20281071	192xN	Protein-protein Interactions	Any
20281149	192xN	Protein-protein Interactions	Any
20281152	192xN	Protein-protein Interactions	Any
264111	276xN	Protein-protein Interactions	Any
264112	276xN	Protein-protein Interactions	Any
263966	384xN	Protein-protein Interactions	Any
263967	384xN	Protein-protein Interactions	Any
264110	552xN	Protein-protein Interactions	Any
18108379	SPH 52.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108381	SPH 52.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108383	SPH 52.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108368	SPH 52.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108384	SPH 52.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108394	SPH 53.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108355	SPH 53.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108359	SPH 53.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108361	SPH 53.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108362	SPH 53.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108366	SPH 53.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108354	SPH 54.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108392	SPH 54.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108348	SPH 54.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	Blood cancers, hematopoiesis, leukemia
18108382	SPH 54.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108395	SPH 54.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
18108365	SPH 54.6 (Brain- Thalamus)	Thalamus	Brain cancer, head injury, obesity, neurological disorders, neuropsychiatric disorders
18108397	SPH 55.1 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
18108398	SPH 55.2 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
18108364	SPH 55.3 (B's Lymphoma- Raji)	Lymphoma derived from B cells	
18108388	SPH 55.4 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
18108358	SPH 55.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
20281099	SPH 56.2 (MG63)		
20281100	SPH 56.3 (UiSMC)		
264404	SPH.1 (Brain)	Whole Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberosus sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264510	SPH.10 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264511	SPH.11 (Placenta)	Placenta	Infertility, birth defects
264512	SPH.12 (Thyroid)	Thyroid	Hyperparathyroidism, Hypoparathyroidism
264555	SPH.13 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264556	SPH.14 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264557	SPH.15 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264558	SPH.16 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264559	SPH.17 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264569	SPH.19 (One Fetal tissue and two cell lines)	Mixed	
264687	SPH.19.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264688	SPH.19.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264689	SPH.19.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264690	SPH.19.4 (Fetal Liver)	Fetal liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264691	SPH.19.5 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264692	SPH.19.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264693	SPH.19.7 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264482	SPH.2 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection

264600	SPH.21 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264601	SPH.22 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264602	SPH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264603	SPH.24 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264604	SPH.25 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264605	SPH.26 (Placenta)	Placenta	Infertility, birth defects
264634	SPH.28 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis , Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264635	SPH.29 (Fetal Kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264483	SPH.3 (Bone Marrow)	Bone marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264636	SPH.30 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264637	SPH.31 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264638	SPH.32 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264639	SPH.33 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264484	SPH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264758	SPH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264760	SPH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation

264762	SPH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis, Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus, Pulmonary stenosis, Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264764	SPH.44.4 (Prostate)	Prostate	Prostate Cancer
264766	SPH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
264768	SPH.44.6 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264769	SPH.44.7 (Uterus)	Uterus	Infertility, birth defects
264905	SPH.48.1 (Burkitt's Lymphoma- Raji)	Burkitt's Lymphoma	Lymphoma, blood cancers
264906	SPH.48.2 (Thalamus- Brain)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264907	SPH.48.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
264908	SPH.48.4 (Fetal Lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
264909	SPH.48.5 (Salivary Gland)	Salivary Gland	Dry mouth, infection
264910	SPH.48.6 (Mammary Gland)	Mammary Gland	Lactation disorders, breast cancer
265006	SPH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
265007	SPH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
265008	SPH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
265009	SPH.50.4 (fetal lung)	Fetal Lung	Cystic Fibrosis, infection, lung cancer
265010	SPH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
265011	SPH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
18108385	SPH.51.1 (MCF-7)	Breast Cancer	Breast Cancer
18108370	SPH.51.2 (CCRF-CEM)	Cancer Cell line	Cancer
18108374	SPH.51.3 (K-562)	Cancer Cell line	Cancer
18108351	SPH.51.4 (OVCAR-3)	Ovarian cancer	Ovarian cancer
18108372	SPH.51.5 (HL-60)	Cancer Cell line	Cancer
264486	SPH.6 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264508	SPH.8 (Fetal Brain)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264509	SPH.9 (Lymph Node)	Lymph Node	Lymphedema , Allergies
20798451	SRH 56.3(UtSMC)		
264487	SRH.1 (Brain)	Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264534	SRH.11 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264535	SRH.12 (Bone marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264563	SRH.19 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264488	SRH.2 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264564	SRH.20 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264565	SRH.21 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264566	SRH.22 (Placenta)	Placenta	Infertility, birth defects
264567	SRH.23 (Thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264591	SRH.25 (Fetal Brain)	Fetal brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264592	SRH.26 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264593	SRH.27(thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264594	SRH.28 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264595	SRH.29 (Lymph Node)	Lymph Node	Lymphedema , Allergies
264489	SRH.3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,

264596	SRH.30 (Placenta)	Placenta	Infertility, birth defects
264628	SRH.33 (fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264629	SRH.34 (lymph Node)	Lymph Node	Lymphedema , Allergies
264630	SRH.35 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
264631	SRH.36 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
264632	SRH.37 (Fetal Brain)	Fetal Brain	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264490	SRH.4 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
264681	SRH.43.1 (fetal thymus - CRL7046)	Fetal Thymus	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, immunodeficiencies
264682	SRH.43.2 (hematopoietic stem cells - CRL2043)	Hematopoietic stem cells	Leukemia, osteoporosis, post-chemotherapeutic stem cell repopulation
264683	SRH.43.3 (osteogenic sarcoma cell lines - HTB96)	Osteogenic Sarcoma	Sarcomas, osteoporosis, osteopetrosis
264684	SRH.43.4 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264685	SRH.43.6 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura , Immunodeficiencies, Graft versus host
264686	SRH.43.7 (pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264757	SRH.44.1 (Kidney)	Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
264759	SRH.44.2 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
264761	SRH.44.3 (Heart)	Heart	Cardiomyopathy, Atherosclerosis, Hypertension, Congenital heart defects, Aortic stenosis , Atrial septal defect (ASD), Atrioventricular (A-V) canal defect, Ductus arteriosus , Pulmonary stenosis , Subaortic stenosis, Ventricular septal defect (VSD), valve diseases, Tuberous sclerosis, Scleroderma, Obesity, Transplantation
264763	SRH.44.4 (Prostate)	Prostate	Prostate Cancer
264765	SRH.44.5 (Spleen)	Spleen	Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura , Immunodeficiencies, Graft versus host

264767	SRH.44.6 (Pituitary)	Pituitary	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
264828	SRH.46.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
264887	SRH.47.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
18108377	SRH.50.1 (B's lymphoma)	Burkitt's Lymphoma	Lymphoma, blood cancers
18108380	SRH.50.2 (thalamus)	Thalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
18108396	SRH.50.3 (adrenal gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
18108391	SRH.50.4 (fetal lung)	Fetal Lung	Airway diseases, infection
18108357	SRH.50.5 (salivary gland)	Salivary Gland	Dry mouth, infection
18108390	SRH.50.6 (mammary gland)	Mammary Gland	Lactation disorders, breast cancer
264532	SRH.9 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
263974	736xN		
263976	736xN		
263981	736xN		
20281166	96xN		
20281169	96xN		
20281171	96xN		
263994	cDNA-ORF Selection		
264080	Mx96		
21906754	NQH 6.1 (HH729)		
22278996	NQH 6.10 (PrEC)	Endothelial cells	heart disease, cancer
22278997	NQH 6.11 (CAEC)	Endothelial cells	heart disease, cancer
22278998	NQH 6.12 (CSC)	Cancer Cell line	Cancer
22278999	NQH 6.13 (NHNPC)	Cancer Cell line	Cancer
22279000	NQH 6.14 (NHMC-RM)	Cancer Cell line	Cancer
22279002	NQH 6.15 (Hypothalamus)	Hypothalamus	Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
21906764	NQH 6.2 (In Dated Platelets)	Platelets	Clotting diseases, stroke
21906765	NQH 6.3 (HuVec)	Endothelial cells	heart disease, cancer
87168474	NQH 6.3 (Sized-HUVEC)	Endothelial cells	heart disease, cancer
21906766	NQH 6.4 (UMVEC- myo)	Cancer Cell line	Cancer
21906767	NQH 6.5 (NHEM-neo)	Cancer Cell line	Cancer
21906768	NQH 6.6 (NHEK)	Cancer Cell line	Cancer
21906769	NQH 6.7 (ByCAEC)	Endothelial cells	heart disease, cancer
22278994	NQH 6.8 (NHA)	Cancer Cell line	Cancer

22278995	NQH 6.9 (PrSC)	Cancer Cell line	Cancer
27486261	NQH 7.1 (Jurkat E6-untreated)	Cancer Cell line	Cancer
27486262	NQH 7.2 (TF1-untreated)	Cancer Cell line	Cancer
27486264	NQH 7.3 (U87-untreated)	Cancer Cell line	Cancer
27486265	NQH 7.4 (THP1-untreated)	Cancer Cell line	Cancer
29331822	NQH 8.1 (Brain- amygdala)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331824	NQH 8.2 (Brain-hippocampus)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331825	NQH 8.3 (Brain- substantia nigra)		Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection
29331826	NQH 8.4 (small intestine)	Small intestine	digestive diseases, obesity, diabetes
29331827	NQH 8.5 (Spinal cord)	Spinal chord	paralysis, neurodegenerative disorders
29331828	NQH 8.6 (stomach)	Stomach	Stomach cancer
29331830	NQH 8.7 (Trachea)	Trachea	Airway diseases, infection
87168518	NQH 9.1 (Sized-MG-63_treatment pool)		
87168559	NQH 9.2 (Sized-HEPG2 untreated)		
35695763	NQH.10.1 (MCF-7untreated)	Cancer Cell line	Cancer
35695855	NQH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
35695917	NQH.10.3 (JAR)	Cancer Cell line	Cancer
35696052	NQH.10.4 (PA-1)	Cancer Cell line	Cancer
35696286	NQH.10.5 (CADMEC)	Endothelial cells	heart disease, cancer
35696423	NQH.10.6 (CADMEC_LA)	Endothelial cells	heart disease, cancer
52644045	NQH.11.1 (SK-PN-DW)	Cancer Cell line	Cancer
52644150	NQH.11.2 (Chorionic Villus Cells)	Chorionic villus	fertility, birth defects
52644229	NQH.11.3 (A549)	Cancer Cell line	Cancer
52644296	NQH.11.4 (U266B1)	Cancer Cell line	Cancer
52644332	NQH.11.5 (Daoy)	Cancer Cell line	Cancer
52644507	NQH.11.6 (SW1783)	Cancer Cell line	Cancer
52645080	NQH.12.1 (U-118MG)	Cancer Cell line	Cancer
52645129	NQH.12.2 (A204)	Cancer Cell line	Cancer
52645156	NQH.12.3 (T24)	Cancer Cell line	Cancer
52646317	NQH.12.4 (G-401)	Cancer Cell line	Cancer
52646365	NQH.12.5 (CaSki)	Cancer Cell line	Cancer
52646842	NQH.12.6 (SHP-77)	Cancer Cell line	Cancer

60424179	NQH.14.1 (Yale75_breast carcinoma)	Breast carcinoma	Breast Cancer
60424269	NQH.14.2 (Yale78B_ovarytumor)	Ovary tumor	Ovarian cancer
60431528	NQH.14.3 (Yale79_prostateBPH)	Prostate	Prostate Cancer
60431602	NQH.14.4 (Yale80_ProstateAdenocarcinoma)	Prostate	Prostate Cancer
60431735	NQH.14.5 (Yale86_UterineMyoma)	Uterine Myoma	Uterine Cancer
60431850	NQH.14.6 (Yale207_Myometrium)	Myometrium	Fertility
60432049	NQH.15.1 (Yale99_cervix)	Cervix	Osteoporosis, cervical cancer
60432113	NQH.15.2 (Yale45_spleenITP)		Hemophilia, Hypercoagulation, Idiopathic thrombocytopenic purpura, Immunodeficiencies, Graft versus host
60432229	NQH.15.3 (Yale16_Skin)	Skin	wound healing, melanoma
60432289	NQH.15.4 (Yale137_Parotid)		
60433356	NQH.15.5 (Yale38_SmallIntestine)	Small intestine	digestive diseases, obesity, diabetes
60433438	NQH.15.6 (Yale28_ColonAscending)	Colon	Colon cancer
65274444	NQH.17.1 (Larynx)	Larynx	Cancer
65274572	NQH.17.2 (Duodenum)	Duodenum	
65274620	NQH.17.3 (Kidney, Primary tumors)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
65274727	NQH.17.4 (Lung Pleura, normal)	Lung	Airway diseases, infection
65274791	NQH.17.5 (Lung, Normal Adult)	Lung	Airway diseases, infection
83373044	NQH.18.230 (Pooled adrenal gland, placenta)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,
85658542	NQH.18.560 (Pooled uterus, BeWo pool)	Uterus	Infertility, birth defects
33656970	NQH.9.1 (MG-63_treatment pool)	Cancer Cell line	Cancer
33657023	NQH.9.2 (HEPG2 untreated)		Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
33657084	NQH.9.3 (PC3_untreated)	Cancer Cell line	Cancer
33657109	NQH.9.4 (TF-1_TPA)	Cancer Cell line	Cancer
33657182	NQH.9.5 (TF-1_TPO)	Cancer Cell line	Cancer
33657349	NQH.9.6 (TF-1_Hemin)	Cancer Cell line	Cancer
33657402	NQH.9.7 (HFDPC)	Cancer Cell line	Cancer
264259	NQH1 (Mixture of eight adult & two fetal tissues)		
264288	NQH2 (Ten tissues plus lymphocyte control)		
264448	NQH3 (Bone Marrow)	Bone Marrow	Hemophilia, hypercoagulation, Idiopathic thrombocytopenic purpura, autoimmune disease, allergies, immunodeficiencies, transplantation, Graft versus host,
265017	NQH4.1 (lymph node)	Lymph Node	Lymphedema, Allergies

265018	NQH4.2 (fetal kidney)	Fetal Kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
66712502	NQH4.2 (Sized)		
265019	NQH4.3 (pituitary gland)		Von Hippel-Lindau (VHL) syndrome, Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
66714117	NQH4.3 (Sized)		
265020	NQH4.4 (testis)	testis	Infertility, birth defects
265021	NQH4.5 (fetal liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
265022	NQH4.6 (thyroid)	Thyroid	Hyperthyroidism and Hypothyroidism
18108376	NQH5.1 (MCF-7)	Breast cancer	Breast Cancer
18108387	NQH5.2 (CCRF-CEM)	Cancer Cell line	Cancer
264952	NRL1: HPLC FRACTIONATION OF RELIG		
263971	Old BB3 Baits		
263969	Old BB5 Baits		
263975	ORFSEL		
263972	OTHER Baits		
263978	pGALORF		
264106	PPBAITS		
264088	QC-YA7		
264089	QC-YA8		
264102	Resequenced Interactors		
264369	RRH.1		
60170394	RRH.10.1 (MCF-7untreated)	Breast cancer	Breast Cancer
60170615	RRH.10.2 (U-937_treatment pool)	Cancer Cell line	Cancer
60170831	RRH.10.3 (JAR)	Cancer Cell line	Cancer
60174639	RRH.11.8 (HeLa)	Cancer Cell line	Cancer
264113	rrQEA Baits		
263973	RRQEA B5 baits		
29146498	SRD 3.1 (SKMC)	Cancer Cell line	Cancer
29146499	SRD 3.2 (SKMC)	Cancer Cell line	Cancer
29147620	SRD 3.3 (RPTEC)	Cancer Cell line	Cancer
29148627	SRD 3.4 (HRCE)	Cancer Cell line	Cancer
29148629	SRD 3.6 (HRE)	Cancer Cell line	Cancer
29148784	SRD 3.7 (HRE)	Cancer Cell line	Cancer
55810764	SRD.7.1 (Lymph Node)	Lymph Node	Lymphedema, Allergies
55811150	SRD.7.2 (pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
55811386	SRD.7.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy, Congenital Adrenal Hyperplasia,

55811576	SRD.7.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
55811957	SRD.7.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
55812038	SRD.7.6 (Fetal Kidney)	Fetal kidney	Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
56181562	SRD.8.1 (Lymph Node)	Lymph Node	Lymphedema , Allergies
56181686	SRD.8.2 (Pancreas)	Pancreas	Pancreatitis, diabetes, pancreatic cancer
56182181	SRD.8.3 (Adrenal Gland)	Adrenal Gland/Suprarenal gland	Adrenoleukodystrophy , Congenital Adrenal Hyperplasia,
56182323	SRD.8.4 (Pituitary Gland)	Pituitary	Von Hippel-Lindau (VHL) syndrome , Alzheimer's disease, Stroke, Tuberous sclerosis, hypercalcaemia, Parkinson's disease, Huntington's disease, Cerebral palsy, Epilepsy, Lesch-Nyhan syndrome, Multiple sclerosis, Ataxia-telangiectasia, Leukodystrophies, Behavioral disorders, Addiction, Anxiety, Pain, Neuroprotection, Obesity
56182435	SRD.8.5 (Fetal Liver)	Fetal Liver	Von Hippel-Lindau (VHL) syndrome, Cirrhosis, Transplantation
56182575	SRD.8.6 (Fetal Kidney)		Diabetes, Autoimmune disease, Renal artery stenosis, Interstitial nephritis, Glomerulonephritis, Polycystic kidney disease, Systemic lupus erythematosus, Renal tubular acidosis, IgA nephropathy, Hypercalcaemia, Lesch-Nyhan syndrome
32833986	SRD4: HL adapter		
56526486	SRD5: I:rr fragments		
33109954	SRD5: long-RXRJ		
56994075	SRD9.1 (CS/SC)	Cancer Cell line	Cancer
263977	TSC Screen I		

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<211> 331

<212> PRT

<213> Homo sapiens

<400> 3222

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		20						25					30		
Gln	Ala	Thr	Gly	Gly	Val	Glu	Pro	Ala	Gly	Trp	Lys	Glu	Met	Arg	Cys
		35					40					45			
His	Leu	Arg	Ala	Asn	Gly	Tyr	Leu	Cys	Lys	Tyr	Gln	Phe	Glu	Val	Leu
	50				55					60					
Cys	Pro	Ala	Pro	Arg	Pro	Gly	Ala	Ala	Ser	Asn	Leu	Ser	Tyr	Arg	Ala
65				70					75					80	
Pro	Phe	Gln	Leu	His	Ser	Ala	Ala	Leu	Asp	Phe	Ser	Pro	Pro	Gly	Thr
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Glu	Val	Ser	Ala	Leu	Cys	Arg	Gly	Gln	Leu	Pro	Ile	Ser	Val	Thr	Cys
		100					105						110		
Ile	Ala	Asp	Glu	Ile	Gly	Ala	Arg	Trp	Asp	Lys	Leu	Ser	Gly	Asp	Val
	115				120						125				
Leu	Cys	Pro	Cys	Pro	Gly	Arg	Tyr	Leu	Arg	Ala	Gly	Lys	Cys	Ala	Glu
	130				135					140					
Leu	Pro	Asn	Cys	Leu	Asp	Asp	Leu	Gly	Gly	Phe	Ala	Cys	Glu	Cys	Ala
145				150					155					160	
Thr	Gly	Phe	Glu	Leu	Gly	Lys	Asp	Gly	Arg	Ser	Cys	Val	Thr	Ser	Gly
		165						170					175		
Glu	Gly	Gln	Pro	Thr	Leu	Gly	Gly	Thr	Gly	Val	Pro	Thr	Arg	Arg	Pro
		180					185					190			
Pro	Ala	Thr	Ala	Thr	Ser	Pro	Val	Pro	Gln	Arg	Thr	Trp	Pro	Ile	Arg
	195					200						205			
Val	Asp	Glu	Lys	Leu	Gly	Glu	Thr	Pro	Leu	Val	Pro	Glu	Gln	Asp	Asn
	210				215						220				
Ser	Val	Thr	Ser	Ile	Pro	Glu	Ile	Pro	Arg	Trp	Gly	Ser	Gln	Ser	Thr
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<210> 3224

<211> 224
 <212> PRT
 <213> Homo sapiens

<400> 3224

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      20           25           30
Val Ile Gly Val Ile Leu Gly Ala Glu Ala Ser Arg Arg Tyr Lys Lys
      35           40           45
Val Ile Pro Gly Ala Glu Pro Leu Ile Cys Ala Ser Ser Leu Leu Ala
      50           55           60
Thr Ala Pro Cys Leu Tyr Leu Ala Leu Val Leu Ala Pro Thr Thr Leu
      65           70           75           80
Leu Ala Ser Tyr Val Phe Leu Gly Leu Gly Glu Leu Leu Leu Ser Cys
      85           90           95
Asn Trp Ala Val Val Ala Asp Ile Leu Leu Ser Val Val Val Pro Arg
      100          105          110
Cys Arg Gly Thr Ala Glu Ala Leu Gln Ile Thr Val Gly His Ile Leu
      115          120          125
Gly Asp Ala Gly Ser Pro Tyr Leu Thr Gly Leu Ile Ser Ser Val Leu
      130          135          140
Arg Pro Gly Ala Leu Thr Pro Leu Gln Arg Phe Arg Ser Leu Gln Gln
      145          150          155          160
Ser Phe Leu Cys Cys Ala Phe Val Ile Ala Leu Gly Gly Gly Cys Phe
      165          170          175
Leu Leu Thr Ala Leu Tyr Leu Glu Arg Asp Glu Thr Arg Ala Trp Gln
      180          185          190
Pro Val Thr Gly Thr Pro Asp Ser Asn Asp Val Asp Ser Asn Asp Leu
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Glu Arg Gln Gly Leu Leu Ser Gly Ala Gly Ala Ser Thr Glu Glu Pro
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<210> 3225
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 <212> DNA
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<400> 3225

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420

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<210> 3226
 <211> 137
 <212> PRT
 <213> Homo sapiens

<400> 3226
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 Cys Phe Pro Val Pro Lys Met Pro Val Pro Cys Ala Leu Gly Glu Glu
 35 40 45
 Leu Val Pro Cys His Arg Gly Thr Gly Pro Ala Val Val Trp Pro Ala
 50 55 60
 Gln Pro Gln Gln Gly Glu Val Glu Pro Gln Pro Gln Pro Thr Gln Arg
 65 70 75 80
 Met Glu Pro Pro Ser Ala Ala Lys Asn Asn His Thr Ala Phe Glu Val
 85 90 95
 Ser His Pro Arg Cys Arg Trp Gly Cys Met Lys Leu His Glu His Gly
 100 105 110
 Met Ser Phe Ile Phe Arg Val Pro Arg Gly His Glu Trp Tyr Gln Asp
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 Pro Trp Arg Cys Pro Trp Phe Pro Met
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<210> 3227
 <211> 1623
 <212> DNA
 <213> Homo sapiens

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 120
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 180
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<210> 3228

<211> 385

<212> PRT

<213> Homo sapiens

<400> 3228

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			20					25					30		
Val	Gln	Val	Gly	Asp	Ser	Leu	Arg	Ala	Ser	Thr	Ile	Arg	Lys	Val	Gln
		35					40				45				
Thr	Glu	Ser	Ser	Thr	Gly	Ser	Val	Gly	Ser	Asn	Arg	Val	Arg	Thr	Thr
	50					55				60					
Leu	Thr	Leu	Cys	Val	Glu	Ala	Ile	Asp	Phe	Asp	Ser	Gln	Ala	Cys	Gln

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 Gly Ala Tyr His Thr Ile Glu Leu Glu Pro Asn Arg Gln Phe Thr Leu
 100 105 110
 Ala Lys Lys Gln Trp Asp Ser Val Val Leu Glu Arg Ile Glu Gln Ala
 115 120 125
 Cys Asp Pro Ala Trp Ser Ala Asp Val Ala Ala Val Met Gln Glu
 130 135 140
 Gly Leu Ala His Ile Cys Leu Val Thr Pro Ser Met Thr Leu Thr Arg
 145 150 155 160
 Ala Lys Val Glu Val Asn Ile Pro Arg Lys Arg Lys Gly Asn Cys Ser
 165 170 175
 Gln His Asp Arg Ala Leu Glu Arg Phe Tyr Glu Gln Val Val Gln Ala
 180 185 190
 Ile Gln Arg His Ile His Phe Asp Val Val Lys Cys Ile Leu Val Ala
 195 200 205
 Ser Pro Gly Phe Val Arg Glu Gln Phe Cys Asp Tyr Met Phe Gln Gln
 210 215 220
 Ala Val Lys Thr Asp Asn Lys Leu Leu Leu Glu Asn Arg Ser Lys Phe
 225 230 235 240
 Leu Gln Val His Ala Ser Ser Gly His Lys Tyr Ser Leu Lys Glu Ala
 245 250 255
 Leu Cys Asp Pro Thr Val Ala Ser Arg Leu Ser Asp Thr Lys Ala Ala
 260 265 270
 Gly Glu Val Lys Ala Leu Asp Asp Phe Tyr Lys Met Leu Gln His Glu
 275 280 285
 Pro Asp Arg Ala Phe Tyr Gly Leu Lys Gln Val Glu Lys Ala Asn Glu
 290 295 300
 Ala Met Ala Ile Asp Thr Leu Leu Ile Ser Asp Glu Leu Phe Arg His
 305 310 315 320
 Gln Asp Val Ala Thr Arg Ser Arg Tyr Val Arg Leu Val Asp Ser Val
 325 330 335
 Lys Glu Asn Ala Gly Thr Val Arg Ile Phe Ser Ser Leu His Val Ser
 340 345 350
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<210> 3229

<211> 1008

<212> DNA

<213> Homo sapiens

<400> 3229

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<210> 3230

<211> 232

<212> PRT

<213> Homo sapiens

<400> 3230

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			20					25					30		
Leu	Lys	Arg	Ile	His	Arg	Ala	Val	Leu	Arg	Gly	Asn	Leu	Glu	Glu	Leu
		35					40					45			
Lys	Tyr	Leu	Leu	Leu	Thr	Tyr	Tyr	Asp	Ile	Asn	Lys	Arg	Asp	Arg	Lys
		50				55					60				
Glu	Arg	Thr	Ala	Leu	His	Leu	Ala	Cys	Ala	Thr	Gly	Gln	Pro	Glu	Met
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Val	His	Leu	Leu	Val	Ser	Arg	Arg	Cys	Glu	Leu	Asn	Leu	Cys	Asp	Arg
				85					90					95	
Glu	Asp	Arg	Thr	Pro	Leu	Ile	Lys	Ala	Val	Gln	Leu	Arg	Gln	Glu	Ala
			100					105					110		
Cys	Ala	Thr	Leu	Leu	Leu	Gln	Asn	Gly	Ala	Asp	Pro	Asn	Ile	Thr	Asp
		115					120					125			
Val	Phe	Gly	Arg	Thr	Ala	Leu	His	Tyr	Ala	Val	Tyr	Asn	Glu	Asp	Thr
	130					135					140				
Ser	Met	Ile	Glu	Lys	Leu	Leu	Ser	His	Gly	Thr	Asn	Ile	Glu	Glu	Cys

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 180 185 190
 Ile Asp Tyr Leu Gly Arg Ser Ala Leu Ile Leu Ala Val Thr Leu Gly
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 Ser Arg Asp Val Tyr Gly Lys Leu
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<210> 3231

<211> 1367

<212> DNA

<213> Homo sapiens

<400> 3231

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<211> 251

<212> PRT

<213> Homo sapiens

<400> 3232

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Tyr	Trp	Phe	Ala	Ala	Thr	Val	Ala	Val	Pro	Leu	Val	Gly	Lys	Leu	Gly
			20					25					30		
Leu	Ile	Ser	Pro	Ala	Tyr	Leu	Phe	Leu	Trp	Pro	Glu	Ala	Phe	Leu	Tyr
		35					40					45			
Arg	Phe	Gln	Ile	Trp	Arg	Pro	Ile	Thr	Ala	Thr	Phe	Tyr	Phe	Pro	Val
	50					55					60				
Gly	Pro	Gly	Thr	Gly	Phe	Leu	Tyr	Leu	Val	Asn	Leu	Tyr	Phe	Leu	Tyr
65					70					75					80
Gln	Tyr	Ser	Thr	Arg	Leu	Glu	Thr	Gly	Ala	Phe	Asp	Gly	Arg	Pro	Ala
			85						90					95	
Asp	Tyr	Leu	Phe	Met	Leu	Leu	Phe	Asn	Trp	Ile	Cys	Ile	Val	Ile	Thr
			100					105					110		
Gly	Leu	Ala	Met	Asp	Met	Gln	Leu	Met	Ile	Pro	Leu	Ile	Met	Ser	
		115					120					125			
Val	Leu	Tyr	Val	Trp	Ala	Gln	Leu	Asn	Arg	Asp	Met	Ile	Val	Ser	Phe
	130					135						140			
Trp	Phe	Gly	Thr	Arg	Phe	Lys	Ala	Cys	Tyr	Leu	Pro	Trp	Val	Ile	Leu
145					150					155					160
Gly	Phe	Asn	Tyr	Ile	Ile	Gly	Gly	Ser	Val	Ile	Asn	Glu	Leu	Ile	Gly
			165					170						175	
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		180					185					190			
Asp	Leu	Gly	Gly	Arg	Asn	Phe	Leu	Ser	Thr	Pro	Gln	Phe	Leu	Tyr	Arg
		195					200					205			
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<212> DNA

<213> Homo sapiens

<400> 3233
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 accgttgttt accttgtggc ttccatctg ttctttgtta tgtttgtatg gtccatttgg
 120
 atgacaattt tcacatctcc cgcttcccc tccaaagagt tctacttgtc caattctgaa
 180
 aaggaacgtt atgaaaaaga attcagccaa gaaagacaac aagaaatttt gagaagagca
 240
 gcaagagctt tacctatcta taccacatca gcttcaaaaa ctatcagata ttgtgaaaaa
 300
 tgtcagctga ttaaacctga tcgggcgcac cactgctcag cctgtgactc atgtattctt
 360
 aagatggatc atccctgtcc ttgggtgaat aactgtgtgg gatcttctaa ttacaaattc
 420
 ttctgtctgt ttttattgta ttccctatta tattgccttt tcgtggccgc acagtttttag
 480
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 ttttttcttt tctttgtgtc tgcaatgttc ttcatcagcg tcctctcact ttccagctac
 600
 cactgctggc tttaaacagc attgtccaca gctccgtctg cagggtcagg gcatggcctc
 660
 tctccgtgtt cctgtgaaga gccttcattg gaatcatccc gggacataca gcttgaatgt
 720
 gctgtctggc tagccccctc acaagtcggt cactctgcac aaggaatccg agagctcatc
 780
 aaggatcagc acggtctggg gccaggtgg ggtggaacac gcacggtcca caagcaattc
 840
 tgtctttctc aaggcttttt cttgtgcagt atgaaatcct tcatatttca tatgaagtat
 900
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 960
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 975

<210> 3234

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3234
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 Glu Asn Gly Lys Thr Val Val Tyr Leu Val Ala Phe His Leu Phe Phe
 20 25 30
 Val Met Phe Val Trp Ser Tyr Trp Met Thr Ile Phe Thr Ser Pro Ala
 35 40 45
 Ser Pro Ser Lys Glu Phe Tyr Leu Ser Asn Ser Glu Lys Glu Arg Tyr
 50 55 60
 Glu Lys Glu Phe Ser Gln Glu Arg Gln Gln Glu Ile Leu Arg Arg Ala
 65 70 75 80
 Ala Arg Ala Leu Pro Ile Tyr Thr Thr Ser Ala Ser Lys Thr Ile Arg

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<210> 3235
<211> 551
<212> DNA
<213> Homo sapiens
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<210> 3236
<211> 183
<212> PRT
<213> Homo sapiens
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2439

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<400> 3237
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120
gatgaggacc gttgggaagt acggggggac cgcaaggccc ggaagcccct ggtggagaag
180
aagcgacgcg cgcgatcaa cgagagtctt caggagtgtc ggctgctgct ggcgggcgcc
240
gagggtgcagg ccaagctgga gaacgccgaa gtgctggagc tgacggtgcg gcgggtccag
300
ggtgtgctgc ggggccgggc gcgcgagcgc gaggcagctgc aggcggaagc gaggcagcgc
360
ttcgctgccg gctacatcca gtgcatgcac gagggtgcaca cgttcgtgtc cacgtgccag
420
gccatcgacg ctaccgtcgc tgccgagctc ctgaaccatc tgctcgagtc catgccgctg
480
cgtgagggca gcagcttcca ggatctgctg ggggacgccc tggcgggggc acctagagcc
540
cctggacgga gtggctggcc tgcggggggc gtcctgggat cccaatacc cagccccccg
600
ggtcctgggg acgacctgtg ctccgacctg gaggaggccc ctgaggctga actgagtcag
660
gctcctgctg agggggcccg cttggtgccc gcagccctgg gcagcctgac cacagcccaa
720
attgcccgga gtgtctggag gccttggtga ccaatgccag ccagagtcct gcgggggtgg
780
gccccgccc ccttggaatc cctccctcct ccagggggtt cagatgtggt ggggtagggc
840
cctggaagtc tcccaggtct tcctccctc ctctgatgga tggcttgag ggcagcccct
900
ggtaaccagc ccagtcaggc ccagccccg tttcttaaga aacttttagg gaccctgcag
960
ctctggagtg ggtggagggg gggagctacg ggcaggagga agaattttgt agagctgcca
1020

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gcgctctccc aggttcaccc acccaggctt caccagccct gtgcgggctc tgggggcaga
 1080
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 1140
 gaacttgcca cttcagcggg gagatgagag gcagggtgcac tcagctgcac tgcccagagc
 1200
 tgtgatgctc tgtacatctt gttttagca cacttgagtt tgtgtattcc attgacatca
 1260
 aatgtgacaa ttttactaaa taaagaattt tggagttagt tacccttgaa aaaaaagtcg
 1320
 acg
 1323

<210> 3238

<211> 249

<212> PRT

<213> Homo sapiens

<400> 3238

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			20					25					30		
Gly	Arg	Asp	Arg	Val	Gly	Arg	Glu	Asp	Glu	Asp	Arg	Trp	Glu	Val	Arg
		35				40						45			
Gly	Asp	Arg	Lys	Ala	Arg	Lys	Pro	Leu	Val	Glu	Lys	Lys	Arg	Arg	Ala
	50					55					60				
Arg	Ile	Asn	Glu	Ser	Leu	Gln	Glu	Leu	Arg	Leu	Leu	Leu	Ala	Gly	Ala
65					70					75				80	
Glu	Val	Gln	Ala	Lys	Leu	Glu	Asn	Ala	Glu	Val	Leu	Glu	Leu	Thr	Val
			85						90					95	
Arg	Arg	Val	Gln	Gly	Val	Leu	Arg	Gly	Arg	Ala	Arg	Glu	Arg	Glu	Gln
		100						105					110		
Leu	Gln	Ala	Glu	Ala	Ser	Glu	Arg	Phe	Ala	Ala	Gly	Tyr	Ile	Gln	Cys
		115					120					125			
Met	His	Glu	Val	His	Thr	Phe	Val	Ser	Thr	Cys	Gln	Ala	Ile	Asp	Ala
	130					135					140				
Thr	Val	Ala	Ala	Glu	Leu	Leu	Asn	His	Leu	Leu	Glu	Ser	Met	Pro	Leu
145					150					155				160	
Arg	Glu	Gly	Ser	Ser	Phe	Gln	Asp	Leu	Leu	Gly	Asp	Ala	Leu	Ala	Gly
			165					170						175	
Pro	Pro	Arg	Ala	Pro	Gly	Arg	Ser	Gly	Trp	Pro	Ala	Gly	Gly	Ala	Pro
		180						185					190		
Gly	Ser	Pro	Ile	Pro	Ser	Pro	Pro	Gly	Pro	Gly	Asp	Asp	Leu	Cys	Ser
		195					200					205			
Asp	Leu	Glu	Glu	Ala	Pro	Glu	Ala	Glu	Leu	Ser	Gln	Ala	Pro	Ala	Glu
	210					215					220				
Gly	Pro	Asp	Leu	Val	Pro	Ala	Ala	Leu	Gly	Ser	Leu	Thr	Thr	Ala	Gln
225					230					235				240	
Ile	Ala	Arg	Ser	Val	Trp	Arg	Pro	Trp							
				245											

<210> 3239

<211> 432

<212> DNA

<213> Homo sapiens

<400> 3239

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 120
 ggtttgttcc tccttttctt cgttctgcgg gtccgaagca atgtgctaaa ggggtgctatc
 180
 caggaccgcg taggtctcct ttaccagttt gtgggcgcca ccccgtaacac aggcattgctg
 240
 aacgctgtga atctgtttcc cgtgctgcga gctgtcagcg accaggagag tcaggacggc
 300
 ctctaccaga agtggcagat gatgctggcc tatgcactgc acgtcctccc cttcagcgtt
 360
 gttgccacca tgattttcag cagtgtgtgc tactggacgc tgggcttaca tcctgaggtt
 420
 gcccgattgg gt
 432

<210> 3240

<211> 144

<212> PRT

<213> Homo sapiens

<400> 3240

Lys	Thr	Lys	Asp	Ser	Pro	Gly	Val	Phe	Ser	Lys	Leu	Gly	Val	Leu	Leu
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Arg	Arg	Val	Thr	Arg	Asn	Leu	Val	Arg	Asn	Lys	Leu	Ala	Val	Ile	Thr
			20					25					30		
Arg	Leu	Leu	Gln	Asn	Leu	Ile	Met	Gly	Leu	Phe	Leu	Leu	Phe	Phe	Val
	35					40					45				
Leu	Arg	Val	Arg	Ser	Asn	Val	Leu	Lys	Gly	Ala	Ile	Gln	Asp	Arg	Val
	50				55					60					
Gly	Leu	Leu	Tyr	Gln	Phe	Val	Gly	Ala	Thr	Pro	Tyr	Thr	Gly	Met	Leu
65				70				75						80	
Asn	Ala	Val	Asn	Leu	Phe	Pro	Val	Leu	Arg	Ala	Val	Ser	Asp	Gln	Glu
			85					90					95		
Ser	Gln	Asp	Gly	Leu	Tyr	Gln	Lys	Trp	Gln	Met	Met	Leu	Ala	Tyr	Ala
			100				105					110			
Leu	His	Val	Leu	Pro	Phe	Ser	Val	Val	Ala	Thr	Met	Ile	Phe	Ser	Ser
	115						120					125			
Val	Cys	Tyr	Trp	Thr	Leu	Gly	Leu	His	Pro	Glu	Val	Ala	Arg	Leu	Gly
	130					135						140			

<210> 3241

<211> 492

<212> DNA

<213> Homo sapiens

<400> 3241

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acgaaataca aaataagagg caggaagagc ccaaagcatc agaaatgtgc cagttataat
 120
 gggccaaaat cccctcttgt gtctccagaa gtatttgaaa aatacgttag gatctgcctc
 180
 acagacatgc tcccaggaca ctgcacagca aggaggtacg gcgggcccag ccagccaagg
 240
 cagaggagga catcactgcc acagcagggg gcctgactgg cagcaaaagg gacgactccg
 300
 gcgaaaagtc agcaggaaac aggacagggg ctggaccaat ggccctccctc agccccacac
 360
 cccacccagg caggagcggg gcctggcccc gggcaggcgg gtgggagagc tactgagtg
 420
 ggcagcaggg catggcccct gatgctgcag gtacccaggc tgcagctgca gaaacctcag
 480
 tgggaaccca gg
 492

<210> 3242

<211> 107

<212> PRT

<213> Homo sapiens

<400> 3242

Met	Gly	Gln	Asn	Pro	Leu	Leu	Cys	Leu	Gln	Lys	Tyr	Leu	Lys	Asn	Thr
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Leu	Gly	Ser	Ala	Ser	Gln	Thr	Cys	Ser	Gln	Asp	Thr	Arg	Gln	Gln	Gly
		20					25					30			
Gly	Thr	Ala	Gly	Pro	Ala	Ser	Gln	Gly	Arg	Gly	Gly	His	His	Cys	His
		35				40					45				
Ser	Arg	Gly	Pro	Asp	Trp	Gln	Gln	Lys	Gly	Arg	Leu	Arg	Arg	Lys	Val
	50				55					60					
Ser	Arg	Lys	Gln	Asp	Arg	Gly	Trp	Thr	Asn	Gly	Leu	Pro	Gln	Pro	His
65			70						75					80	
Thr	Pro	Pro	Arg	Gln	Glu	Arg	Cys	Leu	Ala	Arg	Gly	Arg	Arg	Val	Gly
			85					90						95	
Glu	Leu	Thr	Glu	Trp	Ala	Ala	Gly	His	Gly	Pro					
			100					105							

<210> 3243

<211> 944

<212> DNA

<213> Homo sapiens

<400> 3243

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 120
 tttgaggcaa aggtaaccca gaatctccca atgaaagaag gctgcacaga ggtctctctc
 180
 cttcgagttg ggtggtctgt tgatttttcc cgtccacagc ttggtgaaga tgaattctct
 240
 tacggtttcg atggacgagg actcaaggca gaaaatggac aatttgagga atttgccag
 300

acttttgggg agaatgatgt tattggctgc ttgctaatt ttgagactga agaagtagaa
 360
 ctttccttct ccaagaatgg agaagacctt ggtgtggcat tctggatcag caaggattcc
 420
 ctggcagacc gggcccttct accccatgtc ctctgcaaaa attgtgttgt agaattaaac
 480
 ttcggtcaga aggaggagcc cttcttccca ccaccagaag agtttgtgtt cattcatgct
 540
 gtgcctgttg aggagcgtgt acgcactgca gtccctccca agaccataga ggaatgtgag
 600
 gtgattctga tgggtgggact acccggtatct ggaaagacct agtgggcact gaaatatgca
 660
 aaagaaaacc ctgagaaaag atacaatgtc ctgggagctg agactgtgct caatcaaatg
 720
 aggatgaagg gtctcgagga gccagagatg gacccccaaa gccgagacct tttagttag
 780
 caagcctccc agtgccttag taagctggtc cagattgctt cccggacaaa gaggaacttt
 840
 attcttgatc agtgtaatgt gtacaattct ggccaacggc ggaagctatt gctgttcaag
 900
 accttctctc ggaaagtggg ggtggttgtc cctaagtagg aaga
 944

<210> 3244

<211> 314

<212> PRT

<213> Homo sapiens

<400> 3244

Asp	Leu	His	Phe	Gln	Val	Ser	Lys	Asp	Arg	Tyr	Gly	Gly	Gln	Pro	Leu
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Phe	Ser	Glu	Lys	Phe	Pro	Thr	Leu	Trp	Ser	Gly	Ala	Arg	Ser	Thr	Tyr
			20					25					30		
Gly	Val	Thr	Lys	Gly	Lys	Val	Cys	Phe	Glu	Ala	Lys	Val	Thr	Gln	Asn
		35				40						45			
Leu	Pro	Met	Lys	Glu	Gly	Cys	Thr	Glu	Val	Ser	Leu	Leu	Arg	Val	Gly
	50				55					60					
Trp	Ser	Val	Asp	Phe	Ser	Arg	Pro	Gln	Leu	Gly	Glu	Asp	Glu	Phe	Ser
65				70					75					80	
Tyr	Gly	Phe	Asp	Gly	Arg	Gly	Leu	Lys	Ala	Glu	Asn	Gly	Gln	Phe	Glu
			85					90						95	
Glu	Phe	Gly	Gln	Thr	Phe	Gly	Glu	Asn	Asp	Val	Ile	Gly	Cys	Phe	Ala
		100						105					110		
Asn	Phe	Glu	Thr	Glu	Glu	Val	Glu	Leu	Ser	Phe	Ser	Lys	Asn	Gly	Glu
		115				120						125			
Asp	Leu	Gly	Val	Ala	Phe	Trp	Ile	Ser	Lys	Asp	Ser	Leu	Ala	Asp	Arg
	130				135					140					
Ala	Leu	Leu	Pro	His	Val	Leu	Cys	Lys	Asn	Cys	Val	Val	Glu	Leu	Asn
145				150					155					160	
Phe	Gly	Gln	Lys	Glu	Pro	Phe	Phe	Pro	Pro	Pro	Glu	Glu	Phe	Val	
			165				170						175		
Phe	Ile	His	Ala	Val	Pro	Val	Glu	Glu	Arg	Val	Arg	Thr	Ala	Val	Pro
		180					185						190		
Pro	Lys	Thr	Ile	Glu	Glu	Cys	Glu	Val	Ile	Leu	Met	Val	Gly	Leu	Pro

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<210> 3245
<211> 980
<212> DNA
<213> Homo sapiens
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2445

ctcaccaaag caaaaaaaaaa
980

<210> 3246

<211> 219

<212> PRT

<213> Homo sapiens

<400> 3246

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Val Trp Arg Gly Ala Leu Leu Leu Ala Asp Tyr Ile Leu Phe Arg Gln
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      20              25              30
Leu Ala Ser Ile Ile Ala Ala Thr Met Ala Arg Thr Val Tyr Cys Thr
      35              40              45
Asp Val Gly Ala Asp Leu Leu Ser Met Cys Gln Arg Asn Ile Ala Leu
      50              55              60
Asn Ser His Leu Ala Ala Thr Gly Gly Gly Ile Val Arg Val Lys Glu
      65              70              75              80
Leu Asp Trp Leu Lys Asp Asp Leu Cys Thr Asp Pro Lys Val Pro Phe
      85              90              95
Ser Trp Ser Gln Glu Glu Ile Ser Asp Leu Tyr Asp His Thr Thr Ile
      100             105             110
Leu Phe Ala Ala Glu Val Phe Tyr Asp Asp Asp Leu Thr Asp Ala Val
      115             120             125
Phe Lys Thr Leu Ser Arg Leu Ala His Arg Leu Lys Asn Ala Cys Thr
      130             135             140
Ala Ile Leu Ser Val Glu Lys Arg Leu Asn Phe Thr Leu Arg His Leu
      145             150             155             160
Asp Val Thr Cys Glu Ala Tyr Asp His Phe Arg Ser Cys Leu His Ala
      165             170             175
Leu Glu Gln Leu Thr Asp Gly Lys Leu Arg Phe Val Val Glu Pro Val
      180             185             190
Glu Ala Ser Phe Pro Gln Leu Leu Val Tyr Glu Arg Leu Gln Gln Leu
      195             200             205
Glu Leu Trp Lys Ile Ile Ala Glu Pro Val Thr
      210             215
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<210> 3247

<211> 977

<212> DNA

<213> Homo sapiens

<400> 3247

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180
ccgggtgggc ccagccccgg gagccgggtg cttaccatcc tggagcagat ccccggcag
240
gtgggtgggtg ctgacaagac ctgggagctc taccagaaga cctactgggc cagctacaac
300
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 420
 ctggtacaag acatggactc catggtcagg ctgatgaggt acaatgactt cctccatgac
 480
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 540
 cgctccgacc tcaaccgggc caatggctcc tacccttcc aggccctacg tcagcgtcc
 600
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 660
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 720
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 780
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 840
 acccccgctc caaggccacc ggacttctaa ctccagcccc tcttgggggc ttcgttctct
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 gatctgggggt ctgagtcac tcctcctaga gtgggtcacg aacctgatgg ggctcagaac
 960
 tgacccccctc tctcccc
 977

<210> 3248

<211> 260

<212> PRT

<213> Homo sapiens

<400> 3248

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1			5						10					15	
Trp	Val	Arg	Asn	Ile	Val	Ala	Asn	Arg	Leu	Ala	Ser	Asp	Gly	Ala	Thr
			20					25					30		
Trp	Ala	Asp	Ile	Phe	Lys	Arg	Phe	Asn	Ser	Gly	Thr	Tyr	Asn	Asn	Gln
		35					40					45			
Trp	Met	Ile	Val	Asp	Tyr	Lys	Ala	Phe	Ile	Pro	Gly	Gly	Pro	Ser	Pro
		50				55					60				
Gly	Ser	Arg	Val	Leu	Thr	Ile	Leu	Glu	Gln	Ile	Pro	Gly	Met	Val	Val
65				70					75						80
Val	Ala	Asp	Lys	Thr	Ser	Glu	Leu	Tyr	Gln	Lys	Thr	Tyr	Trp	Ala	Ser
			85						90				95		
Tyr	Asn	Ile	Pro	Ser	Phe	Glu	Thr	Val	Phe	Asn	Ala	Ser	Gly	Leu	Gln
			100					105					110		
Ala	Leu	Val	Ala	Gln	Tyr	Gly	Asp	Trp	Phe	Ser	Tyr	Asp	Gly	Ser	Pro
		115					120					125			
Arg	Ala	Gln	Ile	Phe	Arg	Arg	Asn	Gln	Ser	Leu	Val	Gln	Asp	Met	Asp
		130					135					140			
Ser	Met	Val	Arg	Leu	Met	Arg	Tyr	Asn	Asp	Phe	Leu	His	Asp	Pro	Leu
145				150					155						160
Ser	Leu	Cys	Lys	Ala	Cys	Asn	Pro	Gln	Pro	Asn	Gly	Glu	Asn	Ala	Ile
			165					170					175		
Ser	Ala	Arg	Ser	Asp	Leu	Asn	Pro	Ala	Asn	Gly	Ser	Tyr	Pro	Phe	Gln

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<400> 3249
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120
gctcttcact tttatgcttt ccaccagagt aataatggaa atcctggaaa gccttctcct
180
ttcccatggg ttcccaactga ttgcttttct ctctctctct cccaccccca ctccagggtgc
240
tctggggcca ggtgccaccg gccattgtcc aggcagctgt gtgcaagcca aagaagcatg
300
tggacactgg aagactcctc ggggacagtc ctgcaccgcc tcatccagga gcagctgcgc
360
tacggcaacc tgactgagac gcgcacgctg ctagccatcc agcagcaggc cctgaggggt
420
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480
gacagtcagg tgctgcagca ggccaccagg caggagcccc agggccagga gcaccagggc
540
ggtgagaacc acctggcaga gaacaccctc taccggctat gcccacagcc cagcaaggga
600
gaggagctgc ccacctatga ggaggccaaa gccactcgc agtactatgc ggcccagcag
660
gcagggaccc ggccacatgc gggggaccga gatccccgtg gggccccggg aggcagtctg
720
aggcaggacg aggccctgcg ggagctgagg catgggcacg tgcgctcggt gagtgaacgg
780
ctccttcagt tgtccctgga gaggaacggc gcccgggccc ccagccacat gagctcctcc
840
cacagcttcc cacagctggc ccgcaaccag cagggccccc cactgagggg cccccctgct
900
gagggcccag agtcccagg accccacact cagtaccctc atgttgtact agctcatgag
960
accaccactg ctgtcactga cccacggtac cgtgccccgc gcagcccgc cttccagcat
1020
gctgaagtca ggatcctgca ggcccagggt cctcctgtgt tctccaaca gcagcagcag
1080

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taccagtacc tgcagcaatc tcaggagcac cccctcccc cacatccagc tgctctcggc
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1200
tcctcagcca cctcgggcag tgcccacctg gccagatgg aggccgtgct gagggagaat
1260
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1380
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<211> 849

<212> PRT

<213> Homo sapiens

<400> 3250

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<213> Homo sapiens

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<213> Homo sapiens

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Gly	Ser	Arg	Tyr	Glu	Gly	Glu	Trp	Ala	Asn	Asp	Leu	Arg	His	Gly	His
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		115					120					125			
Ala	His	Gln	Arg	His	Gly	Gln	Gly	Thr	Tyr	Leu	Tyr	Ala	Glu	Thr	Gly
		130				135					140				
Ser	Lys	Tyr	Val	Gly	Thr	Trp	Val	Asn	Gly	Gln	Glu	Gly	Thr	Ala	
145					150				155					160	
Glu	Leu	Ile	His	Leu	Asn	His	Arg	Tyr							

165

<210> 3257

<211> 368

<212> DNA

<213> Homo sapiens

<400> 3257

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nncccggggg acatagactc cccacactac agccggcagg gcatgtcccc caccttctcc
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120
agtgaagaca tcagccagac ctccaagtac agtcccatct actcgccaga cccctactat
180
gcttcggagt ctgagtactg gacctaccat gggcccccca aagtgccccg agccagaagg
240
ttctcgtctg gaggagagga ggatgatttt gaccgcagca tgcacaagct ccaaagtgga
300
attggccggc tgattctgaa ggaagaaatg aaggccccgt cgagctccta tgcagatccc
360
tggcgcgc
368

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<210> 3258

<211> 122

<212> PRT

<213> Homo sapiens

<400> 3258

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Xaa Pro Gly Tyr Ile Asp Ser Pro Thr Tyr Ser Arg Gln Gly Met Ser
1      5      10      15
Pro Thr Phe Ser Arg Ser Pro His His Tyr Tyr Arg Ser Gly Asp Leu
20     25     30
Ser Thr Ala Thr Lys Ser Glu Thr Ser Glu Asp Ile Ser Gln Thr Ser
35     40     45
Lys Tyr Ser Pro Ile Tyr Ser Pro Asp Pro Tyr Tyr Ala Ser Glu Ser
50     55     60
Glu Tyr Trp Thr Tyr His Gly Ser Pro Lys Val Pro Arg Ala Arg Arg
65     70     75     80
Phe Ser Ser Gly Gly Glu Glu Asp Asp Phe Asp Arg Ser Met His Lys
85     90     95
Leu Gln Ser Gly Ile Gly Arg Leu Ile Leu Lys Glu Glu Met Lys Ala
100    105    110
Arg Ser Ser Ser Tyr Ala Asp Pro Trp Arg
115    120

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<210> 3259

<211> 747

<212> DNA

<213> Homo sapiens

<400> 3259

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acgcgtgaag ggcgcaccct ctgctgcagc actggccacc ccggacacgc tgcagggccca
60

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gtgctcagcc ttcgtacagc tctgggccc cctgcagccc atcttggtg gcaacaaccg
 120
 caccattgaa cccggagcgc tgcggcgggg caacatgagc tccctgggct ttacgagcaa
 180
 ggagcagcgg aacctggggc ttctcgtgca cctcatgacc agcaacccca aaatcctgta
 240
 cgcgcctgcg ggctctgagg tcgaccgcgt catcctcaag gccaacgaga cttttgcttt
 300
 tgtggggaac gtgactcact atgccaggt ctggctcaac atctcggcgg agatccgcag
 360
 cttcctggag cagggcaggc tgcagcaaca cctgcgctgg ctgcagcagt atgtagcaga
 420
 gctgcggctg caccctgagg cactgaacct gtcactggat gagctgccgc cggccctgag
 480
 acaggacaac ttctcgtgca ccagtggcat ggccctcctg cagcagctgg ataccattga
 540
 caacgcggcc tgcggctgga tccagttcat gtccaaggtg agcgtggaca tcttcaaggg
 600
 cttccccgac gaggagagca ttgtcaacta caccctcaac caggcctacc aggacaacgt
 660
 cactgttttt gccagtgtga tcttccagac ccggaaggac ggctcgtccc gcctcaagtg
 720
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 747

<210> 3260

<211> 197

<212> PRT

<213> Homo sapiens

<400> 3260

Met	Ser	Ser	Leu	Gly	Phe	Thr	Ser	Lys	Glu	Gln	Arg	Asn	Leu	Gly	Leu
1			5						10					15	
Leu	Val	His	Leu	Met	Thr	Ser	Asn	Pro	Lys	Ile	Leu	Tyr	Ala	Pro	Ala
			20					25					30		
Gly	Ser	Glu	Val	Asp	Arg	Val	Ile	Leu	Lys	Ala	Asn	Glu	Thr	Phe	Ala
			35				40					45			
Phe	Val	Gly	Asn	Val	Thr	His	Tyr	Ala	Gln	Val	Trp	Leu	Asn	Ile	Ser
			50				55				60				
Ala	Glu	Ile	Arg	Ser	Phe	Leu	Glu	Gln	Gly	Arg	Leu	Gln	Gln	His	Leu
65						70				75				80	
Arg	Trp	Leu	Gln	Gln	Tyr	Val	Ala	Glu	Leu	Arg	Leu	His	Pro	Glu	Ala
			85					90						95	
Leu	Asn	Leu	Ser	Leu	Asp	Glu	Leu	Pro	Pro	Ala	Leu	Arg	Gln	Asp	Asn
			100					105					110		
Phe	Ser	Leu	Pro	Ser	Gly	Met	Ala	Leu	Leu	Gln	Gln	Leu	Asp	Thr	Ile
			115				120					125			
Asp	Asn	Ala	Ala	Cys	Gly	Trp	Ile	Gln	Phe	Met	Ser	Lys	Val	Ser	Val
130						135					140				
Asp	Ile	Phe	Lys	Gly	Phe	Pro	Asp	Glu	Glu	Ser	Ile	Val	Asn	Tyr	Thr
145					150					155				160	
Leu	Asn	Gln	Ala	Tyr	Gln	Asp	Asn	Val	Thr	Val	Phe	Ala	Ser	Val	Ile
				165				170						175	
Phe	Gln	Thr	Arg	Lys	Asp	Gly	Ser	Ser	Arg	Leu	Thr	Cys	Thr	Thr	Arg

180
Ser Ala Arg Thr Pro
195

185

190

<210> 3261

<211> 1323

<212> DNA

<213> Homo sapiens

<400> 3261

nnacgcgtac agccaccttc cttaccgccg gccctgccgg gagcctgctt cttatcattt
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gcacctcatt gctttcctca cctgccatct cacacgtggc tgcctgtgtg tgccctgtg
120
tgctgtgcca attgtgtttt ttgtctctgt gtacattttg gttttatttg gggttgctgt
180
tgatgatttc ctttgttccg gtgttctgtc tcccctcgct ggctgtgtgg gggtgcctg
240
gcccgtgct tgcgcctcc atagatcccc gttgcgagc catctgtcat ggacgacatt
300
gaggtgtggc tcaggaccga cctgaagggt gatgatctgg aggaggggtg cacaagtga
360
gagtttgata aattccttga agaaagagcc aaagctgctg aaatggttcc cgacctcccc
420
tcgcccccca tggaggctcc tgccccagcc tcaaaccctt ctggccggaa gaagccagag
480
cggtcagagg atgcccctct cgccctgtga gcagctctgt ggtttgctc cccagatggc
540
gggtccccgc ttgcaccccg tggacaccgg gcactggcca ctctacatc cccagctcca
600
cacggcctgc acacctgtgt ttccatggaa atgccaccgt gtctgctccc aggcctcccc
660
ctagtcagga ccagcttcag ccacttcttt tctctgagtg gtgggacaac tgcagccaga
720
gactctctcc cctcccacca tgggcccctc tgcccattgt tcctcccagg aagagcgggc
780
agagtggccc agccccaggc agtgcctcct gagcagacca cccggactgt ctttctctca
840
ccgcccctg gagaaagagc acgcccggcc ccgcccgtg ctcacctctg cctggctcag
900
tgacctctc aggcattctg cctcctggg cccctctctc cctgaagggg ctttgtggca
960
tctctggaag agcagggtgt gctgcactca tgggcctggg ctactcctt ggacttgta
1020
ccttgtaga tttggcttac cagcatttga gaaggctctg ctgggtctcc atggtggggg
1080
tctctcacct tcttgacct ctctccatca ttcagctgcc agcccaggct tcacacccaa
1140
gctggctcag cagccgagcc tggcaccgag ggtccctgca ggctccctgg gcaggagag
1200
ggccaaggac aattgggagg gcagcaggca gcccgagat ggtggccatg tggcacgctg
1260
ctgagacgac actaccaata aaccaaactg ccacgcacaa aaaaaaaaaa aaaaaaaaaa
1320

aaa
1323

<210> 3262
<211> 81
<212> PRT
<213> Homo sapiens

<400> 3262
Ile Pro Val Ala Gln Pro Ser Val Met Asp Asp Ile Glu Val Trp Leu
1 5 10 15
Arg Thr Asp Leu Lys Gly Asp Asp Leu Glu Glu Gly Val Thr Ser Glu
20 25 30
Glu Phe Asp Lys Phe Leu Glu Glu Arg Ala Lys Ala Ala Glu Met Val
35 40 45
Pro Asp Leu Pro Ser Pro Pro Met Glu Ala Pro Ala Pro Ala Ser Asn
50 55 60
Pro Ser Gly Arg Lys Lys Pro Glu Arg Ser Glu Asp Ala Leu Phe Ala
65 70 75 80
Leu

<210> 3263
<211> 1128
<212> DNA
<213> Homo sapiens

<400> 3263
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60
cggggacgca agggccgggg ccgggggtccc ccgtcctcct ctgactccga gcccagggcc
120
gagctggaga gagaggccaa gaaatcagcg aagaagccgc agtcctcaag cacagagccc
180
gccaggaaac ctggccagaa ggagaagaga gtgcggcccg aggagaagca acaagccaag
240
cccgtgaagg tggagcggac ccggaagcgg tccgagggct tctcgatgga caggaaggta
300
gagaagaaga aagagccctc cgtggaggag aagctgcaga agctgcacag tgagatcaag
360
tttgccctaa aggtcgacag ccgggacgtg aaggggtgcc tgaatgccct agaggagctg
420
ggaaccctgc aggtgacctc tcagatcctc cagaagaaca cagacgtggt ggccaccttg
480
aagaagattc gccgttataa agcgaacaag gacgtaatgg agaaggcagc agaagtctat
540
acccgggtca agtcgcggtt cctcggccca aagatcgagg cgggtgcagaa agtgaacaag
600
gctgggatgg agaaggagaa ggccgaggag aagctggccg gggaggagct ggccggggag
660
gaggccccc aggagaaggc ggaggacaag ccagcaccg atctctcagc ccagtgat
720
ggcgaggcca catcacagaa gggggagagc gcagaggaca aggagcacga ggagggtcgg
780

gactcggagg aggggccaag gtgtggctcc tctgaagacc tgcacgacag cgtacgggag
 840
 ggtcccgacc tggacaggcc tgggagcgac cggcaggagc gcgagagggc acggggggac
 900
 tcggaggccc tggacgagga gagctgagcc gcgggcagcc aggcccagcc cccgcccag
 960
 ctgaggtgc ccctctcctt ccccggtcg caggagagca gagcagagaa ctgtggggaa
 1020
 cgctgtgctg tttgtatttg ttcccttggg ttttttttc ctgcctaatt tctgtgattt
 1080
 ccaaccaaca tgaaatgact ataaatgggt tttttaatga aaaaaaaaa
 1128

<210> 3264

<211> 308

<212> PRT

<213> Homo sapiens

<400> 3264

Ser	Arg	Tyr	Arg	Arg	Ser	Ser	Gly	Asp	Glu	Leu	Arg	Glu	Asp	Asp	Glu
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Pro	Val	Lys	Lys	Arg	Gly	Arg	Lys	Gly	Arg	Gly	Arg	Gly	Pro	Pro	Ser
		20						25					30		
Ser	Ser	Asp	Ser	Glu	Pro	Glu	Ala	Glu	Leu	Glu	Arg	Glu	Ala	Lys	Lys
		35					40					45			
Ser	Ala	Lys	Lys	Pro	Gln	Ser	Ser	Ser	Thr	Glu	Pro	Ala	Arg	Lys	Pro
	50					55				60					
Gly	Gln	Lys	Glu	Lys	Arg	Val	Arg	Pro	Glu	Glu	Lys	Gln	Gln	Ala	Lys
65					70					75					80
Pro	Val	Lys	Val	Glu	Arg	Thr	Arg	Lys	Arg	Ser	Glu	Gly	Phe	Ser	Met
				85					90					95	
Asp	Arg	Lys	Val	Glu	Lys	Lys	Lys	Glu	Pro	Ser	Val	Glu	Glu	Lys	Leu
			100					105					110		
Gln	Lys	Leu	His	Ser	Glu	Ile	Lys	Phe	Ala	Leu	Lys	Val	Asp	Ser	Pro
		115					120					125			
Asp	Val	Lys	Gly	Cys	Leu	Asn	Ala	Leu	Glu	Glu	Leu	Gly	Thr	Leu	Gln
		130				135					140				
Val	Thr	Ser	Gln	Ile	Leu	Gln	Lys	Asn	Thr	Asp	Val	Val	Ala	Thr	Leu
145					150					155					160
Lys	Lys	Ile	Arg	Arg	Tyr	Lys	Ala	Asn	Lys	Asp	Val	Met	Glu	Lys	Ala
				165					170					175	
Ala	Glu	Val	Tyr	Thr	Arg	Leu	Lys	Ser	Arg	Val	Leu	Gly	Pro	Lys	Ile
		180						185					190		
Glu	Ala	Val	Gln	Lys	Val	Asn	Lys	Ala	Gly	Met	Glu	Lys	Glu	Lys	Ala
		195					200					205			
Glu	Glu	Lys	Leu	Ala	Gly	Glu	Glu	Leu	Ala	Gly	Glu	Glu	Ala	Pro	Gln
		210				215					220				
Glu	Lys	Ala	Glu	Asp	Lys	Pro	Ser	Thr	Asp	Leu	Ser	Ala	Pro	Val	Asn
225					230					235					240
Gly	Glu	Ala	Thr	Ser	Gln	Lys	Gly	Glu	Ser	Ala	Glu	Asp	Lys	Glu	His
				245					250					255	
Glu	Glu	Gly	Arg	Asp	Ser	Glu	Glu	Gly	Pro	Arg	Cys	Gly	Ser	Ser	Glu
			260					265					270		
Asp	Leu	His	Asp	Ser	Val	Arg	Glu	Gly	Pro	Asp	Leu	Asp	Arg	Pro	Gly

275 280 285
 Ser Asp Arg Gln Glu Arg Glu Arg Ala Arg Gly Asp Ser Glu Ala Leu
 290 295 300
 Asp Glu Glu Ser
 305

<210> 3265

<211> 524

<212> DNA

<213> Homo sapiens

<400> 3265
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 ctttttcgtg gttttcaaaa tgttccatt gagggcgat tactttata atcaacaaaa
 120
 gagaaagtat aacttcattt tagaaattct cacctaaggc atttgaaaaa taatccaaaa
 180
 ggtacattat tggtgatttt tcttccttct agaaaggatc ttgttcgagt agaagccaca
 240
 gtcattgaaa agacagaatc atggccaaga atcattatga gattcaggaa aaggaaaaac
 300
 ttcaagaaga aaagaagtaa gttagagaaa gtaccgctgg gccctgttgc acggtgctgg
 360
 ttgccaggc gcatgctggc ggagggtgtg gggcacgtgg gtctcgggac aggaagccca
 420
 ggcaggtctc aacctggctg ccaactgccc cttgccacc tcatactaga gggagcacc
 480
 agagggtcca gcctcgtcc ccttcctc cagctccac gcgt
 524

<210> 3266

<211> 82

<212> PRT

<213> Homo sapiens

<400> 3266
 Met Arg Phe Arg Lys Arg Lys Asn Phe Lys Lys Lys Arg Ser Lys Leu
 1 5 10 15
 Glu Lys Val Pro Leu Gly Pro Val Ala Arg Cys Trp Leu Pro Arg Arg
 20 25 30
 Met Arg Thr Glu Gly Val Gly His Val Gly Leu Gly Thr Gly Ser Pro
 35 40 45
 Gly Arg Ser Gln Pro Gly Cys His Cys Pro Leu Ala Thr Leu Ile Leu
 50 55 60
 Glu Gly Ala Pro Arg Gly Ser Ser Leu Ala Pro Leu Leu Leu His Ala
 65 70 75 80
 Pro Arg

<210> 3267

<211> 393

<212> DNA

<213> Homo sapiens

<400> 3267

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tggaatacat tgaataaaaa ggtcgcacaa agaattgcac agctacagga agctttgttg
120
cattgtggga agtttcaaga tgccttggag ccattgctca gctgggtggc agataccgag
180
gagctcatag ccaatcagaa acctccatct gctgagtata aagtgggtgaa agcacagatc
240
caagaacaga agttgctcca gcggctccta gatgatcgaa aggccacagt agacatgctt
300
caagcagaag gaggcagaat agcccagtca gcagagctgg ctgatagaga gaaaatcact
360
ggacagctgg agagtcttga aagtagatgg act
393

<210> 3268

<211> 131

<212> PRT

<213> Homo sapiens

<400> 3268

Val	Glu	Tyr	Ala	Cys	Arg	Val	Gln	Gly	Leu	Glu	His	Asp	Met	Glu	Glu
1				5				10					15		
Ile	Asn	Ala	Arg	Trp	Asn	Thr	Leu	Asn	Lys	Lys	Val	Ala	Gln	Arg	Ile
			20					25					30		
Ala	Gln	Leu	Gln	Glu	Ala	Leu	Leu	His	Cys	Gly	Lys	Phe	Gln	Asp	Ala
		35				40						45			
Leu	Glu	Pro	Leu	Leu	Ser	Trp	Leu	Ala	Asp	Thr	Glu	Glu	Leu	Ile	Ala
		50				55				60					
Asn	Gln	Lys	Pro	Pro	Ser	Ala	Glu	Tyr	Lys	Val	Val	Lys	Ala	Gln	Ile
65					70					75				80	
Gln	Glu	Gln	Lys	Leu	Leu	Gln	Arg	Leu	Leu	Asp	Asp	Arg	Lys	Ala	Thr
				85				90					95		
Val	Asp	Met	Leu	Gln	Ala	Glu	Gly	Gly	Arg	Ile	Ala	Gln	Ser	Ala	Glu
			100				105					110			
Leu	Ala	Asp	Arg	Glu	Lys	Ile	Thr	Gly	Gln	Leu	Glu	Ser	Leu	Glu	Ser
		115					120					125			
Arg	Trp	Thr													
		130													

<210> 3269

<211> 1423

<212> DNA

<213> Homo sapiens

<400> 3269

ctgtatcaaa aataatagta actttttgaa tatacacaaat ttatctagaa tctattttcc
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tttgaagctg taactttatg agcgattatt tactaccttt gagaaatgtg ttttagtata
120
aaatatagga tgtggaagcg aaaaaatata tgggtagcaa gtgaggtgta ctcaaaaata
180

agcaaaagtc acgtgggtct gattttatac cctcgctgga aagcttggtc tcagacacac
 240
 tgttactgca agtgtgtgtg aggggggaaac tctcacacac ttgcagttg aggacagggc
 300
 tagactttga ggtggaccct ggctcccagg gctgtgtact cccagcccggt gtttctcttt
 360
 tgctcagact gaacaagtgg aacgaaatta cattaaagaa aagaaggcag cagtgaagaa
 420
 atttgaagac aagaagggtg agctgaaaga gaacctgatt gctgagctag aagaaaagaa
 480
 gaaaatgatt gaaaacgaaa tgctgacaat ggaactgaat ggagattcta tggaggtgaa
 540
 acctatcatg accagaaagt tgcggaggcg accaaatgat cccgtcccca tcccagacaa
 600
 gaggaggaaa cctgctccag cccagctaaa ctatttggtta acagatgaac agatcatgga
 660
 ggatctgaga acattaaata agcttaagtc acccaagaga ccagcatctc catcctctcc
 720
 tgagcacttg cctgcaacac ccgcggaatc tccagcacag agatttgagg cgcggataga
 780
 agatggcaaa ctgtattatg acaaaagatg gtaccacaag agccaggcca tctatctgga
 840
 gtcaaaggac aaccagaaac tgagctgctg gatcagttct gtaggagcca atgagatctg
 900
 ggtgaggaag acaagtgaca gcaccaagat gaggatctac ctgggtcagc ttcagcgcg
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 1020
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 1080
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 1140
 gggcactttt gtggccgat gcttccaact ttgtcagtct tttctgcctc aacttcttcc
 1200
 agacatcagt caccatgaga ctgttttact ttcaggcgta ttgggggggtt tgatttactt
 1260
 tccttttatt tctttatttt ttgcttatac ttgtttttga aaacctctc tgagtttgaa
 1320
 gggacagcta tttttattga ttatctttaa gtctctctac catggagaag agcaggaagg
 1380
 gatacactct ccagtgcatt ttcatgtttt gaatcggatt agt
 1423

<210> 3270

<211> 169

<212> PRT

<213> Homo sapiens

<400> 3270

Met	Ile	Glu	Asn	Glu	Met	Leu	Thr	Met	Glu	Leu	Asn	Gly	Asp	Ser	Met
1			5					10						15	
Glu	Val	Lys	Pro	Ile	Met	Thr	Arg	Lys	Leu	Arg	Arg	Arg	Pro	Asn	Asp
		20						25					30		
Pro	Val	Pro	Ile	Pro	Asp	Lys	Arg	Arg	Lys	Pro	Ala	Pro	Ala	Gln	Leu

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      35              40              45
Asn Tyr Leu Leu Thr Asp Glu Gln Ile Met Glu Asp Leu Arg Thr Leu
      50              55              60
Asn Lys Leu Lys Ser Pro Lys Arg Pro Ala Ser Pro Ser Ser Pro Glu
65              70              75              80
His Leu Pro Ala Thr Pro Ala Glu Ser Pro Ala Gln Arg Phe Glu Ala
      85              90              95
Arg Ile Glu Asp Gly Lys Leu Tyr Tyr Asp Lys Arg Trp Tyr His Lys
      100             105             110
Ser Gln Ala Ile Tyr Leu Glu Ser Lys Asp Asn Gln Lys Leu Ser Cys
      115             120             125
Val Ile Ser Ser Val Gly Ala Asn Glu Ile Trp Val Arg Lys Thr Ser
      130             135             140
Asp Ser Thr Lys Met Arg Ile Tyr Leu Gly Gln Leu Gln Arg Gly Leu
145             150             155             160
Phe Val Ile Arg Arg Arg Ser Ala Ala
      165

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<210> 3271
 <211> 464
 <212> DNA
 <213> Homo sapiens

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<400> 3271
tcatgagcag ggcccaattc tggcttctct gtggctcgcca tccatgtgct gggcgtcact
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gaaggcactg gggatacagc cgagcacaag atggacagag atccctggcc cctcggagca
120
ggcagtctgt ggctctggcc cctccagttc cttgtcacca ggagataggc aatgcagctg
180
atgagaaggg ccccggcagc aagagatcca atgatggtgg ccgccaggat cccagcgttg
240
gtgggcaggt gtgtactggg cagctcctta ttcttttcag ctacctggac ctcagtcttg
300
gccttcatag tccattcaga gttgatggta atggctactt ggtaggtgcc actgtctgta
360
ggctgggcgc ggcgcagcag catggaacca ttggggaagc ccacgatgtc tcgctgtccc
420
atggcactgc catccctctg aggcggttgt atccccaggg atgt
464

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<210> 3272
 <211> 140
 <212> PRT
 <213> Homo sapiens

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<400> 3272
Met Gly Gln Arg Asp Ile Val Gly Phe Pro Asn Gly Ser Met Leu Leu
1      5      10      15
Arg Arg Ala Gln Pro Thr Asp Ser Gly Thr Tyr Gln Val Ala Ile Thr
      20      25      30
Ile Asn Ser Glu Trp Thr Met Lys Ala Lys Thr Glu Val Gln Val Ala
      35      40      45
Glu Lys Asn Lys Glu Leu Pro Ser Thr His Leu Pro Thr Asn Ala Gly

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      50              55              60
Ile Leu Ala Ala Thr Ile Ile Gly Ser Leu Ala Ala Gly Ala Leu Leu
65              70              75              80
Ile Ser Cys Ile Ala Tyr Leu Leu Val Thr Arg Asn Trp Arg Gly Gln
      85              90              95
Ser His Arg Leu Pro Ala Pro Arg Gly Gln Gly Ser Leu Ser Ile Leu
      100              105              110
Cys Ser Ala Val Ser Pro Val Pro Ser Val Thr Pro Ser Thr Trp Met
      115              120              125
Ala Thr Thr Glu Lys Pro Glu Leu Gly Pro Ala His
      130              135              140

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<210> 3273
 <211> 387
 <212> DNA
 <213> Homo sapiens

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<400> 3273
ngcgcgccag ggatggaaaa ctttattctg tatgaggaga tcggaagagg aagcaagact
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120
aagtgcagaa ggcctgaaat aaccaactgg gtccgtctca cccgtgaaat aaaacacaag
180
aatattgtaa cttttcatga atggtatgaa acaagcaacc acctctggct agtggtggaa
240
ctccgcacag gtggttcctt aaaaacagtt attgctcaag atgaaaacct cccagaagat
300
gttggtgagag aatttggaat tgacctgatt agtggattac atcatcttca taaacttggc
360
attctctttg tgacatttct cctagga
387

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<210> 3274
 <211> 129
 <212> PRT
 <213> Homo sapiens

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<400> 3274
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1      5      10      15
Gly Ser Lys Thr Val Val Tyr Lys Gly Arg Arg Lys Gly Thr Ile Asn
      20      25      30
Phe Val Ala Ile Leu Cys Thr Asp Lys Cys Arg Arg Pro Glu Ile Thr
      35      40      45
Asn Trp Val Arg Leu Thr Arg Glu Ile Lys His Lys Asn Ile Val Thr
      50      55      60
Phe His Glu Trp Tyr Glu Thr Ser Asn His Leu Trp Leu Val Val Glu
65      70      75      80
Leu Arg Thr Gly Gly Ser Leu Lys Thr Val Ile Ala Gln Asp Glu Asn
      85      90      95
Leu Pro Glu Asp Val Val Arg Glu Phe Gly Ile Asp Leu Ile Ser Gly
      100      105      110
Leu His His Leu His Lys Leu Gly Ile Leu Phe Val Thr Phe Leu Leu

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115 120 125
 Gly

 <210> 3275
 <211> 1266
 <212> DNA
 <213> Homo sapiens

 <400> 3275
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 120
 ttttctttta tagagacatg aataacagat aactgaagt ataaacaaaa attggcctga
 180
 agcgtccggt ggccggctta gttaggagct atggctaaac atcatcctga tttgatcttt
 240
 tgccgcaagc aggctggtgt tgccatcgga agactgtgtg aaaaatgtga tggcaagtgt
 300
 gtgatttgtg actcctatgt gcgtccctgc actctggtgc gcatatgtga tgagtgtaac
 360
 tatggatctt accaggggag ctgtgtgatc tgtggaggac ctggggtctc tgatgcctat
 420
 tattgtaagg agtgcaccat ccaggagaag gacagagatg gctgccccaa gattgtcaat
 480
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 600
 tgcctactac taccagcaga aaggagcag agcccagagc atcaccagga gtgcctgcta
 660
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 720
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 780
 aatggttttt cttgaattcg agaagcatag atctgttctc catattggta tgttctccct
 840
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 900
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 960
 aacctttggt gtgtggtggg aagctatcag aacaagaaat gtaggcattt cccgtttttt
 1020
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 1080
 cttgtccagc tacagtgggg tacagtagct ggctattcac aggcacatc atagcccact
 1140
 agtctcatat tattttcctt ttgagaaatt ggaaactctt tctgttgcta ttatattaat
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 1260
 aaaaaa
 1266

<210> 3276
 <211> 110
 <212> PRT
 <213> Homo sapiens

<400> 3276
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 20 25 30
 Cys Asp Ser Tyr Val Arg Pro Cys Thr Leu Val Arg Ile Cys Asp Glu
 35 40 45
 Cys Asn Tyr Gly Ser Tyr Gln Gly Arg Cys Val Ile Cys Gly Gly Pro
 50 55 60
 Gly Val Ser Asp Ala Tyr Tyr Cys Lys Glu Cys Thr Ile Gln Glu Lys
 65 70 75 80
 Asp Arg Asp Gly Cys Pro Lys Ile Val Asn Leu Gly Ser Ser Lys Thr
 85 90 95
 Asp Leu Phe Tyr Glu Arg Lys Lys Tyr Gly Phe Lys Lys Arg
 100 105 110

<210> 3277
 <211> 1435
 <212> DNA
 <213> Homo sapiens

<400> 3277
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 120
 cagacttccg tctccttaaa atgttcatgc gtaagtgcgt ggcagaagcg gctcaagcgc
 180
 actcgtgcgt cattgctgtc agggccgagg gagcggtgca aggcgcgcgc gtgacgtcag
 240
 gacgccgcgg tcaggacgtc gaagccaaag aagaccagag ccagccgggt ggcacagcgg
 300
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 420
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 720
 gctactacta tcccatgagc atgtaccaga gctatggctc cccttcccag tatgggatgg
 780

ccggctccta tggctagcca caccacagca gccatccgca ccccaacacc aagggactct
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 1020
 acggggccagg cctatgggccc acacacctac accgaacctg ccaagcccaa gaagggccaa
 1080
 cagctgtgga accgcatgaa acccgcccct gggactggag gttcaagtcc aacatccaga
 1140
 agcgaccctt tgetgttacc acccagagct ttggctccaa cgcagagggc cagcacagtg
 1200
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 1320
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<210> 3278

<211> 104

<212> PRT

<213> Homo sapiens

<400> 3278

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Tyr	Ser	Met	Val	Ala	Gly	Ala	Gly	Arg	Glu	Asn	Gly	Met	Glu	Thr	Pro
			20					25					30		
Met	His	Glu	Asn	Pro	Glu	Trp	Glu	Lys	Ala	Arg	Gln	Ala	Leu	Ala	Ser
		35				40					45				
Ile	Ser	Lys	Ser	Gly	Ala	Ala	Gly	Gly	Ser	Ala	Lys	Ser	Ser	Ser	Asn
	50				55					60					
Gly	Pro	Val	Ala	Ser	Ala	Ser	Thr	Cys	Pro	Arg	Gln	Lys	Pro	Gln	Leu
65				70				75						80	
Cys	Ser	Ser	Ser	Ser	Thr	Thr	Ser	Gly	Thr	Ser	Ser	Thr	Thr	Met	Pro
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Thr	Pro	Thr	Ala	Thr	Thr	Ile	Pro								
							100								

<210> 3279

<211> 1130

<212> DNA

<213> Homo sapiens

<400> 3279

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cctgagccag aaccaggcac catggtggag aagggatcag atagctctc agagaagggt
 180
 ggggtgcctg ggacccccag caccagagc ctaggcagcc ggaacttcac ccgcaacagc
 240
 aagaagatgc agagctggta cagtatgctg agccccactt ataagcagcg taatgaggac
 300
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 360
 gccctgcagc gtgagatcct gctccagggc cgctctacc tctctgagaa ctggatctgc
 420
 ttctacagca acatcttccg ctgggagacc acgatctcca tccagctgaa ggaagtgaca
 480
 tgtctgaaga aggaaaagac ggccaagctg atccccaacg ccatccagat ctgcacggag
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 900
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 960
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 1020
 cccttggatc tgctgcccag tgaggagcta ttgacagaca caagtaactc ctcttcaccc
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 1130

<210> 3280

<211> 376

<212> PRT

<213> Homo sapiens

<400> 3280

Xaa	Arg	Ala	His	Arg	Ala	Ala	Ser	Met	Phe	Asp	Thr	Thr	Pro	His	Ser
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Gly	Arg	Ser	Thr	Pro	Ser	Ser	Ser	Pro	Ser	Leu	Arg	Lys	Arg	Leu	Gln
			20					25					30		
Leu	Leu	Pro	Pro	Ser	Arg	Pro	Pro	Pro	Glu	Pro	Glu	Pro	Gly	Thr	Met
			35				40					45			
Val	Glu	Lys	Gly	Ser	Asp	Ser	Ser	Ser	Glu	Lys	Gly	Gly	Val	Pro	Gly
			50			55					60				
Thr	Pro	Ser	Thr	Gln	Ser	Leu	Gly	Ser	Arg	Asn	Phe	Ile	Arg	Asn	Ser
65					70				75					80	
Lys	Lys	Met	Gln	Ser	Trp	Tyr	Ser	Met	Leu	Ser	Pro	Thr	Tyr	Lys	Gln
			85					90						95	
Arg	Asn	Glu	Asp	Phe	Arg	Lys	Leu	Phe	Ser	Lys	Leu	Pro	Glu	Ala	Glu

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      100      105      110
Arg Leu Ile Val Asp Tyr Ser Cys Ala Leu Gln Arg Glu Ile Leu Leu
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Gln Gly Arg Leu Tyr Leu Ser Glu Asn Trp Ile Cys Phe Tyr Ser Asn
      130      135      140
Ile Phe Arg Trp Glu Thr Thr Ile Ser Ile Gln Leu Lys Glu Val Thr
      145      150      155      160
Cys Leu Lys Lys Glu Lys Thr Ala Lys Leu Ile Pro Asn Ala Ile Gln
      165      170      175
Ile Cys Thr Glu Ser Glu Lys His Phe Phe Thr Ser Phe Gly Ala Arg
      180      185      190
Asp Arg Cys Phe Leu Leu Ile Phe Arg Leu Trp Gln Asn Ala Leu Leu
      195      200      205
Glu Lys Thr Leu Ser Pro Arg Glu Leu Trp His Leu Val His Gln Cys
      210      215      220
Tyr Gly Ser Glu Leu Gly Leu Thr Ser Glu Asp Glu Asp Tyr Val Ser
      225      230      235      240
Pro Leu Gln Leu Asn Gly Leu Gly Thr Pro Lys Glu Val Gly Asp Val
      245      250      255
Ile Ala Leu Ser Asp Ile Thr Ser Ser Gly Ala Ala Asp Arg Ser Gln
      260      265      270
Glu Pro Ser Pro Val Gly Ser Arg Arg Gly His Val Thr Pro Asn Leu
      275      280      285
Ser Arg Ala Ser Ser Asp Ala Asp His Gly Ala Glu Glu Asp Lys Glu
      290      295      300
Glu Gln Val Asp Ser Gln Pro Asp Ala Ser Ser Ser Gln Thr Val Thr
      305      310      315      320
Pro Val Ala Glu Pro Pro Ser Thr Glu Pro Thr Gln Pro Asp Gly Pro
      325      330      335
Thr Thr Leu Gly Pro Leu Asp Leu Leu Pro Ser Glu Glu Leu Leu Thr
      340      345      350
Asp Thr Ser Asn Ser Ser Ser Thr Gly Glu Glu Ala Asp Leu Ala
      355      360      365
Ala Leu Leu Pro Asp Leu Ser Gly
      370      375

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<210> 3281

<211> 842

<212> DNA

<213> Homo sapiens

<400> 3281

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120
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180
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300
ctgggttcaca aagtgtgttg tttccaggaa gaacagatgg gggcgctga gggcaaaggg
360

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cctgagtgtg ggtcgaggat atgccggctg ctcgctcagg ggctgggttt tcattttgtg
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 840
 tc
 842

<210> 3282
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 3282
 Met Pro Thr Asn Pro Gly Leu His Leu Ala Leu Ala Pro Val Ser Val
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 Pro Asp Thr Ser Leu Gln Val Leu Leu Val Ala Gly Pro Thr Lys Ala
 20 25 30
 Pro Trp Pro Arg Gln Pro Gly Gly Cys Trp Thr Val Gly Leu Pro Ala
 35 40 45
 Thr Ser Phe Ala Arg Gly Lys Glu His His Val Gly His Ile His Glu
 50 55 60
 Gly Thr Gly Asn Ser Val Val Pro Ser Val Thr Pro Cys Gln Asp Thr
 65 70 75 80
 Gln Asp Glu Asn Pro Ala Pro Glu Arg Ala Ala Gly Ile Ser Ser Thr
 85 90 95
 His Thr Gln Ala Leu Cys Pro Gln Ala Pro Pro Ser Val Leu Pro Gly
 100 105 110
 Asn Asn Thr Leu Cys Glu Pro Val Val Glu Pro Gly Thr Ala Trp Ala
 115 120 125
 Ser Glu Gln Ser His Glu Ile Arg Val Arg Thr Pro Ser Cys Arg Gly
 130 135 140
 Arg Asp
 145

<210> 3283
 <211> 3268
 <212> DNA
 <213> Homo sapiens

<400> 3283
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gcggagaacc taccgccagt cctcatggag cacaaggcca ccaccatcca gaagcacgtg
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<210> 3284
 <211> 1012
 <212> PRT
 <213> Homo sapiens

<400> 3284
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 35 40 45
 Met Glu His Lys Ala Thr Thr Ile Gln Lys His Val Arg Gly Trp Met
 50 55 60
 Ala Arg Arg His Phe Gln Arg Leu Arg Asp Ala Ala Ile Val Ile Gln
 65 70 75 80
 Cys Ala Phe Arg Met Leu Lys Ala Arg Arg Glu Leu Lys Ala Leu Arg
 85 90 95
 Ile Glu Ala Arg Ser Ala Glu His Leu Lys Arg Leu Asn Val Gly Met
 100 105 110
 Glu Asn Lys Val Val Gln Leu Gln Arg Lys Ile Asp Glu Gln Asn Lys
 115 120 125
 Glu Phe Lys Thr Leu Ser Glu Gln Leu Ser Val Thr Thr Ser Thr Tyr
 130 135 140
 Thr Met Glu Val Glu Arg Leu Lys Lys Glu Leu Val His Tyr Gln Gln
 145 150 155 160
 Ser Pro Gly Glu Asp Thr Ser Leu Arg Leu Gln Glu Glu Val Glu Ser
 165 170 175
 Leu Arg Thr Glu Leu Gln Arg Ala His Ser Glu Arg Lys Ile Leu Glu
 180 185 190
 Asp Ala His Ser Arg Glu Lys Asp Glu Leu Arg Lys Arg Val Ala Asp
 195 200 205
 Leu Glu Gln Glu Asn Ala Leu Leu Lys Asp Glu Lys Glu Gln Leu Asn
 210 215 220
 Asn Gln Ile Leu Cys Gln Ser Lys Asp Glu Phe Ala Gln Asn Ser Val
 225 230 235 240
 Lys Glu Asn Leu Leu Met Lys Lys Glu Leu Glu Glu Glu Arg Ser Arg
 245 250 255
 Tyr Gln Asn Leu Val Lys Glu Tyr Ser Gln Leu Glu Gln Arg Tyr Asp
 260 265 270
 Asn Leu Arg Asp Glu Met Thr Ile Ile Lys Gln Thr Pro Gly His Arg
 275 280 285
 Arg Asn Pro Ser Asn Gln Ser Ser Leu Glu Ser Asp Ser Asn Tyr Pro
 290 295 300
 Ser Ile Ser Thr Ser Glu Ile Gly Asp Thr Glu Asp Ala Leu Gln Gln
 305 310 315 320
 Val Glu Glu Ile Gly Leu Glu Lys Ala Ala Met Asp Met Thr Val Phe
 325 330 335
 Leu Lys Leu Gln Lys Arg Val Arg Glu Leu Glu Gln Glu Arg Lys Lys
 340 345 350
 Leu Gln Val Gln Leu Glu Lys Arg Glu Gln Gln Asp Ser Lys Lys Val
 355 360 365
 Gln Ala Glu Pro Pro Gln Thr Asp Ile Asp Leu Asp Pro Asn Ala Asp

370	375	380
Leu Ala Tyr Asn Ser	Leu Lys Arg Gln Glu	Leu Glu Ser Glu Asn Lys
385	390	395
Lys Leu Lys Asn Asp	Leu Asn Glu Leu Arg	Lys Ala Val Ala Asp Gln
405	410	415
Ala Thr Gln Asn Asn Ser Ser His Gly Ser Pro Asp Ser Tyr Ser Leu		
420	425	430
Leu Leu Asn Gln Leu Lys Leu Ala His Glu Glu Leu Glu Val Arg Lys		
435	440	445
Glu Glu Val Leu Ile Leu Arg Thr Gln Ile Val Ser Ala Asp Gln Arg		
450	455	460
Arg Leu Ala Gly Arg Asn Ala Glu Pro Asn Ile Asn Ala Arg Ser Ser		
465	470	475
Trp Pro Asn Ser Glu Arg His Val Asp Gln Glu Asp Ala Ile Glu Ala		
485	490	495
Tyr His Gly Val Cys Gln Thr Asn Arg Leu Leu Glu Ala Gln Leu Gln		
500	505	510
Ala Gln Ser Leu Glu His Glu Glu Glu Val Glu His Leu Lys Ala Gln		
515	520	525
Leu Glu Ala Leu Lys Glu Glu Met Asp Lys Gln Gln Gln Thr Phe Cys		
530	535	540
Gln Thr Leu Leu Leu Ser Pro Glu Ala Gln Val Glu Phe Gly Val Gln		
545	550	555
Gln Glu Ile Ser Arg Leu Thr Asn Glu Asn Leu Asp Leu Lys Glu Leu		
565	570	575
Val Glu Lys Leu Glu Lys Asn Glu Arg Lys Leu Lys Lys Gln Leu Lys		
580	585	590
Ile Tyr Met Lys Lys Ala Gln Asp Leu Glu Ala Ala Gln Ala Leu Ala		
595	600	605
Gln Ser Glu Arg Lys Arg His Glu Leu Asn Arg Gln Val Thr Val Gln		
610	615	620
Arg Lys Glu Lys Asp Phe Gln Gly Met Leu Glu Tyr His Lys Glu Asp		
625	630	635
Glu Ala Leu Leu Ile Arg Asn Leu Val Thr Asp Leu Lys Pro Gln Met		
645	650	655
Leu Ser Gly Thr Val Pro Cys Leu Pro Ala Tyr Ile Leu Tyr Met Cys		
660	665	670
Ile Arg His Ala Asp Tyr Thr Asn Asp Asp Leu Lys Val His Ser Leu		
675	680	685
Leu Thr Ser Thr Ile Asn Gly Ile Lys Lys Val Leu Lys Lys His Asn		
690	695	700
Asp Asp Phe Glu Met Thr Ser Phe Trp Leu Ser Asn Thr Cys Arg Leu		
705	710	715
Leu His Cys Leu Lys Gln Tyr Ser Gly Asp Glu Gly Phe Met Thr Gln		
725	730	735
Asn Thr Ala Lys Gln Asn Glu His Cys Leu Lys Asn Phe Asp Leu Thr		
740	745	750
Glu Tyr Arg Gln Val Leu Ser Asp Leu Ser Ile Gln Ile Tyr Gln Gln		
755	760	765
Leu Ile Lys Ile Ala Glu Gly Val Leu Gln Pro Met Ile Val Ser Ala		
770	775	780
Met Leu Glu Asn Glu Ser Ile Gln Gly Leu Ser Gly Val Lys Pro Thr		
785	790	795
Gly Tyr Arg Lys Arg Ser Ser Ser Met Ala Asp Gly Asp Asn Ser Tyr		

805 810 815
 Cys Leu Glu Ala Ile Ile Arg Gln Met Asn Ala Phe His Thr Val Met
 820 825 830
 Cys Asp Gln Gly Leu Asp Pro Glu Ile Ile Leu Gln Val Phe Lys Gln
 835 840 845
 Leu Phe Tyr Met Ile Asn Ala Val Thr Leu Asn Asn Leu Leu Leu Arg
 850 855 860
 Lys Asp Val Cys Ser Trp Ser Thr Gly Met Gln Leu Arg Tyr Asn Ile
 865 870 875 880
 Ser Gln Leu Glu Glu Trp Leu Arg Gly Arg Asn Leu His Gln Ser Gly
 885 890 895
 Ala Val Gln Thr Met Glu Pro Leu Ile Gln Ala Ala Gln Leu Leu Gln
 900 905 910
 Leu Lys Lys Lys Thr Gln Glu Asp Ala Glu Ala Ile Cys Ser Leu Cys
 915 920 925
 Thr Ser Leu Ser Thr Gln Gln Ile Val Lys Ile Leu Asn Leu Tyr Thr
 930 935 940
 Pro Leu Asn Glu Phe Glu Glu Arg Val Thr Val Ala Phe Ile Arg Thr
 945 950 955 960
 Ile Gln Ala Gln Leu Gln Glu Arg Asn Asp Pro Gln Gln Leu Leu Leu
 965 970 975
 Asp Ala Lys His Met Phe Pro Val Leu Phe Pro Phe Asn Pro Ser Ser
 980 985 990
 Leu Thr Met Asp Ser Ile His Ile Pro Ala Cys Leu Asn Leu Glu Phe
 995 1000 1005
 Leu Asn Glu Val
 1010

<210> 3285

<211> 1518

<212> DNA

<213> Homo sapiens

<400> 3285

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 aacctgatga caccaccact ttattttgag ctaaactctc atttaagtga gaacaggaca
 120
 ggtttcacca ctgcctcctt tggcaacttg agtggtggtg ttcccaccga gtttatggct
 180
 gcaaagatag gtcttttctc gtatttatgt ataaacaggt accagttttg attttattta
 240
 atcatttcat acattaacat acatgacaca tcaaaatgag aaatgcacag ttttaaccgtt
 300
 caacagctgg ccttacttca aaagaacact atattcatat taaacattta cagtcttttc
 360
 atctaacttt acacatgtcc taaatcattt tccagcactt ctcacataga agtctagttt
 420
 tgctctttta aatcaccatc tgtatcaccc ctagtagacg cgagggtttc cccaattaca
 480
 tgctgaagag agccagccac caccacacct aaagacatcc aagcagctcc agagcctgcc
 540
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 600

tgaaccagca ctaaaggctg taggatgtga ctacatcaca gttccagaag gaaggggacc
 660
 atggccaaga gaagccctaa atgacagaag ctcattaaaa ccaagtcccc caaacctcct
 720
 gaaacatcgt tagcaaggag ctactgcttt cctttcttaa acatgttttg ggcattgacca
 780
 cactctggaa gtggtgaact gttacacatt tgggtgtgtgt gtacataaca tcaaaaacta
 840
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 900
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 960
 ctttacaccc catcatagca cattatttgt gcacaactag tgagggtctgt gcgggtcatc
 1020
 atccccataa ccaagtcggt ctgtgttgag tcatatcatt ctgtgctggt tttagaagtc
 1080
 accataggaa acatgaagtc acatcctggt caaaaaactg tccattttctc aaaaacagag
 1140
 aaaaacctga gatacgaggc agcaactagc gacacttaca ggaagggaaa gaacaatgac
 1200
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 1260
 acccaactg tagctgataa aactcaagcc aggaggatgt ttgaaagcca atctgacta
 1320
 tcaattgttc cagtgcctc ctatgttcag ctgccaggac cgattccata cagtgttgt
 1380
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 1500
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 1518

<210> 3286

<211> 142

<212> PRT

<213> Homo sapiens

<400> 3286

Met	Lys	Ser	His	Pro	Gly	Gln	Lys	Thr	Val	His	Phe	Ser	Lys	Thr	Glu
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Lys	Asn	Leu	Arg	Tyr	Glu	Ala	Ala	Thr	Ser	Asp	Thr	Tyr	Arg	Lys	Gly
			20					25					30		
Lys	Asn	Asn	Asp	Asn	Thr	Arg	Pro	Ala	Pro	Pro	Pro	Lys	Ser	Cys	Cys
		35				40						45			
Cys	Glu	Leu	Arg	Leu	Gln	Lys	Arg	Thr	His	Thr	Val	Ala	Asp	Lys	Thr
	50					55					60				
Gln	Ala	Arg	Arg	Met	Phe	Glu	Ser	Gln	Ser	Ala	Leu	Ser	Leu	Val	Pro
65					70					75				80	
Val	Thr	Ser	Tyr	Val	Gln	Leu	Pro	Gly	Pro	Ile	Pro	Tyr	Ser	Asp	Cys
				85				90					95		
Arg	Leu	Arg	Thr	Glu	Asp	Ala	Pro	Leu	Leu	Ser	Leu	His	Phe	Asp	Leu
			100					105					110		
Leu	Phe	Pro	Leu	Lys	Thr	Arg	Arg	Pro	Ala	Phe	Pro	Lys	Thr	Ala	Trp

115 120 125
 Pro Trp Leu Cys Thr Leu Phe Thr Thr Asp Gln Asn Ser Ile
 130 135 140

<210> 3287

<211> 921

<212> DNA

<213> Homo sapiens

<400> 3287

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 120
 gcgtaagccc aatccgggaa actcgttgcc cctctcctgg gaaaggaacg tccctcccca
 180
 ggggttgcgag tgactcgggc accatcaccc tgtgctgtaa agacctgcga gtgctgcagc
 240
 tggaaataga gggcgcggaa gcgacgctgg gcatcgcccc ctccatcgag gtgtgccgag
 300
 ggagctcccc agccctttaa gctctccctg tctcgcgtag aggggaataa aaaggtgctt
 360
 ctgttcaaag aggctccgca gccgcagcta aatggcaggg ggatgcaggg tggtcggggg
 420
 tactttgaga ggccgaagct gaagctacag gactgagggg ctggaaaggg cgcgggcgag
 480
 acaattccga cctcctccag agccccctgac ttccttctcc ggacgctgtc ctccctggaa
 540
 tcagtcacca cctccttccc tttattctac cgtcccaagg gcctgagatt gggcgactcc
 600
 tggcacttcc tcccgccgga actctactgc aagagagtag ctcgcaagt gggcgcggtc
 660
 gtaggggccc ggggaaggtg aagcgccggg cctggaagag gcgcggggac agggcactcc
 720
 ctgggtgccc tagacctggc ctctctcttc cctgcgctgc agaccaacgc ggccggaaaa
 780
 aggctggagg gggcttggca gccaaagctaa ttcgggcgaa tttctatgat tatgattttt
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 900
 aatctattct gagaactctt c
 921

<210> 3288

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3288

Met Thr Asp Ser Arg Glu Asp Ser Val Arg Arg Arg Lys Ser Gly Ala
 1 5 10 15
 Leu Gly Arg Val Gly Ile Val Ser Pro Ala Pro Phe Pro Ala Pro Gln
 20 25 30
 Ser Cys Ser Phe Ser Phe Gly Leu Ser Lys Tyr Pro Gly Pro Pro Cys


```

          35          40          45
Ile Pro Leu Pro Phe Ser Cys Gly Cys Gly Ala Ser Leu Asn Arg Ser
   50          55          60
Thr Phe Leu Phe Pro Ser Thr Arg Asp Arg Glu Ser Leu Lys Gly Ser
   65          70          75          80
Gly Ala Pro Ser Ala His Leu Asp Gly Ala Gly Asp Ala Gln Arg Arg
          85          90          95
Phe Arg Ala Leu Tyr Phe Gln Leu Gln His Ser Gln Val Phe Thr Ala
          100          105          110
Gln Gly Asp Gly Ala Arg Val Thr Arg Asn Pro Gly Glu Gly Arg Ser
          115          120          125
Phe Pro Arg Arg Gly Ala Thr Ser Phe Pro Asp Trp Ala Tyr Ala Gly
          130          135          140
Gly Arg Gln Leu
145

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<210> 3289

<211> 554

<212> DNA

<213> Homo sapiens

<400> 3289

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acgcgtagtg atctgtgcga ggtcacacag caaatctgtg ggaggctagg gttcaaacct
60
cacagcatgg actcttccct gtgtcccggt cctgccttcg ctcctccca gctcttctct
120
cccagcctcc tagcccaata tcagggcccg aggcactgga gaacttccgg ctaaggcagg
180
ctctccctcc cattcacaga gccctgccag ggtggctggc aatgggtgaag tccagggcag
240
agatggggac agaggggacg ccttggattc gactctgtgg tgggtggacc acctccctga
300
gaccagcat ccacgtcggg cagcacatgc taccagtc acagaagagg aaacagaggc
360
tccgagagga agggactgtg tccagggcgg gaccaggcc cttctgcact gggtaatga
420
gccaaagcaca tcacccagc ccttggggag caggagccgg gccttcagg gtagggagct
480
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540
ataagctgca attg
554

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<210> 3290

<211> 129

<212> PRT

<213> Homo sapiens

<400> 3290

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Met Ile Pro Gly Cys Leu Pro Trp Ser Phe Ala Phe Pro Ser Ser Ser
   1           5           10           15
Pro Cys Lys Ala Arg Leu Leu Leu Pro Lys Gly Trp Gly Asp Val Leu
          20          25          30
Gly Ser Leu Thr Gln Cys Arg Arg Ala Trp Val Pro Pro Trp Thr Gln

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<400> 3291
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120
tgggccctt ctcccgccac gctgcggtg aggtccccc ccccgctctc taccatagct
180
gcctctgtcc ctccgactg gctgttcacc tggctagctg tgtccgttcc tcaaccggga
240
agcgagtctn ggcgtcgacc gctgccgcc cccagttac cccctccac cccgccgtcc
300
cttccctagc ctacatagcc cttggccatg gcccggcctg gtcccacctc tgatgtcccg
360
ccccccacag gtggacagac gccttcgnnt gggcctgagc acttgcgccc ggcacatgtc
420
cgctcaccgc gtgtccgggg ccctggcgcg ggtcctggaa gtaccctagc gggccacacc
480
ctgacagccg agctgatggc gcaccccgcc taccctagtg tgccctccacc ggcggctgcg
540
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600
ccgcgcccac gctgcgggcc cagcttgccc aggatggcgt gcagctttgc gccctcgacg
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720
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780
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960
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1020

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1075

<210> 3292

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3292

Xaa	Xaa	Met	Gly	Cys	Ala	Leu	Arg	Asp	Cys	Arg	Trp	Ser	Ala	Val	Trp
1			5					10					15		
Val	Ala	Ala	Leu	Gly	Trp	Arg	Pro	Pro	Arg	Val	Pro	Ser	Pro	Ala	Pro
		20					25					30			
Trp	Ser	Ala	Thr	Pro	Gly	Pro	Pro	Trp	Ala	Pro	Ser	Pro	Ala	Thr	Pro
	35					40					45				
Ala	Val	Arg	Leu	Pro	Ala	Pro	Ser	Pro	Thr	Ile	Ala	Ala	Ser	Val	Pro
	50				55				60						
Pro	His	Trp	Leu	Phe	Thr	Trp	Leu	Ala	Val	Ser	Val	Ser	Gln	Pro	Gly
65				70					75				80		
Ser	Glu	Ser	Xaa	Arg	Arg	Pro	Leu	Pro	Pro	Pro	Gln	Leu	Pro	Pro	Pro
			85					90					95		
Thr	Pro	Pro	Ser	Leu	Pro										

<210> 3293

<211> 2362

<212> DNA

<213> Homo sapiens

<400> 3293

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120
gcaggacgcc gacacctacc cctcagcaga cgccggagag aaatgagtag caacaaagag
180
cagcgggtcag cagtgttcgt gatcctcttt gccctcatca ccattctcat cctctacagc
240
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540
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600
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660
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720

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780
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1740
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1800
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1920
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1980
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2160
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2340

aaaaaaaaaa aaaaaaaaaa aa
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<210> 3294

<211> 353

<212> PRT

<213> Homo sapiens

<400> 3294

Xaa Ser Pro Lys Pro Ala Leu Pro Ala Gly Asp Glu Glu Thr Glu Ala
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20 25 30
Thr Ser Leu Pro Pro Gly Pro Pro Ala Gly Arg Arg His Leu Pro Leu
35 40 45
Ser Arg Arg Arg Arg Glu Met Ser Ser Asn Lys Glu Gln Arg Ser Ala
50 55 60
Val Phe Val Ile Leu Phe Ala Leu Ile Thr Ile Leu Ile Leu Tyr Ser
65 70 75 80
Ser Asn Ser Ala Asn Glu Val Phe His Tyr Gly Ser Leu Arg Gly Arg
85 90 95
Ser Arg Arg Pro Val Asn Leu Lys Lys Trp Ser Ile Thr Asp Gly Tyr
100 105 110
Val Pro Ile Leu Gly Asn Lys Thr Leu Pro Ser Arg Cys His Gln Cys
115 120 125
Val Ile Val Ser Ser Ser Ser His Leu Leu Gly Thr Lys Leu Gly Pro
130 135 140
Glu Ile Glu Arg Ala Glu Cys Thr Ile Arg Met Asn Asp Ala Pro Thr
145 150 155 160
Thr Gly Tyr Ser Ala Asp Val Gly Asn Lys Thr Thr Tyr Arg Val Val
165 170 175
Ala His Ser Ser Val Phe Arg Val Leu Arg Arg Pro Gln Glu Phe Val
180 185 190
Asn Arg Thr Pro Glu Thr Val Phe Ile Phe Trp Gly Pro Pro Ser Lys
195 200 205
Met Gln Lys Pro Gln Gly Ser Leu Val Arg Val Ile Gln Arg Ala Gly
210 215 220
Leu Val Phe Pro Asn Met Glu Ala Tyr Ala Val Ser Pro Gly Arg Met
225 230 235 240
Arg Gln Phe Asp Asp Leu Phe Arg Gly Glu Thr Gly Lys Asp Arg Glu
245 250 255
Lys Ser His Ser Trp Leu Ser Thr Gly Trp Phe Thr Met Val Ile Ala
260 265 270
Val Glu Leu Cys Asp His Val His Val Tyr Gly Met Val Pro Pro Asn
275 280 285
Tyr Cys Ser Gln Arg Pro Arg Leu Gln Arg Met Pro Tyr His Tyr Tyr
290 295 300
Glu Pro Lys Gly Pro Asp Glu Cys Val Thr Tyr Ile Gln Asn Glu His
305 310 315 320
Ser Arg Lys Gly Asn His His Arg Phe Ile Thr Glu Lys Arg Val Phe
325 330 335
Ser Ser Trp Ala Gln Leu Tyr Gly Ile Thr Phe Ser His Pro Ser Trp
340 345 350
Thr

<210> 3295

<211> 690

<212> DNA

<213> Homo sapiens

<400> 3295

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120
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180
gctgggggat gggctctgca ctgcagagac cagcaggac taaagaagag aggacatggg
240
gaactggaaa aataagcctt ccaggattgt ggggagaaa acgctgtggg agaggccagg
300
atgctgcatt aggcacagga taacctggga acccaggcac atgggtctctg ctctccgaag
360
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420
tagtggcttt acagtgggta cctgtcaga aaccagcact gggggccctg ccacccccac
480
atggaaggag tgtcctatct gtaaggagcg ctttctgtct gagagtgaca aggatgcctt
540
ggaggaccac atggatggac acttcttttt cagcaccag ggaccccttc acctttgagt
600
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<210> 3296

<211> 120

<212> PRT

<213> Homo sapiens

<400> 3296

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Met Gly Asn Trp Lys Asn Lys Pro Ser Arg Ile Val Gly Arg Lys Thr
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Leu Trp Glu Arg Pro Gly Cys Cys Ile Arg His Arg Ile Thr Trp Glu
20     25     30
Pro Arg His Met Gly Pro Ala Leu Arg Ser Leu Gln Val Lys Lys Gly
35     40     45
Thr Glu His Ala Asp Pro Leu Pro Phe Pro Ser Val Ser Leu Ser Gly
50     55     60
Phe Thr Val Gly Thr Leu Ser Glu Thr Ser Thr Gly Gly Pro Ala Thr
65     70     75     80
Pro Thr Trp Lys Glu Cys Pro Ile Cys Lys Glu Arg Phe Pro Ala Glu
85     90     95
Ser Asp Lys Asp Ala Leu Glu Asp His Met Asp Gly His Phe Phe Phe
100    105    110
Ser Thr Gln Gly Pro Leu His Leu

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115

120

<210> 3297

<211> 3176

<212> DNA

<213> Homo sapiens

<400> 3297

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120
ctgcctcagc ctcccaagta gctgggatta taggtgcccc ccaccctgcc tggctaattt
180
ttgtattttt agtaaagatg gggttttgta acattggcca ggctggcttc aaactcctga
240
cctcaactga actgccccca tcgggcttcc aaagtgttgg gattagaggt ctgagctact
300
gggccccggc aaacttggaa acattttttt ccttcctagt gcctcagttt tctcaaatgt
360
aaaatgggaa taaaatatct accttctaag acttttctga gggctctaata actgttatat
420
acattatctc atttaatctt cacaacaacc tttaaaatag ggatacgatc atttctcaatt
480
tacagttgag tgaaagtgag gcagttcaga tggcttgact aaggttacct ggcatttgag
540
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<211> 251

<212> PRT

<213> Homo sapiens

<400> 3298

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<212> DNA

<213> Homo sapiens

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<211> 219

<212> PRT

<213> Homo sapiens

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Ser Ile Gln Gln Phe Thr Glu Met Asn Leu Leu Ser Asp Tyr Arg Phe
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Leu Glu Asp Val Ala Arg Thr Ala Asp His Ile Ser Arg Asp Ala Phe
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Leu Lys Arg Pro Ile Ser Asn Lys Tyr Met Tyr Phe Met Lys Asn Arg
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Ala Arg Ser Lys Gly Ile Asn Leu Lys Leu Leu Pro Asn Gly Phe Thr
      100          105          110
Lys Arg Lys Glu Asn Ser Thr Phe Phe Asp Lys Lys Lys Gln Gln Phe
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Cys Trp His Val Lys Leu Gln Phe Pro Gln Ser Gln Ala Glu Tyr Ile
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Tyr Ile Asp Pro Glu Lys Ser Asp Pro Val Ile Arg Gln Arg Leu Lys
      165          170          175
Ala Tyr Ile Arg Ser Gln Thr Gly Val Gln Ile Leu Met Lys Ile Glu
      180          185          190
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<211> 2109

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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      35           40           45
Arg Asp Gly Glu Gly Pro Val Arg Glu Ala Thr Val Lys Pro Phe Ala
      50           55           60
Ile Asp Ile Phe Pro Val Thr Asn Lys Asp Phe Arg Asp Phe Val Arg
      65           70           75           80
Glu Lys Lys Tyr Arg Thr Glu Ala Glu Met Phe Gly Trp Ser Phe Val
      85           90           95
Phe Glu Asp Phe Val Ser Asp Glu Leu Arg Asn Lys Ala Thr Gln Pro
      100          105          110
Met Lys Val Lys Phe Thr His Gly Gly Thr Gly Ser Ser Gln Thr Ala
      115          120          125
Pro Thr Cys Gly Arg Glu Ser Ser Pro Arg Glu Thr Lys Leu Arg Met
      130          135          140
Ala Ser Met Glu Ser Pro Xaa Val Asn Ala Phe Pro Ala Gln Asn Asn
      145          150          155          160
Tyr Gly Leu Tyr Asp Leu Leu Gly Asn Val Trp Glu Trp Thr Ala Ser
      165          170          175
Pro Tyr Gln Ala Ala Glu Gln Asp Met Arg Val Leu Arg Gly His Pro
      180          185          190
Gly Ser Thr Gln Leu Met Ala Leu Pro Ile Thr Gly Pro Gly Ser Pro
      195          200          205
Pro Gly Trp Ala Thr Leu Gln Ile Gln Pro Gln Thr Thr Ser Val Ser
      210          215          220
Ala Val Leu Gln Thr Gln Ala Gly Arg Gln Gly Ser Cys Lys Gln Pro
      225          230          235          240
Gly Gly Asp Lys Glu Lys Ser Leu Leu Gly Ser Leu Ser Phe Pro Gly
      245          250          255
His Val Ala Asn Ser Ala Ile Pro Ser Ser Arg Ala Ser Ala Ser Gly
      260          265          270
Lys Asn Phe Pro Phe Pro Val Ser His Pro Ser Val Ala Gly Ala Ser
      275          280          285
His Gln Gly Arg Arg Gly Leu Ser Leu Leu Cys Phe Gly Glu Gly Ala
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<211> 699

<212> DNA

<213> Homo sapiens

<400> 3303

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2160
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2340
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2400
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2460
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2520
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2580
atggatttat ttggtgccct catacagaat gctgtagaaa atgtaaagaa gagaaagctc
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2700
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2717

<210> 3306

<211> 319
 <212> PRT
 <213> Homo sapiens

<400> 3306
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 20 25 30
 Ile Ser Leu Val Met Lys Thr Pro Arg Val Ala Lys Asn Glu Ala Leu
 35 40 45
 Trp His Pro Thr Leu Asn Leu Pro Leu Ser Pro Gln Gly Thr Val Arg
 50 55 60
 Thr Ala Val Glu Phe Gln Val Met Thr Gln Thr Gln Ser Leu Ser Phe
 65 70 75 80
 Leu Leu Gly Ser Ser Ala Ser Leu Asp Cys Gly Phe Ser Met Ala Pro
 85 90 95
 Gly Leu Asp Leu Ile Ser Val Glu Trp Arg Leu Gln His Lys Gly Arg
 100 105 110
 Gly Gln Leu Val Tyr Ser Trp Thr Ala Gly Gln Gly Gln Ala Val Arg
 115 120 125
 Lys Gly Ala Thr Leu Xaa Ala Cys Thr Thr Gly His Gly Xaa Arg Asp
 130 135 140
 Ala Ser Leu Thr Leu Pro Gly Leu Thr Ile Gln Asp Glu Gly Thr Tyr
 145 150 155 160
 Ile Cys Gln Ile Thr Thr Ser Leu Tyr Arg Ala Gln Gln Ile Ile Gln
 165 170 175
 Leu Asn Ile Gln Ala Ser Pro Lys Val Arg Leu Ser Leu Ala Asn Glu
 180 185 190
 Ala Leu Leu Pro Thr Leu Ile Cys Asp Ile Ala Gly Tyr Tyr Pro Leu
 195 200 205
 Asp Val Val Val Thr Trp Thr Arg Glu Glu Leu Gly Gly Ser Pro Ala
 210 215 220
 Gln Val Ser Gly Ala Ser Phe Ser Ser Leu Arg Gln Ser Val Ala Gly
 225 230 235 240
 Thr Tyr Ser Ile Ser Ser Ser Leu Thr Ala Glu Pro Gly Leu Cys Arg
 245 250 255
 Cys His Leu His Leu Pro Gly His Thr His Leu Ser Gly Gly Ala Pro
 260 265 270
 Trp Gly Gln His Pro Gly Cys Pro Thr Arg Ala Glu Asn Ser Leu Gly
 275 280 285
 Ser His Leu Cys Gln Gln Ser Leu Pro Ser Cys Thr Asp Val Pro Gly
 290 295 300
 Ala Ser Glu Thr Ala Ser Thr Tyr Arg Thr Trp Ala Ala Ser Gly
 305 310 315

<210> 3307
 <211> 352
 <212> DNA
 <213> Homo sapiens

<400> 3307
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 120
 gaggtgggag cctgccttg gccagggtag cgtgttgac ggttcttggg actgtgacat
 180
 tggaaggcga ggcaggtcac cagcactgtc ctctgcagga tgggctggga ttcatttggc
 240
 agcttctcag ggcctgtgtc cggctggttg gtccctgtgc tgcccaaacc aggtgtccac
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 352

<210> 3308

<211> 110

<212> PRT

<213> Homo sapiens

<400> 3308

Met	Gly	Leu	Pro	Arg	Ala	Leu	Ala	Leu	Pro	Ser	Gly	Gly	Arg	Ser	Gly
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Ser	Leu	His	Pro	Asp	Pro	Gly	Ala	Ser	Leu	Pro	Cys	Pro	Val	Leu	Ile
			20					25					30		
Pro	Arg	Trp	Glu	Pro	Cys	Leu	Gly	Gln	Gly	Gly	Arg	Val	Asp	Gly	Ser
			35					40					45		
Trp	Asp	Cys	Asp	Ile	Gly	Arg	Arg	Gly	Arg	Ser	Pro	Ala	Leu	Ser	Ser
	50					55					60				
Ala	Gly	Trp	Ala	Gly	Ile	His	Leu	Ala	Ala	Ser	Gln	Gly	Leu	Cys	Pro
65					70					75				80	
Ala	Gly	Trp	Ser	Leu	Cys	Cys	Pro	Asn	Gln	Val	Ser	Thr	Phe	Pro	Ala
				85					90					95	
Pro	Met	Arg	Arg	Glu	Gly	Gly	Arg	Trp	Trp	Leu	Gly	Trp	Arg		
				100				105					110		

<210> 3309

<211> 737

<212> DNA

<213> Homo sapiens

<400> 3309

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 120
 cccagggacc ccaagtacca gggctctcgg gcacgtggcc gggagatccg gaaggagctt
 180
 gttcacctgt accccaggga ggcccagctt gaggagcagt tctacctgca ggcgctgaag
 240
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 300
 cacatggctg gagacaagcc agttttctcc ttccaacctc ggggccacct ggaaattggc
 360
 gagaaactcg acatcatccg tcagaagcgc ctgtcccacg tgtctggcca ccggtcctat
 420
 tacctgcgcg gggctggagc cctcctgcag cacggcctgg tcaacttcac attcaacaag
 480

cttctccgcc ggggcttcac ccccatgacg gtgccagacc ttctccgcgg agcagtgttt
 540
 gaaggctgtg ggatgacacc aaatgccaac ccatcccaaa ttacaacat cgaccctgcc
 600
 cgcttcaaag atctcaacct tgctggaaca gcggaggtgg ggcttgacagg ctacttcacg
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 720
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 737

<210> 3310

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3310

Ala	His	Leu	Cys	Cys	Pro	Gln	Asp	Pro	Lys	Tyr	Gln	Gly	Leu	Arg	Ala
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Arg	Gly	Arg	Glu	Ile	Arg	Lys	Glu	Leu	Val	His	Leu	Tyr	Pro	Arg	Glu
			20					25					30		
Ala	Gln	Leu	Glu	Glu	Gln	Phe	Tyr	Leu	Gln	Ala	Leu	Lys	Leu	Pro	Asn
		35					40					45			
Gln	Thr	His	Pro	Asp	Val	Pro	Val	Gly	Asp	Glu	Ser	Gln	Ala	Arg	Val
	50					55					60				
Leu	His	Met	Val	Gly	Asp	Lys	Pro	Val	Phe	Ser	Phe	Gln	Pro	Arg	Gly
65					70					75				80	
His	Leu	Glu	Ile	Gly	Glu	Lys	Leu	Asp	Ile	Ile	Arg	Gln	Lys	Arg	Leu
			85					90					95		
Ser	His	Val	Ser	Gly	His	Arg	Ser	Tyr	Leu	Arg	Gly	Ala	Gly	Ala	
			100					105					110		
Leu	Leu	Gln	His	Gly	Leu	Val	Asn	Phe	Thr	Phe	Asn	Lys	Leu	Leu	Arg
		115					120					125			
Arg	Gly	Phe	Thr	Pro	Met	Thr	Val	Pro	Asp	Leu	Leu	Arg	Gly	Ala	Val
		130					135					140			
Phe	Glu	Gly	Cys	Gly	Met	Thr	Pro	Asn	Ala	Asn	Pro	Ser	Gln	Ile	Tyr
145					150					155				160	
Asn	Ile	Asp	Pro	Ala	Arg	Phe	Lys	Asp	Leu	Asn	Leu	Ala	Gly	Thr	Ala
			165					170						175	
Glu	Val	Gly	Leu	Ala	Gly	Tyr	Phe	Met	Asp	His	Thr	Val	Ala	Phe	Arg
		180						185					190		
Asp	Leu	Pro	Val	Arg	Met	Val	Cys	Ser	Ser	Thr	Cys	Tyr	Arg	Ala	Glu
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Thr	Asn														
	210														

<210> 3311

<211> 486

<212> DNA

<213> Homo sapiens

<400> 3311

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 120
 aggaaagatc aaggagtaaa ccagaagaag aagaaaaaga ggacttcaaa gctgggaagg
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 atgagttctt gcagcaacgt ctgtgggtcc aggcaggcac aggtgcagc tgagggtggt
 240
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 300
 atttgggagt atgaggatga tttccagatc caaagatcac ctaacagggtg gagctcagta
 360
 ttctggaagg ttggactcat ctcaggtaca gtttttgtga tcctcggatt gactgttctg
 420
 gcagtgggct ttcttgtgcc ccccaaaatc gaagcatttg gcgaagccga ttttgtggtg
 480
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 486

<210> 3312

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3312

Met Ser Ser Cys Ser Asn Val Cys Gly Ser Arg Gln Ala Gln Ala Ala
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 Ala Glu Gly Gly Tyr Gln Arg Tyr Gly Val Arg Ser Tyr Leu His Gln
 20 25 30
 Phe Tyr Glu Asp Cys Thr Ala Ser Ile Trp Glu Tyr Glu Asp Asp Phe
 35 40 45
 Gln Ile Gln Arg Ser Pro Asn Arg Trp Ser Ser Val Phe Trp Lys Val
 50 55 60
 Gly Leu Ile Ser Gly Thr Val Phe Val Ile Leu Gly Leu Thr Val Leu
 65 70 75 80
 Ala Val Gly Phe Leu Val Pro Pro Lys Ile Glu Ala Phe Gly Glu Ala
 85 90 95
 Asp Phe Val Val Val Asp
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<210> 3313

<211> 1791

<212> DNA

<213> Homo sapiens

<400> 3313

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 120
 cccggggcgg gtcgagttgg cggcgggcgc ggccgantgc gttctcgtca gccggaaggg
 180
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 240
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 300

atgatgatgc catttaaacy acaggctcta gtggaatttg aaaacataga tagtgccaaa
360
gaatgtgtga catttgctgc agatgaaccc gtgtacattg ctgggtcaaca ggcttttttc
420
aactattcta caagcaaaag gatcactcgg ccaggaaata ctgatgatcc atcaggaggc
480
aacaagttc ttctgctctc aattcagaat ccgctttatc caattacagt ggatgtttta
540
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660
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900
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1380
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1500
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1560
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1620
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1740
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1791

<210> 3314

<211> 537

<212> PRT

<213> Homo sapiens

<400> 3314

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 20 25 30
 Ala Arg Thr Ala Val Lys Arg Arg Pro Gly Ala Gly Arg Val Gly Gly
 35 40 45
 Gly Gly Gly Arg Xaa Arg Ser Arg Gln Pro Glu Gly Leu Arg Ser His
 50 55 60
 His Lys Val Ser Val Ser Pro Val Val His Val Arg Gly Leu Cys Glu
 65 70 75 80
 Ser Val Val Glu Ala Asp Leu Val Glu Ala Leu Glu Lys Phe Gly Thr
 85 90 95
 Ile Cys Tyr Val Met Met Met Pro Phe Lys Arg Gln Ala Leu Val Glu
 100 105 110
 Phe Glu Asn Ile Asp Ser Ala Lys Glu Cys Val Thr Phe Ala Ala Asp
 115 120 125
 Glu Pro Val Tyr Ile Ala Gly Gln Gln Ala Phe Phe Asn Tyr Ser Thr
 130 135 140
 Ser Lys Arg Ile Thr Arg Pro Gly Asn Thr Asp Asp Pro Ser Gly Gly
 145 150 155 160
 Asn Lys Val Leu Leu Ser Ile Gln Asn Pro Leu Tyr Pro Ile Thr
 165 170 175
 Val Asp Val Leu Tyr Thr Val Cys Asn Pro Val Gly Lys Val Gln Arg
 180 185 190
 Ile Val Ile Phe Lys Arg Asn Gly Ile Gln Ala Met Val Glu Phe Glu
 195 200 205
 Ser Val Leu Cys Ala Gln Lys Ala Lys Ala Ala Leu Asn Gly Ala Asp
 210 215 220
 Ile Tyr Ala Gly Cys Cys Thr Leu Lys Ile Glu Tyr Ala Arg Pro Thr
 225 230 235 240
 Arg Leu Asn Val Ile Arg Asn Asp Asn Asp Ser Trp Asp Tyr Thr Lys
 245 250 255
 Pro Tyr Leu Gly Arg Arg Asp Arg Gly Lys Gly Arg Gln Arg Gln Ala
 260 265 270
 Ile Leu Gly Glu His Pro Ser Ser Phe Arg His Asp Gly Tyr Gly Ser
 275 280 285
 His Gly Pro Leu Leu Pro Leu Pro Ser Arg Tyr Arg Met Gly Ser Arg
 290 295 300
 Asp Thr Pro Glu Leu Val Ala Tyr Pro Leu Pro Gln Ala Ser Ser Ser
 305 310 315 320
 Tyr Met His Gly Gly Asn Pro Ser Gly Ser Val Val Met Val Ser Gly
 325 330 335
 Leu His Gln Leu Lys Met Asn Cys Ser Arg Val Phe Asn Leu Phe Cys
 340 345 350
 Leu Tyr Gly Asn Ile Glu Lys Val Lys Phe Met Lys Thr Ile Pro Gly
 355 360 365
 Thr Ala Leu Val Glu Met Gly Asp Glu Tyr Ala Val Glu Arg Ala Val
 370 375 380
 Thr His Leu Asn Asn Val Lys Leu Phe Gly Lys Arg Leu Asn Val Cys
 385 390 395 400
 Val Ser Lys Gln His Ser Val Val Pro Ser Gln Ile Phe Glu Leu Glu

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<400> 3315
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120
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180
aaaacatccc tgagttcacc accttggccg gaagttgttc tgccagaccc agttgaggag
240
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420
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480
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540
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600
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660
caaaaggata aaaataaaact cctgcttccc aaggagacca ggtttctgtg ttctggttta
720
aagccgtgca tgcctgttgt agatagttta actggagcag catgtctgta agcaccaggc
780
ccccgagcca gagaaaaacag gaactggggg agaatgacaa gcatggccct cccagggtg
840
gataaatagt attcttgcca gccctccacc ccatgtggcg gcggcagggc ccaggggagt
900

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ggggcgggga tgcagattga tcttggagct gcag
934

<210> 3316

<211> 187

<212> PRT

<213> Homo sapiens

<400> 3316

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      20           25           30
Val Pro Lys Thr Ser Leu Ser Ser Pro Pro Trp Pro Glu Val Val Leu
      35           40           45
Pro Asp Pro Val Glu Glu Thr Arg His His Ala Glu Val Val Lys Lys
      50           55           60
Val Asn Glu Met Ile Val Thr Gly Gln Tyr Gly Arg Leu Phe Ala Val
      65           70           75           80
Val His Phe Ala Ser Arg Gln Trp Lys Val Thr Ser Glu Asp Leu Ile
      85           90           95
Leu Ile Gly Asn Glu Leu Asp Leu Ala Cys Gly Glu Arg Ile Arg Leu
      100          105          110
Glu Lys Val Leu Leu Val Gly Ala Asp Asn Phe Thr Leu Leu Gly Lys
      115          120          125
Pro Leu Leu Gly Lys Asp Leu Val Arg Val Glu Ala Thr Val Ile Glu
      130          135          140
Lys Thr Glu Ser Trp Pro Arg Ile Ile Met Arg Phe Arg Lys Arg Lys
      145          150          155          160
Asn Phe Lys Lys Lys Arg Ile Val Thr Thr Pro Gln Thr Val Leu Arg
      165          170          175
Ile Asn Ser Ile Glu Ile Ala Pro Cys Leu Leu
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<210> 3317

<211> 1665

<212> DNA

<213> Homo sapiens

<400> 3317

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120
aaaagaagct gagaaaaaaa gatgccaaaga ctggaagcat cgaagatggg gagccctttc
180
caagtgtctac gttatgaagc tgccaaatta agaactga gcaaatgtaa ttctcccgta
240
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300
aagtttttag aaacctactg tgtggaggaa gagaagacca gtgccaaccc tgagactctg
360
ctggggggaga tggaggcgaa gacaagagag ctcatgtgcta gaagaaccac acctcttttg
420

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gaatatatta aaaatagaaa attagaaaag cagagaattc gagaagagaa gcgagaagaa
 480
 cggaggagga gagagttaga aaagaaacgt ttgcgggaag aggaaaaaag aagaagaaga
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 gaagaagaaa gatgcaaaaa aaaagagaca gataaacaga agaaaattgc agagaaagaa
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 720
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 780
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 900
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 960
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 1020
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 1140
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 1200
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<210> 3318

<211> 253

<212> PRT

<213> Homo sapiens

<400> 3318

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Leu	Glu	Tyr	Ile	Lys	Asn	Arg	Lys	Leu	Glu	Lys	Gln	Arg	Ile	Arg	Glu
			20					25					30		
Glu	Lys	Arg	Glu	Glu	Arg	Arg	Arg	Arg	Glu	Leu	Glu	Lys	Lys	Arg	Leu

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      50              55              60
Lys Glu Thr Asp Lys Gln Lys Lys Ile Ala Glu Lys Glu Val Arg Ile
65              70              75              80
Lys Leu Leu Lys Lys Pro Glu Lys Gly Glu Glu Pro Thr Thr Glu Lys
      85              90              95
Pro Lys Glu Arg Gly Glu Glu Ile Asp Thr Gly Gly Gly Lys Gln Glu
      100             105             110
Ser Cys Ala Pro Gly Ala Val Val Lys Ala Arg Pro Met Glu Gly Ser
      115             120             125
Leu Glu Glu Pro Gln Glu Thr Ser His Ser Gly Ser Asp Lys Glu His
      130             135             140
Arg Asp Val Glu Arg Ser Gln Glu Gln Glu Ser Glu Ala Gln Arg Tyr
145             150             155             160
His Val Asp Asp Gly Arg Arg His Arg Ala His His Glu Pro Glu Arg
      165             170             175
Leu Ser Arg Arg Ser Glu Asp Glu Gln Arg Trp Gly Lys Gly Pro Gly
      180             185             190
Gln Asp Arg Gly Lys Lys Gly Ser Gln Asp Ser Gly Ala Pro Gly Glu
      195             200             205
Ala Met Glu Arg Leu Gly Arg Ala Gln Arg Cys Asp Asp Ser Pro Ala
210             215             220
Pro Arg Lys Glu Arg Leu Ala Asn Lys Val Phe Ile Lys Pro Lys Lys
225             230             235             240
Lys Asn Val Ser Gly Cys Leu Lys Val Gln Ala Ala Cys
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<210> 3319

<211> 1541

<212> DNA

<213> Homo sapiens

<400> 3319

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ctctgctccc gccgagggac agccggatcg cccctctgct tcccgaact gccctgatca
180
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300
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<211> 256

<212> PRT

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Lys	Gly	Ala	Ser	Leu	Leu	Tyr	Arg	Lys	Phe	Val	His	Pro	Ser	Leu	Ser
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Arg	His	Glu	Lys	Glu	Ile	Asp	Ala	Tyr	Ile	Val	Gln	Ala	Lys	Glu	Arg
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<212> DNA

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<212> PRT

<213> Homo sapiens

<400> 3322

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			20					25					30		
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<211> 254

<212> PRT

<213> Homo sapiens

<400> 3326

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 Val Pro Thr Thr Pro Glu Asp Phe Leu Ser Asn Val Asp Glu Met Asp
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 Thr Gly Glu Asn Ala Gly Gln Thr Pro Met Asn Ile Asn Pro Gln Gln
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 Thr Arg Phe Pro Asp Phe Leu Asp Cys Leu Pro Gly Thr Asn Val Asp
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<210> 3327

<211> 2263

<212> DNA

<213> Homo sapiens

<400> 3327

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<211> 521

<212> PRT

<213> Homo sapiens

<400> 3328

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Ala	Glu	Asn	Lys	Thr	Val	Val	Ala	Pro	Met	Leu	Asp	Ser	Arg	Ala	Ala
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 Ser Val Glu Pro Leu Leu Ile Tyr Pro Thr His Tyr Thr Gly Asp Asp
 450 455 460
 Gly Tyr Val Ser Asp Thr Glu Thr Ser Val Val Trp Asn Asn Glu His
 465 470 475 480
 Val Lys Thr Asp Trp Asp Arg Ala Lys Ser Gln Lys Met Arg Glu Gln
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<211> 705

<212> DNA

<213> Homo sapiens

<400> 3329

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<211> 235

<212> PRT

<213> Homo sapiens

<400> 3330

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		100						105					110		
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<211> 1644

<212> DNA

<213> Homo sapiens

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<211> 128

<212> PRT

<213> Homo sapiens

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Met Ser Ser Cys Arg Val Asp Lys Pro Ser Glu Ile Val Asp Val Gly
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Asp Lys Val Trp Val Lys Leu Ile Gly Arg Glu Met Lys Asn Asp Arg
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Ile Lys Val Ser Leu Ser Met Lys Val Val Asn Gln Gly Thr Gly Lys
      85           90           95
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<212> DNA

<213> Homo sapiens

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<211> 672

<212> PRT

<213> Homo sapiens

<400> 3334

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Ala	Ala	Val	Gln	Pro	Ala	Glu	Val	Thr	Val	Glu	Val	Gly	Glu	Asp
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His	Met	His	His	Val	Arg	Asp	Arg	Glu	Met	Pro	Glu	Ala	Leu	Glu
	50				55					60				Phe
Asn	Leu	Ser	Ala	Asn	Pro	Glu	Ser	Ser	Thr	Ile	Phe	Gln	Arg	Asn
65				70						75				80
Gln	Thr	Glu	Ala	Leu	Glu	Phe	Asn	Pro	Ser	Ala	Asn	Pro	Glu	Ala
			85					90					95	
Thr	Ile	Phe	Gln	Arg	Asn	Ser	Gln	Thr	Asp	Val	Val	Glu	Ile	Arg
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Ser	Asn	Cys	Thr	Asn	His	Val	Ser	Ala	Val	Arg	Phe	Ser	Gln	Gln
	115					120					125			Tyr
Ser	Leu	Cys	Ser	Thr	Ile	Phe	Leu	Asp	Asp	Ser	Thr	Ala	Ile	Gln
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Tyr	Leu	Thr	Met	Thr	Ile	Ser	Val	Thr	Leu	Glu	Ile	Pro	His	His
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Ile	Thr	Gln	Arg	Asp	Ala	Asp	Arg	Thr	Leu	Ser	Ile	Pro	Asp	Glu
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Ser	Thr	Ser	Gln	Glu	Asp	Pro	Gln	Phe	Ser	Val	Pro	Pro	Thr	Ala
	210				215						220			Asn
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Ala Cys Thr Pro Ile Ser Ser Ser Lys Ser Asn Gly Leu Ser Lys Asp
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Met Asp Thr Gly Leu Gly Asp Ser Ile Cys Phe Ser Pro Ser Ile Ser
          355          360          365
Ser Thr Thr Ser Pro Lys Leu Asn Pro Pro Pro Ser Pro His Ala Asn
          370          375          380
Lys Lys Lys His Leu Lys Lys Lys Ser Thr Asn Asn Phe Met Ile Val
          385          390          395          400
Ser Ala Thr Gly Gln Thr Trp His Phe Glu Ala Thr Thr Tyr Glu Glu
          405          410          415
Arg Asp Ala Trp Val Gln Ala Ile Gln Ser Gln Ile Leu Ala Ser Leu
          420          425          430
Gln Ser Cys Glu Ser Ser Lys Ser Lys Ser Gln Leu Thr Ser Gln Ser
          435          440          445
Glu Ala Met Ala Leu Gln Ser Ile Gln Asn Met Arg Gly Asn Ala His
          450          455          460
Cys Val Asp Cys Glu Thr Gln Asn Pro Lys Trp Ala Ser Leu Asn Leu
          465          470          475          480
Gly Val Leu Met Cys Ile Glu Cys Ser Gly Ile His Arg Ser Leu Gly
          485          490          495
Thr Arg Leu Ser Arg Val Arg Ser Leu Glu Leu Asp Asp Trp Pro Val
          500          505          510
Glu Leu Arg Lys Val Met Ser Ser Ile Gly Asn Glu Leu Ala Asn Ser
          515          520          525
Ile Trp Glu Glu Ser Ser Gln Gly Arg Thr Lys Pro Ser Val Asp Ser
          530          535          540
Thr Arg Glu Glu Lys Glu Arg Trp Ile Arg Ser Lys Tyr Glu Glu Lys
          545          550          555          560
Leu Phe Leu Ala Pro Leu Pro Cys Thr Glu Leu Ser Leu Gly Gln Gln
          565          570          575
Leu Leu Arg Ala Thr Ala Asp Glu Asp Leu Gln Thr Ala Ile Leu Leu
          580          585          590
Leu Ala His Gly Ser Arg Glu Glu Val Asn Glu Thr Cys Gly Glu Gly
          595          600          605
Asp Gly Cys Thr Ala Leu His Leu Ala Cys Arg Lys Gly Asn Val Val
          610          615          620
Leu Ala Gln Leu Leu Ile Trp Tyr Gly Val Asp Val Met Ala Arg Asp
          625          630          635          640
Ala His Gly Asn Thr Ala Leu Thr Tyr Ala Arg Gln Ala Ser Ser Gln
          645          650          655
Glu Cys Ile Asn Val Leu Leu Gln Tyr Gly Cys Pro Asp Lys Cys Val
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<210> 3335

<211> 477

<212> DNA

<213> Homo sapiens

<400> 3335

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120

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cccagactgc ttgttgaagg ggttgagggtg ggcctgccgg aaacgggcca gcttctcatc
 180
 atattccata gcatcccacc tgcctgcct gccagggccc aggggctcgc agggacagga
 240
 tggccattcc tctagggctg ctggccacgg aagcctggcc gtgggttcgg cacctgctga
 300
 ccgccgcctc gcatttgccc tgagacaggg ctggacagcc aggattaccg ctgtgccgag
 360
 tgccggggcg ccatctctct gcgggggtgtg cccagtggag ccaggcagtg cgactacacc
 420
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 477

<210> 3336

<211> 59

<212> PRT

<213> Homo sapiens

<400> 3336

Pro	Pro	Pro	Arg	Ile	Cys	Pro	Glu	Thr	Gly	Leu	Asp	Ser	Gln	Asp	Tyr
1				5					10					15	
Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile	Ser	Leu	Arg	Gly	Val	Pro	Ser
		20						25					30		
Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly	Gln	Tyr	Tyr	Cys	Ser	Pro	Cys
		35					40					45			
His	Trp	Asn	Ala	Leu	Ala	Val	Ile	Pro	Ala	Arg					
	50					55									

<210> 3337

<211> 679

<212> DNA

<213> Homo sapiens

<400> 3337

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 120
 agcttagcct ccaaagacac agatagagtg agagagagag acagagagag acacagagac
 180
 agacagagac caaaacagaa gcggcaaacg gcaaaaacga agcagaatca atgcaagtta
 240
 gagaaaaaaa taaaactaaa catcagagca gggaaaagtc atctactccg tatcacacct
 300
 gtgtattagc ttaaccagaa ataagctgga agaggagtgc agtagcctct cagcccccta
 360
 aagatgttgg tcataccccc tctttcaccg tctgagtcga gaggacacca agccaaacaa
 420
 actgtgcccc aaactgggtc atctagtcct cccaggtcct tccttgctaa ctcgaggaaa
 480
 caaggaaaac caactttgga tggcaacttc aacaaggtaa ccctccttcc ttcaatggcc
 540
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679

<210> 3338

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3338

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Lys	Lys	Gly	Lys	Lys	Lys	Arg	Lys	Arg	Asp	Thr	Pro	Gln	Arg	Gly	Gly
		20					25					30			
Lys	Glu	Val	Arg	Trp	Gly	Ser	Leu	Ser	Leu	Ala	Ser	Lys	Asp	Thr	Asp
	35					40					45				
Arg	Val	Arg	Glu	Arg	Asp	Arg	Glu	Arg	His	Arg	Asp	Arg	Gln	Arg	Pro
	50				55				60						
Lys	Gln	Lys	Arg	Gln	Thr	Ala	Lys	Thr	Lys	Gln	Asn	Gln	Cys	Lys	Leu
65				70					75				80		
Glu	Lys	Lys	Ile	Lys	Leu	Asn	Ile	Arg	Ala	Gly	Lys	Ser	His	Leu	Leu
			85					90					95		
Arg	Ile	Thr	Pro	Val	Tyr										
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<210> 3339

<211> 1341

<212> DNA

<213> Homo sapiens

<400> 3339

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120
agaagccagt tccatccagg atccactatc tacacaccta tgttacaaca ttatatcaaa
180
tctggtatct gaagaaaaga tacacattta atatgttcat ttaagttacg tattttgcag
240
aaagattaaa aattcattca cacaaaactc aaaaactgta ttaaaagttt gaatataaaa
300
ctcagatcca cctggaatga ctaaagaatg gaagttctgt atccacctgt gttaaaaactg
360
gtaaatgtaa tgatatctgt taccaataaa acgcattcgt ttattcaatg taagtaagtt
420
atctaatttt aacaatatgg caccctaaaa accaactgta tttttatgat gaggcacttt
480
tgttagtgat gaaacaaaaa gaacaaattt gctgcacact gatgccagcg attttcttca
540
gtgattttgg gtatatgcta tgtagtaagt tgcaacaaat accttgctca tttgtataca
600
actatccgat atatttttaa tatatatata tatatatggt cttctggctg tagtaatgca
660

ctgtaaagct atttcacagt gcaaaatgat gaaaccagcc caaatgaagg ctgcataata
 720
 acaattctga tacaagaaaa tattgacaga gttactggaa cgtgtaacag tagttttttt
 780
 acttgctaga gtggacatac cccagttta aagacagggg tgaaactctg ctttagtgcc
 840
 tggggtttca gacagtttat gaggttgggc attcgctgca gaactagcat ttttgctcac
 900
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 960
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 1020
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 1200
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<210> 3340

<211> 86

<212> PRT

<213> Homo sapiens

<400> 3340

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Ser	Val	Asn	Ile	Phe	Leu	Tyr	Gln	Asn	Cys	Tyr	Tyr	Ala	Ala	Phe	Ile
		20					25					30			
Trp	Ala	Gly	Phe	Ile	Ile	Leu	His	Cys	Glu	Ile	Ala	Leu	Gln	Cys	Ile
		35				40					45				
Thr	Thr	Ala	Arg	Arg	Thr	Tyr	Ile	Tyr	Ile	Tyr	Ile	Lys	Asn	Ile	Ser
	50				55				60						
Asp	Ser	Cys	Ile	Gln	Met	Ser	Lys	Val	Phe	Val	Ala	Thr	Tyr	Tyr	Ile
65			70					75						80	
Ala	Tyr	Thr	Gln	Asn	His										
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<210> 3341

<211> 1132

<212> DNA

<213> Homo sapiens

<400> 3341

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 120

ctggagcatg accacagacc cattcagggg ggctggcgga ctcttcatcc tggacagtcc
 180
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 240
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 480
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 aagatgaaga agcgcacatg cctcgtcctg gactgcctct gtgctcatga cttcagcgat
 660
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 720
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 780
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 840
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 960
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 1020
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 1132

<210> 3342

<211> 308

<212> PRT

<213> Homo sapiens

<400> 3342

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 Gly Pro Phe Ile Leu Gly Pro Arg Leu Gly Asn Ser Pro Val Pro Ser
 35 40 45
 Ile Val Gln Cys Leu Ala Arg Lys Asp Gly Thr Asp Asp Phe Tyr Gln
 50 55 60
 Leu Lys Ile Leu Thr Leu Glu Glu Arg Gly Asp Gln Gly Ile Glu Ser
 65 70 75 80
 Gln Glu Glu Arg Gln Gly Lys Met Leu Leu His Thr Glu Tyr Ser Leu
 85 90 95
 Leu Ser Leu Leu His Thr Gln Asp Gly Val Val His His His Gly Leu


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      100      105      110
Phe Gln Asp Arg Thr Cys Glu Ile Val Glu Asp Thr Glu Ser Ser Arg
      115      120      125
Met Val Lys Lys Met Lys Lys Arg Ile Cys Leu Val Leu Asp Cys Leu
      130      135      140
Cys Ala His Asp Phe Ser Asp Lys Thr Ala Asp Leu Ile Asn Leu Gln
145      150      155      160
His Tyr Val Ile Lys Glu Lys Arg Leu Ser Glu Arg Glu Thr Val Val
      165      170      175
Ile Phe Tyr Asp Val Val Arg Val Val Glu Ala Leu His Gln Lys Asn
      180      185      190
Ile Val His Arg Asp Leu Lys Leu Gly Asn Met Val Leu Asn Lys Arg
      195      200      205
Thr His Arg Ile Thr Ile Thr Asn Phe Cys Leu Gly Lys His Leu Val
      210      215      220
Ser Glu Gly Asp Leu Leu Lys Asp Gln Arg Gly Ser Pro Ala Tyr Ile
225      230      235      240
Ser Pro Asp Val Leu Ser Gly Arg Pro Tyr Arg Gly Lys Pro Ser Asp
      245      250      255
Met Trp Ala Leu Gly Val Val Leu Phe Thr Met Leu Tyr Gly Gln Phe
      260      265      270
Pro Phe Tyr Asp Ser Ile Pro Gln Glu Leu Phe Arg Lys Ile Lys Ala
      275      280      285
Ala Glu Tyr Thr Ile Pro Glu Asp Gly Arg Val Ser Glu Asn Thr Val
      290      295      300
Cys Leu Ile Arg
305

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<210> 3343

<211> 594

<212> DNA

<213> Homo sapiens

<400> 3343

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120
ttcagcatga actgggtcgt gggcagcgcg gacctggaga ttatcaacgc caccactggg
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240
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300
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420
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594

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<210> 3344
 <211> 143
 <212> PRT
 <213> Homo sapiens

<400> 3344
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 20 25 30
 Arg Gln Pro Gly Lys Ser Pro Pro Phe Ser Met Asn Trp Val Val Gly
 35 40 45
 Ser Ala Asp Leu Glu Ile Ile Asn Ala Thr Thr Gly Arg Arg Ser Cys
 50 55 60
 Gly Gly Pro Ser Arg Leu Cys Lys His Val Leu Ser Ala Arg Trp Ala
 65 70 75 80
 Arg Leu Tyr Gly Arg Leu Ser Thr Arg Thr Pro Ser Pro Gly Asp Thr
 85 90 95
 Pro Ser Met Tyr Cys Glu Ala Lys Leu Gly Ala His Thr Tyr Gln Ser
 100 105 110
 Val Lys Gln Gln Leu Phe Lys Ala Phe Gln Lys Ala Gly Leu Gly Thr
 115 120 125
 Trp Val Arg Lys Pro Pro Glu Gln Gln Gln Phe Leu Leu Thr Leu
 130 135 140

<210> 3345
 <211> 1149
 <212> DNA
 <213> Homo sapiens

<400> 3345
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 180
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 240
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<210> 3346

<211> 263

<212> PRT

<213> Homo sapiens

<400> 3346

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		20						25					30		
Glu	Glu	Val	Pro	Asp	Val	Thr	Pro	Glu	Glu	Ala	Leu	Pro	Glu	Leu	Pro
		35					40				45				
Pro	Gly	Glu	Pro	Glu	Phe	Arg	Cys	Pro	Glu	Arg	Val	Met	Asp	Leu	Gly
	50					55					60				
Leu	Ser	Glu	Asp	His	Phe	Ser	Arg	Pro	Val	Gly	Leu	Phe	Leu	Ala	Ser
65					70					75					80
Asp	Val	Gln	Gln	Leu	Arg	Gln	Ala	Ile	Glu	Glu	Cys	Lys	Gln	Val	Ile
			85					90						95	
Leu	Glu	Leu	Pro	Glu	Gln	Ser	Glu	Lys	Gln	Lys	Asp	Ala	Val	Val	Arg
		100						105					110		
Leu	Ile	His	Leu	Arg	Leu	Lys	Leu	Gln	Glu	Leu	Lys	Asp	Pro	Asn	Glu
		115				120						125			
Asp	Glu	Pro	Asn	Ile	Arg	Val	Leu	Leu	Glu	His	Arg	Phe	Tyr	Lys	Glu
	130					135					140				
Lys	Ser	Lys	Ser	Val	Lys	Gln	Thr	Cys	Asp	Lys	Cys	Asn	Thr	Ile	Ile
145					150					155					160
Trp	Gly	Leu	Ile	Gln	Thr	Trp	Tyr	Thr	Cys	Thr	Gly	Cys	Tyr	Tyr	Arg
			165					170						175	
Cys	His	Ser	Lys	Cys	Leu	Asn	Leu	Ile	Ser	Lys	Pro	Cys	Val	Ser	Ser
		180					185						190		
Lys	Val	Ser	His	Gln	Ala	Glu	Tyr	Glu	Leu	Asn	Ile	Cys	Pro	Glu	Thr
		195					200					205			
Gly	Leu	Asp	Ser	Gln	Asp	Tyr	Arg	Cys	Ala	Glu	Cys	Arg	Ala	Pro	Ile
	210					215					220				
Ser	Leu	Arg	Gly	Val	Pro	Ser	Glu	Ala	Arg	Gln	Cys	Asp	Tyr	Thr	Gly

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<210> 3347

<211> 2267

<212> DNA

<213> Homo sapiens

<400> 3347

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120
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240
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1260

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 1980
 gtaaccacc ctgtggcgct agtcgcagtg ctctggccaa cactatagca gggcttatcc
 2040
 ttctccctca tgtgtagtga aacaaaatgt aacaccttgg gttcattcag ttccattccc
 2100
 tatgtctacc tgtgtcaata taattccctg atttggaggc agctctctc attttcccca
 2160
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 2220
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 2267
 <210> 3348
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 3348
 Arg Cys Val Thr Cys Ala Met Glu Pro Lys Val Ala Glu Leu Lys Gln
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 Lys Ile Glu Asp Thr Leu Cys Pro Phe Gly Phe Glu Val Tyr Pro Phe
 20 25 30
 Gln Val Ala Trp Tyr Asn Glu Leu Leu Pro Pro Ala Phe His Leu Pro
 35 40 45
 Leu Pro Gly Pro Thr Leu Ala Phe Leu Val Leu Ser Thr Pro Ala Met
 50 55 60
 Phe Asp Arg Ala Leu Lys Pro Phe Leu Gln Ser Cys His Leu Arg Met
 65 70 75 80
 Leu Thr Asp Pro Val Asp Gln Cys Val Ala Tyr His Leu Gly Arg Val
 85 90 95
 Gly Glu Ser Leu Pro Glu Leu Gln Ile Glu Ile Ile Ala Asp Tyr Glu
 100 105 110

Val His Pro Asn Arg Arg Pro Lys Ile Leu Ala Gln Thr Ala Ala His
 115 120 125
 Val Ala Gly Ala Ala Tyr Tyr Tyr Gln Arg Gln Asp Val Glu Ala Asp
 130 135 140
 Pro Trp Gly Asn Gln Arg Ile Ser Gly Val Cys Ile His Pro Arg Phe
 145 150 155 160
 Gly Gly Trp Phe Ala Ile Arg Gly Val Val Leu Leu Pro Gly Ile Glu
 165 170 175
 Val Pro Asp Leu Pro Pro Arg Lys Pro His Asp Cys Val Pro Thr Arg
 180 185 190
 Ala Asp Arg Ile Ala Leu Leu Glu Gly Phe Asn Phe His Trp Arg Asp
 195 200 205
 Trp Thr Tyr Arg Asp Ala Val Thr Pro Gln Glu Arg Tyr Ser Glu Glu
 210 215 220
 Gln Lys Ala Tyr Phe Ser Thr Pro Pro Ala Gln Arg Leu Ala Leu Leu
 225 230 235 240
 Gly Leu Ala Gln Pro Ser Glu Lys Pro Ser Ser Pro Ser Pro Asp Leu
 245 250 255
 Pro Phe Thr Thr Pro Ala Pro Lys Lys Pro Gly Asn Pro Ser Arg Ala
 260 265 270
 Arg Ser Trp Leu Ser Pro Arg Val Ser Pro Pro Ala Ser Pro Gly Pro
 275 280 285

<210> 3349

<211> 1132

<212> DNA

<213> Homo sapiens

<400> 3349

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 120
 tcggcccaaa gaaaacctgg agctcatcct gacgcagtcg gtggagagta aggcccgggc
 180
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 240
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 300
 aagaagctgt ttgaagagga gaaattgctg agacaagaag gaaaattaga gaagatccag
 360
 accaaggcag gtgaggcgac agtgaaattt ctaaaaagct gtcgcctgga ggtagggatg
 420
 aagaacaatg tcaaattgga gctgaaccct gaaatagttg cccgccactt cttaagaat
 480
 cttggtgttg tggttgcccc acatacatta aagttaccag cagagcctat cacacggtgg
 540
 ggcgagtatt ggtgtgaggt gacggtaaataa gggcttgata ctgtgagagt gcctatgtct
 600
 gtcgtgaact ttgagaagcc caagacaaa agatataagt actggttagc ccagcaagct
 660
 gccaaaggcta tggccccccac cagccccccag atctaaatct actctccctc caaggcagca
 720

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cttgaggaat actccatacc tgagtagaca gccatgtggc catcgcgagct actaattttc
120
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atgatgtctt tagctccaat aattcatggt ggcaagcaca gtgaacgaca tcttgcctc
 180
 gctgctgcgc cgcgatgcgc tgagcgccgc caaggagggtg ttgtaccacc tggacatcta
 240
 cttcagcagc cagctgcaga gcgcgccgct gcccacgtg gacaagggcc ccgtggagct
 300
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 360
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 420
 ggactctgtt cgcgagatta ttttttcac ccttttcagc cctcaagggg acaaagccga
 480
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 600
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 720
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 1080
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 1200
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 1260
 cacgagagat gaccttagaa ccttgttctc caggctcccc cgtaataacc tcctccagct
 1320
 ggtgatctcg ggtcccgctg agcagtcgcc tcacgcgcg ctccccccgg ggttctaccc
 1380
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 1422

<210> 3352

<211> 97

<212> PRT

<213> Homo sapiens

<400> 3352

Met Trp Pro Ser Gln Leu Leu Ile Phe Met Met Leu Leu Ala Pro Ile
 1 5 10 15
 Ile His Gly Gly Lys His Ser Glu Arg His Pro Ala Leu Ala Ala Ala


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                20                25                30
Pro Arg Cys Ala Glu Arg Arg Gln Gly Gly Val Val Pro Pro Gly His
                35                40                45
Leu Leu Gln Gln Pro Ala Ala Glu Arg Ala Ala Ala His Arg Gly Gln
                50                55                60
Gly Pro Arg Gly Ala Ala Gly Gly Val Arg Val Pro Gly Ala Gln Gly
65                70                75                80
Ala Gln Arg Ala Ala Gln Glu Thr Glu Phe Pro Ser Gly Ala Ser Thr
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Ser

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<210> 3353

<211> 420

<212> DNA

<213> Homo sapiens

<400> 3353

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120
ggctccctac ctgacctcac caacctgcac ttccccccac cactgcccac cccctggac
180
cctgaagaga cagcctaccc tagcctgagt gggggcaaca gtacctcaa ttgaccac
240
accatgactc acctgggcat cagcaggggc atgggcctgg gcccaggcta tgatgcacca
300
gggcgtcccc ctggatacca gtaaactgtc cactgaccag cggttacccc cataccata
360
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420

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<210> 3354

<211> 107

<212> PRT

<213> Homo sapiens

<400> 3354

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Xaa Lys Leu Ser Ser Ser Ser Arg Pro Arg Ser Cys Glu Val Pro
1                5                10                15
Gly Ile Asn Ile Phe Pro Ser Pro Asp Gln Pro Ala Asn Val Pro Val
                20                25                30
Leu Pro Pro Ala Met Asn Thr Gly Gly Ser Leu Pro Asp Leu Thr Asn
                35                40                45
Leu His Phe Pro Pro Pro Leu Pro Thr Pro Leu Asp Pro Glu Glu Thr
                50                55                60
Ala Tyr Pro Ser Leu Ser Gly Gly Asn Ser Thr Ser Asn Leu Thr His
65                70                75                80
Thr Met Thr His Leu Gly Ile Ser Arg Gly Met Gly Leu Gly Pro Gly
                85                90                95
Tyr Asp Ala Pro Gly Arg Pro Pro Gly Tyr Gln
                100                105

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<210> 3355
 <211> 474
 <212> DNA
 <213> Homo sapiens

<400> 3355
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 120
 gacaagagtc atgcttttct ccccatcatt ccaaaccacc agagaggtca gctagaagac
 180
 agactgaaca accaggcgcg taccatagct ttccttcttg aacaagcctt ccgcatcaag
 240
 gaggacatct ctgcttgctt gcaggggacc catggctttc gaaaagagga atcgctcgcc
 300
 aggaagttac tggaaagcca catccagacc atcaccagca tcgtcaaaaa actcagccaa
 360
 aatattgaga ttttagaaga ccaaataaga gctcgagatc aggcggccac aggaactaac
 420
 tttgcagtac acgagataaa catcaaacac ctacaaggag ttgggagatc tttc
 474

<210> 3356
 <211> 131
 <212> PRT
 <213> Homo sapiens

<400> 3356
 Met Ser Thr Lys Asn Ser Thr Asp Leu Val Glu Tyr Val Asp Lys Ser
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 His Ala Phe Leu Pro Ile Ile Pro Asn Thr Gln Arg Gly Gln Leu Glu
 20 25 30
 Asp Arg Leu Asn Asn Gln Ala Arg Thr Ile Ala Phe Leu Leu Glu Gln
 35 40 45
 Ala Phe Arg Ile Lys Glu Asp Ile Ser Ala Cys Leu Gln Gly Thr His
 50 55 60
 Gly Phe Arg Lys Glu Glu Ser Leu Ala Arg Lys Leu Leu Glu Ser His
 65 70 75 80
 Ile Gln Thr Ile Thr Ser Ile Val Lys Lys Leu Ser Gln Asn Ile Glu
 85 90 95
 Ile Leu Glu Asp Gln Ile Arg Ala Arg Asp Gln Ala Ala Thr Gly Thr
 100 105 110
 Asn Phe Ala Val His Glu Ile Asn Ile Lys His Leu Gln Gly Val Gly
 115 120 125
 Arg Ser Phe
 130

<210> 3357
 <211> 2268
 <212> DNA
 <213> Homo sapiens

<400> 3357

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agcagccatt atggatttgg atgtgctctt tatacccatg tctctaattg cagatggagg
120
agggcctata aaaataattc cttcttgctt acaaagttca gcaaattcca tgttttctga
180
aagaaaaccg catcctggat ggatagcctg tgcagcagag gtcttggcca cttgaatgat
240
tttctccata gataggtagc tctgctggga ggaacgggtt tggcgtgtgg gacgcagctg
300
cctctgtact ggggagtcac ggagtggccg ggctccaggg acatggcggc ggctctgcg
360
gtgtcgggtgc tgctgggtggc ggcgagagg aaccgggtggc atcgtctccc gagcctgctc
420
ctgccgccga ggacatgggt gtggaggcaa agaaccatga agtacacaac agccacagga
480
agaaacatta ccaaggtcct cattgcaaac agaggagaaa ttgcctgcag ggtgatgcgc
540
acagccaaaa aactgggtgt acagactgtg gcggtttata gtgaggctga cagaaattcc
600
atgcatgtag atatggcaga tgaagcatat tccatcgcc cgcctccctc ccagcagagc
660
tacctatcta tggagaaaat cattcaagtg gccaaagacct ctgctgcaca ggctatccat
720
ccaggatgcg gttttctttc agaaaacatg gaatttgctg aactttgtaa gcaagaagga
780
attattttta taggccctcc tccatctgca attagagaca tgggtataaa gagcacatcc
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tcagaccagt gcctgaagga acacgccagg agaattggct atcctgtcat gattaaagcc
960
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1020
cagttagagt cagcacggag agaagctaag aagtctttca atgatgatgc tatgctgatc
1080
gagaagtttg tagacacacc gaggcagtga gaagtccagg tgtttggtga tcacatggc
1140
aatgctgtgt acttgtttga aagagactgt agtgtgcaga ggcgacatca gaagatcatt
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1260
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1320
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1380
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1440
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tatgcagaag atcctagcaa taacttcatt cctgtggcag gccattagt gcacctctct
1560
actcctcgag cagacccttc caccaggatt gaaactggag tacggcaagg agacgaagtt
1620

tccgtgcatt atgaccccat gattgcgaag ctggctgtgt gggcagcaga tcgccaggcg
 1680
 gcattgacaa aactgaggta cagccttcgt cagtacaata ttgttggtact gcacaccaac
 1740
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 1800
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 1860
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 1920
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 1980
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 2040
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 2100
 ttccagacca ctacaataaa atgtagccat agctgtaacg tataaccatg atgggtctta
 2160
 tagcatgcag attgaagata aaactttcca agtccttggt aatctttaca gcgagggaga
 2220
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 2268

<210> 3358

<211> 493

<212> PRT

<213> Homo sapiens

<400> 3358

Gln	Thr	Val	Ala	Val	Tyr	Ser	Glu	Ala	Asp	Arg	Asn	Ser	Met	His	Val
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Asp	Met	Ala	Asp	Glu	Ala	Tyr	Ser	Ile	Gly	Pro	Ala	Pro	Ser	Gln	Gln
		20						25				30			
Ser	Tyr	Leu	Ser	Met	Glu	Lys	Ile	Ile	Gln	Val	Ala	Lys	Thr	Ser	Ala
		35				40					45				
Ala	Gln	Ala	Ile	His	Pro	Gly	Cys	Gly	Phe	Leu	Ser	Glu	Asn	Met	Glu
	50					55				60					
Phe	Ala	Glu	Leu	Cys	Lys	Gln	Glu	Gly	Ile	Ile	Phe	Ile	Gly	Pro	Pro
65				70					75					80	
Pro	Ser	Ala	Ile	Arg	Asp	Met	Gly	Ile	Lys	Ser	Thr	Ser	Lys	Ser	Ile
			85					90					95		
Met	Ala	Ala	Ala	Gly	Val	Pro	Val	Val	Glu	Gly	Tyr	His	Gly	Glu	Asp
			100					105					110		
Gln	Ser	Asp	Gln	Cys	Leu	Lys	Glu	His	Ala	Arg	Arg	Ile	Gly	Tyr	Pro
		115					120					125			
Val	Met	Ile	Lys	Ala	Val	Arg	Gly	Gly	Gly	Gly	Lys	Gly	Met	Arg	Ile
	130					135					140				
Val	Arg	Ser	Glu	Gln	Glu	Phe	Gln	Glu	Gln	Leu	Glu	Ser	Ala	Arg	Arg
145				150						155				160	
Glu	Ala	Lys	Lys	Ser	Phe	Asn	Asp	Asp	Ala	Met	Leu	Ile	Glu	Lys	Phe
			165						170					175	
Val	Asp	Thr	Pro	Arg	His	Val	Glu	Val	Gln	Val	Phe	Gly	Asp	His	His
			180					185					190		
Gly	Asn	Ala	Val	Tyr	Leu	Phe	Glu	Arg	Asp	Cys	Ser	Val	Gln	Arg	Arg

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      195              200              205
His Gln Lys Ile Ile Glu Glu Ala Pro Ala Pro Gly Ile Lys Ser Glu
  210              215              220
Val Arg Lys Lys Leu Gly Glu Ala Ala Val Arg Ala Ala Lys Ala Val
  225              230              235              240
Asn Tyr Val Gly Ala Gly Thr Val Glu Phe Ile Met Asp Ser Lys His
      245              250              255
Asn Phe Cys Phe Met Glu Met Asn Thr Arg Leu Gln Val Glu His Pro
      260              265              270
Val Thr Glu Met Ile Thr Gly Thr Asp Leu Val Glu Trp Gln Leu Arg
      275              280              285
Ile Ala Ala Gly Glu Lys Ile Pro Leu Ser Gln Glu Glu Ile Thr Leu
      290              295              300
Gln Gly His Ala Phe Glu Ala Arg Ile Tyr Ala Glu Asp Pro Ser Asn
  305              310              315              320
Asn Phe Met Pro Val Ala Gly Pro Leu Val His Leu Ser Thr Pro Arg
      325              330              335
Ala Asp Pro Ser Thr Arg Ile Glu Thr Gly Val Arg Gln Gly Asp Glu
      340              345              350
Val Ser Val His Tyr Asp Pro Met Ile Ala Lys Leu Val Val Trp Ala
      355              360              365
Ala Asp Arg Gln Ala Ala Leu Thr Lys Leu Arg Tyr Ser Leu Arg Gln
      370              375              380
Tyr Asn Ile Val Gly Leu His Thr Asn Ile Asp Phe Leu Leu Asn Leu
  385              390              395              400
Ser Gly His Pro Glu Phe Glu Ala Gly Asn Val His Thr Asp Phe Ile
      405              410              415
Pro Gln His His Lys Gln Leu Leu Leu Ser Arg Lys Ala Ala Ala Lys
      420              425              430
Glu Ser Leu Cys Gln Ala Ala Leu Gly Leu Ile Leu Lys Glu Lys Ala
      435              440              445
Met Thr Asp Thr Phe Thr Leu Gln Ala His Asp Gln Phe Ser Pro Phe
      450              455              460
Ser Ser Ser Ser Gly Arg Arg Leu Asn Ile Ser Tyr Thr Arg Asn Met
  465              470              475              480
Thr Leu Lys Asp Gly Lys Asn Ser Phe Arg Leu Leu Gly
      485              490

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<210> 3359

<211> 652

<212> DNA

<213> Homo sapiens

<400> 3359

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gcctatacct actgtagctt ctccacgtat ggaccctaaa ggctactgct gctactacgg
120
ggctagacag ttactgtctc agctctagga tgtgcgttct tccactagaa gctcttctga
180
gggaggtaat taaaaaacag tggaatggaa aaacagtgcg gtagtcatcc tgtaatatgc
240
tccttgtaaa caatgtatac attcctgcta ggtgccatat tcattgcttt aagctcaagt
300

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cgcatcttac tagtgaagta ttctgccaat gaagaaaaca agtatgatta tcttccaact
 360
 actgtgaatg tgtgctcaga actgggtgaag ctagttttct gtgtgcttgt gtcattctgt
 420
 gttataaaga aagatcatca aagtagaaat ttgaaatatg ctctctggaa ggaattctct
 480
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 540
 tatgtcctgt cctatcttca accagccatg gctgttatct tctcaaattt tagcattata
 600
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 652

<210> 3360

<211> 149

<212> PRT

<213> Homo sapiens

<400> 3360

Met	Glu	Lys	Gln	Cys	Cys	Ser	His	Pro	Val	Ile	Cys	Ser	Leu	Ser	Thr
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Met	Tyr	Thr	Phe	Leu	Leu	Gly	Ala	Ile	Phe	Ile	Ala	Leu	Ser	Ser	Ser
			20				25						30		
Arg	Ile	Leu	Leu	Val	Lys	Tyr	Ser	Ala	Asn	Glu	Glu	Asn	Lys	Tyr	Asp
		35					40					45			
Tyr	Leu	Pro	Thr	Thr	Val	Asn	Val	Cys	Ser	Glu	Leu	Val	Lys	Leu	Val
		50				55					60				
Phe	Cys	Val	Leu	Val	Ser	Phe	Cys	Val	Ile	Lys	Lys	Asp	His	Gln	Ser
65					70					75				80	
Arg	Asn	Leu	Lys	Tyr	Ala	Ser	Trp	Lys	Glu	Phe	Ser	Asp	Phe	Met	Lys
			85					90					95		
Trp	Ser	Ile	Pro	Ala	Phe	Leu	Tyr	Phe	Leu	Asp	Asn	Leu	Ile	Val	Phe
			100					105					110		
Tyr	Val	Leu	Ser	Tyr	Leu	Gln	Pro	Ala	Met	Ala	Val	Ile	Phe	Ser	Asn
		115					120					125			
Phe	Ser	Ile	Ile	Thr	Thr	Ala	Leu	Leu	Phe	Arg	Ile	Val	Leu	Lys	Arg
		130				135					140				
Arg	Leu	Asn	Trp	Ile											
145															

<210> 3361

<211> 1040

<212> DNA

<213> Homo sapiens

<400> 3361

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 120
 ggagtcgcct gcgcgcgcag cggaggccag tgcgcggcg catagcgagc ccgggtctgt
 180
 gatcgccgag gcgggagtga agatagtcca agtcctaaga gacagcgctt ctctcattca
 240

gtctttgatt atacatcagc atcaccagct ccctcaccac caatgcgacc atgggagatg
 300
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 360
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 420
 gatcgtctgt ctgcacataa ttccattagt caagatgaaa actatcacca tctcccttac
 480
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 540
 ctgtacatc ctgctgctca tccaccccag cagaatgcag tcatggttga catacatgat
 600
 cagctccatc aaggaacagt ccctgtttct tacacagtaa caacagtggc accacatggg
 660
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 720
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 780
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 840
 gatccatttc ttatacatcc tctcacctt tctccccatc atctctctca tttgccacca
 900
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<210> 3362

<211> 252

<212> PRT

<213> Homo sapiens

<400> 3362

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Pro	Ser	Gln	His	Phe	Ser	Gly	Glu	Arg	Cys	Asn	Thr	Pro	Ala	Arg	
			20					25					30		
Asn	Arg	Arg	Ser	Pro	Pro	Val	Arg	Arg	Gln	Arg	Gly	Arg	Arg	Asp	Arg
			35					40					45		
Leu	Ser	Arg	His	Asn	Ser	Ile	Ser	Gln	Asp	Glu	Asn	Tyr	His	His	Leu
			50					55				60			
Pro	Tyr	Ala	Gln	Gln	Gln	Ala	Ile	Glu	Glu	Pro	Arg	Ala	Phe	His	Pro
65					70					75				80	
Pro	Asn	Val	Ser	Pro	Arg	Leu	Leu	His	Pro	Ala	Ala	His	Pro	Pro	Gln
				85					90					95	
Gln	Asn	Ala	Val	Met	Val	Asp	Ile	His	Asp	Gln	Leu	His	Gln	Gly	Thr
			100					105					110		
Val	Pro	Val	Ser	Tyr	Thr	Val	Thr	Thr	Val	Ala	Pro	His	Gly	Ile	Pro
			115					120					125		
Leu	Cys	Thr	Gly	Gln	His	Ile	Pro	Ala	Cys	Ser	Thr	Gln	Gln	Val	Pro
			130				135					140			
Gly	Cys	Ser	Val	Val	Phe	Ser	Gly	Gln	His	Leu	Pro	Val	Cys	Ser	Val

```

145             150             155             160
Pro Pro Pro Met Leu Gln Ala Cys Ser Val Gln His Leu Pro Val Pro
             165             170             175
Tyr Ala Ala Phe Pro Pro Leu Ile Ser Ser Asp Pro Phe Leu Ile His
             180             185             190
Pro Pro His Leu Ser Pro His His Pro Pro His Leu Pro Pro Pro Gly
             195             200             205
Gln Phe Val Pro Phe Gln Thr Gln Gln Ser Arg Ser Pro Leu Gln Arg
             210             215             220
Ile Glu Asn Glu Val Glu Leu Leu Gly Glu His Leu Pro Gly Ala His
225             230             235             240
Pro Gln His Pro His Leu Leu Ile Asn Ile Ser Thr
             245             250

```

<210> 3363

<211> 718

<212> DNA

<213> Homo sapiens

<400> 3363

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cagaaggacc ccaggatggc gggtcatcatg cccaggaacg ttggtgatgg ggaatgggtt
60
ggccagcatg atcagggacc ccgtcatgcc catgattttt tgggtggcat tggcgaccga
120
gtagctcagg agtgtctccg gagccactg gagaagcccc ccaacggcct cctcttcccc
180
cagcacgggg actatcagta cggccgcaac aacatctaaa cagaccactt ccaatacage
240
cggcagagct acccaaactc gtacagtttg aaccgctatg atgtgtagag tccaaaggac
300
aggaccagac tgttggtgac tccttccccg gccccacag cagtatcaga aacttctgac
360
aatcagttaa tgtacaaccc agccgagggg acggtgcata actctccatc agaagccctg
420
gggttctctg cccccgtga gccgcaggag gatgcgttgc ctgcagtgca gacggccgtg
480
agctctgggc aaacctaaac agagaccagt gtcccatgct ctttcttctt ggagcctgtc
540
atctgagggc cgtgtccctg cggagatctt ggccacgttg tacctttcca tgtggaatta
600
ttccccaagc agtgtagctc agagcacttg tgtctgcatt ccagataaca ttcaggacct
660
gtgtgaaaag ctgggggtcac tgtggctgta gaccatgaac tggcagtggg ggtgtcca
718

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<210> 3364

<211> 163

<212> PRT

<213> Homo sapiens

<400> 3364

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Met Gly His Trp Ser Leu Phe Arg Phe Ala Gln Ser Ser Arg Pro Ser
1             5             10             15
Ala Leu Gln Ala Thr His Pro Pro Ala Ala His Gly Gly Pro Gly Thr

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```

      20      25      30
Pro Gly Leu Leu Met Glu Ser Tyr Ala Pro Ser Pro Arg Leu Gly Cys
      35      40      45
Thr Phe Thr Asp Cys Gln Lys Phe Leu Ile Leu Leu Trp Gly Pro Gly
      50      55      60
Lys Glu Ser Pro Thr Val Trp Ser Cys Pro Leu Asp Ser Thr His His
      65      70      75      80
Ser Gly Ser Asn Cys Thr Ser Leu Gly Ser Ser Ala Gly Cys Ile Gly
      85      90      95
Ser Gly Leu Phe Arg Cys Cys Cys Gly Arg Thr Asp Ser Pro Arg Ala
      100      105      110
Gly Gly Arg Gly Gly Arg Trp Gly Ala Ser Pro Val Gly Ser Gly Asp
      115      120      125
Thr Pro Glu Leu Leu Gly Arg Gln Cys His Pro Lys Asn His Gly His
      130      135      140
Asp Gly Val Pro Asp His Ala Gly Gln Pro Ile Pro His His Gln Arg
      145      150      155      160
Ser Trp Ala

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<210> 3365

<211> 2389

<212> DNA

<213> Homo sapiens

<400> 3365

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gcaggaagat ggcggcggtta gcggaggtgt gagtggacgc gggactcagc ggccggattt
60
tctcttccct tcttttccct tttccttccc tatttgaaat tggcatcgag ggggctaagt
120
tcgggtggca gcgccgggcg caacgcaggg gtcacggcga cggcggcggc ggctgacggc
180
tggaagggtta ggcttccttc accgctcgtc ctcttcttc gctccgctcg gtgtcaggcg
240
cggcggcggc gcggcgggcg gacttcgtcc ctcttctgc tccccccac accggagcgg
300
gcactcttcg cttcgccatc ccccgaccct tcaccccgag gactgggcgc ctcttccggc
360
gcagctgagg gagcgggggc cggctctctg ctcggttgtc gagcctccat gtcggataat
420
cagaactgga actcgtcggg ctcgaggag gatccagaga cggagtctgg gccgcctgtg
480
gagcgtcgcg gggctctcag taagtggaca aactacatc atgggtggca ggatcgttgg
540
gtagttttga aaaataatgc tctgagttac tacaaatctg aagatgaaac agagtatggc
600
tgcagaggat ccatctgtct tagcaaggct gtcacacac ctacagattt tgatgaatgt
660
cgatttgata ttagtgtaaa tgatagtgtt tggatcttc gtgctcagga tccagatcat
720
agacagcaat ggatagatgc cattgaacag cacaagactg aatctggata tggatctgaa
780
tccagcttgc gtcgacatgg ctcaatggtg tccctggtgt ctggagcaag tggctactct
840

```

gcaacatcca cctcttcatt caagaaaggc cacagtttac gtgagaagtt ggctgaaatg
900
gaaacattta gagacatctt atgtagacaa gttgacacgc tacagaagta ctttgatgcc
960
tgtgctgatg ctgtctctaa ggatgaactt caaagggata aagtggtaga agatgatgaa
1020
gatgactttc ctacaacgag ttctgatggt gacttcttgc atagtaccaa cggcaataaa
1080
gaaaagttat ttccacatgt gacaccaaaa ggaattaatg gtatagactt taaaggggaa
1140
gcgataactt ttaaagcaac tactgctgga atccttgcaa cactttctca ttgtattgaa
1200
ctaattggtta aacgtgagga cagctggcag aagagactgg ataaggaaac tgagaagaaa
1260
agaagaacag aggaagcata taaaaatgca atgacagaac ttaagaaaaa atccccacttt
1320
ggaggaccag attatgaaga aggccctaac agtctgatta atgaagaaga gttctttgat
1380
gctgttgaag ctgctcttga cagacaagat aaaatagaag aacagtcaca gagtgaaaag
1440
gtgagattac attggcctac atccttgccc tctggagatg ccttttcttc tgtggggaca
1500
catagatttg tccaaaagcc ctatagtgc tcttctcca tgtcttccat tgatctagtc
1560
agtgcctctg atgatgttca cagattcagc tcccaggttg aagagatggt gcagaaccac
1620
atgacttact cattacagga tgtaggcgga gatgccatt ggcagttggt tgtagaagaa
1680
ggagaaatga aggtatacag aagagaagta gaagaaaatg ggattgttct ggatccttta
1740
aaagctaccc atgcagttaa aggcgtcaca ggacatgaag tctgcaatta tttctggaat
1800
gttgacgttc gcaatgactg ggaaacaact atagaaaact ttcattgtggt ggaacatta
1860
gctgataatg caatcatcat ttatcaaaca cacaagaggg tgtggcctgc ttctcagcga
1920
gacgtattat atctttctgt cattcgaaag ataccagcct tgactgaaaa tgaccctgaa
1980
acttgatag tttgtaattt ttctgtggat catgacagtg ctctctctaa caaccgatgt
2040
gtccgtgcc aaataaatgt tgctatgatt tgtcaaacct tggtaagccc accagagggga
2100
aaccaggaaa ttagcaggga caacattcta tgcaagatta catatgtagc taatgtgaac
2160
cctggaggat gggcaccagc ctcatgttta agggcagtgg caaagcgaga gtatcctaaa
2220
tttctaaaac gttttacttc ttacgtccaa gaaaaaactg caggaaagcc tattttgttc
2280
tagtattaac aggtactaga agatatgttt tatctttttt taactttatt tgactaatat
2340
gactgtcaat actaaaattt agttgttgaa agtatttact atgtttttt
2389

<210> 3366

<211> 624

<212> PRT

<213> Homo sapiens

<400> 3366

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Met Ser Asp Asn Gln Asn Trp Asn Ser Ser Gly Ser Glu Glu Asp Pro
 1          5          10          15
Glu Thr Glu Ser Gly Pro Pro Val Glu Arg Cys Gly Val Leu Ser Lys
 20          25          30
Trp Thr Asn Tyr Ile His Gly Trp Gln Asp Arg Trp Val Val Leu Lys
 35          40          45
Asn Asn Ala Leu Ser Tyr Tyr Lys Ser Glu Asp Glu Thr Glu Tyr Gly
 50          55          60
Cys Arg Gly Ser Ile Cys Leu Ser Lys Ala Val Ile Thr Pro His Asp
 65          70          75          80
Phe Asp Glu Cys Arg Phe Asp Ile Ser Val Asn Asp Ser Val Trp Tyr
 85          90          95
Leu Arg Ala Gln Asp Pro Asp His Arg Gln Gln Trp Ile Asp Ala Ile
100          105          110
Glu Gln His Lys Thr Glu Ser Gly Tyr Gly Ser Glu Ser Ser Leu Arg
115          120          125
Arg His Gly Ser Met Val Ser Leu Val Ser Gly Ala Ser Gly Tyr Ser
130          135          140
Ala Thr Ser Thr Ser Ser Phe Lys Lys Gly His Ser Leu Arg Glu Lys
145          150          155          160
Leu Ala Glu Met Glu Thr Phe Arg Asp Ile Leu Cys Arg Gln Val Asp
165          170          175
Thr Leu Gln Lys Tyr Phe Asp Ala Cys Ala Asp Ala Val Ser Lys Asp
180          185          190
Glu Leu Gln Arg Asp Lys Val Val Glu Asp Asp Glu Asp Asp Phe Pro
195          200          205
Thr Thr Arg Ser Asp Gly Asp Phe Leu His Ser Thr Asn Gly Asn Lys
210          215          220
Glu Lys Leu Phe Pro His Val Thr Pro Lys Gly Ile Asn Gly Ile Asp
225          230          235          240
Phe Lys Gly Glu Ala Ile Thr Phe Lys Ala Thr Thr Ala Gly Ile Leu
245          250          255
Ala Thr Leu Ser His Cys Ile Glu Leu Met Val Lys Arg Glu Asp Ser
260          265          270
Trp Gln Lys Arg Leu Asp Lys Glu Thr Glu Lys Lys Arg Arg Thr Glu
275          280          285
Glu Ala Tyr Lys Asn Ala Met Thr Glu Leu Lys Lys Lys Ser His Phe
290          295          300
Gly Gly Pro Asp Tyr Glu Glu Gly Pro Asn Ser Leu Ile Asn Glu Glu
305          310          315          320
Glu Phe Phe Asp Ala Val Glu Ala Ala Leu Asp Arg Gln Asp Lys Ile
325          330          335
Glu Glu Gln Ser Gln Ser Glu Lys Val Arg Leu His Trp Pro Thr Ser
340          345          350
Leu Pro Ser Gly Asp Ala Phe Ser Ser Val Gly Thr His Arg Phe Val
355          360          365
Gln Lys Pro Tyr Ser Arg Ser Ser Ser Met Ser Ser Ile Asp Leu Val
370          375          380
Ser Ala Ser Asp Asp Val His Arg Phe Ser Ser Gln Val Glu Glu Met

```

```

385          390          395          400
Val Gln Asn His Met Thr Tyr Ser Leu Gln Asp Val Gly Gly Asp Ala
          405          410          415
Asn Trp Gln Leu Val Val Glu Glu Gly Glu Met Lys Val Tyr Arg Arg
          420          425          430
Glu Val Glu Glu Asn Gly Ile Val Leu Asp Pro Leu Lys Ala Thr His
          435          440          445
Ala Val Lys Gly Val Thr Gly His Glu Val Cys Asn Tyr Phe Trp Asn
          450          455          460
Val Asp Val Arg Asn Asp Trp Glu Thr Thr Ile Glu Asn Phe His Val
465          470          475          480
Val Glu Thr Leu Ala Asp Asn Ala Ile Ile Ile Tyr Gln Thr His Lys
          485          490          495
Arg Val Trp Pro Ala Ser Gln Arg Asp Val Leu Tyr Leu Ser Val Ile
          500          505          510
Arg Lys Ile Pro Ala Leu Thr Glu Asn Asp Pro Glu Thr Trp Ile Val
          515          520          525
Cys Asn Phe Ser Val Asp His Asp Ser Ala Pro Leu Asn Asn Arg Cys
          530          535          540
Val Arg Ala Lys Ile Asn Val Ala Met Ile Cys Gln Thr Leu Val Ser
545          550          555          560
Pro Pro Glu Gly Asn Gln Glu Ile Ser Arg Asp Asn Ile Leu Cys Lys
          565          570          575
Ile Thr Tyr Val Ala Asn Val Asn Pro Gly Gly Trp Ala Pro Ala Ser
          580          585          590
Val Leu Arg Ala Val Ala Lys Arg Glu Tyr Pro Lys Phe Leu Lys Arg
          595          600          605
Phe Thr Ser Tyr Val Gln Glu Lys Thr Ala Gly Lys Pro Ile Leu Phe
610          615          620

```

<210> 3367

<211> 366

<212> DNA

<213> Homo sapiens

<400> 3367

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acgcgtgcag gagaggagag gccaggagat agggagggca gtttgtggat tgaaatgacc
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gagaattacg ccacagaggt gttggaggct ggcacgtgg catctcagga gcacggaggg
120
tgccttcccc acttcaggcc tcttagtgtc aaggatgtga gaggcaaggg ctgctgggag
180
agtattttac ggactgaagg aggcgtgccg cctgccctgc cctcctactg gtggaggaag
240
gagggtgctgg gagccccaca actcagggcc ccccgacgcc cagtaaggcc actgtacacc
300
cctcctgacc cagaccataa ccagcctccg attgtgcttt tgaccctgtt tccttcaggc
360
accagg
366

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<210> 3368

<211> 104

<212> PRT

<213> Homo sapiens

<400> 3368

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Met Thr Glu Asn Tyr Ala Thr Glu Val Leu Glu Ala Gly Ile Val Ala
 1           5           10           15
Ser Gln Glu His Gly Gly Cys Leu Pro His Phe Arg Pro Leu Ser Val
          20          25          30
Lys Asp Val Arg Gly Lys Gly Cys Trp Glu Ser Ile Leu Arg Thr Glu
          35          40          45
Gly Gly Val Pro Pro Ala Leu Pro Ser Tyr Trp Trp Arg Lys Glu Val
          50          55          60
Leu Gly Ala Pro Gln Leu Arg Ala Pro Arg Arg Pro Val Arg Pro Leu
65          70          75          80
Tyr Thr Pro Pro Asp Pro Asp His Asn Gln Pro Pro Ile Val Leu Leu
          85          90          95
Thr Leu Phe Pro Ser Gly Thr Arg
          100

```

<210> 3369

<211> 1405

<212> DNA

<213> Homo sapiens

<400> 3369

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cttggtccag ggaaaagctt tcagcagcaa agggaagcca tgaacaaac catagaagaa
60
gataaggagc agaaaaatca ggaaaactgt ggtgcaaaga agaataaaaa gaagaggaaa
120
aagggttttat ataatgccaa taaaaatgat gattatgaca acgaggagat cttaacctat
180
gaggaaatgt cactttatca tcagccagca aataggaaga gacctatcat cttgattggt
240
ccacagaact gtggccagaa tgaattgcgt cagaggctca tgaacaaaga aaaggaccgc
300
tttgcatctg cagttcctca tacaaccggg agtaggcgag accaagaagt agccggtaga
360
gattaccact ttgtttcgcg gcaagcattc gaggcagaca tagcagctgg aaagttcatt
420
gagcatgggtg aatttgagaa gaatttgtat ggaactagca tagattctgt acggcaagtg
480
atcaactctg gcaaaatatg tcttttaagt cttcgtacac agtcattgaa gactctccgg
540
aattcagatt tgaaccata tattatcttc attgcacccc cttcacaaga aagacttcgg
600
gcattattgg ccaaagaagg caagaatcca aagcctgaag agttgagaga aatcattgag
660
aagacaagag agatggagca gaacaatggc cactactttg atacggcaat tgtgaattcc
720
gatcttgata aagcctatca ggaattgctt aggttaatta acaaacttga tactgaacct
780
cagtgggtac catccacttg gctgaggtga aagaaacatc cattctgtgg catgttgga
840
ttgatctggc aaaaactgcc aataggagga ctgcccgaca ctgcagcaag attgaggata
900

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agatggaagg cagcagtata agctgtagat ctgttcttag atctcttgaa ttagtgagac
 960
 gacagttccc ttaggcagtt tgtgcatggc atcctttatt ctctatacat ggcttttagcg
 1020
 gttcttgccct cattttggga ttctaaatgg aagctttcaa cagagcattc cattttgtcc
 1080
 tgttaaaacc ttttgttttc acctaaaccc tttctgctta gttgtatctc tgtgaaaaac
 1140
 ttgtatacac aagcgtccat gtctcacaca aatattgatg tgattattct taagtgttaa
 1200
 atcattaaca cttaaagac ttcatggga atattgagca gagggactgt gcttctatgc
 1260
 actgggcaag gcagtatttg cttaggaaac taatttagtc atcagagata ctttcctaaa
 1320
 aaggaaaaat aaaaaacaaa atgggtgccac ttggggtga agctactttg ttaggcttga
 1380
 attcatttat atgtcttttg attct
 1405

<210> 3370

<211> 269

<212> PRT

<213> Homo sapiens

<400> 3370

Leu	Val	Pro	Gly	Lys	Ser	Phe	Gln	Gln	Gln	Arg	Glu	Ala	Met	Lys	Gln
1				5					10					15	
Thr	Ile	Glu	Glu	Asp	Lys	Glu	Gln	Lys	Asn	Gln	Glu	Asn	Cys	Gly	Ala
			20					25					30		
Lys	Lys	Asn	Lys	Lys	Lys	Arg	Lys	Lys	Val	Leu	Tyr	Asn	Ala	Asn	Lys
		35				40						45			
Asn	Asp	Asp	Tyr	Asp	Asn	Glu	Glu	Ile	Leu	Thr	Tyr	Glu	Glu	Met	Ser
	50				55					60					
Leu	Tyr	His	Gln	Pro	Ala	Asn	Arg	Lys	Arg	Pro	Ile	Ile	Leu	Ile	Gly
65				70					75					80	
Pro	Gln	Asn	Cys	Gly	Gln	Asn	Glu	Leu	Arg	Gln	Arg	Leu	Met	Asn	Lys
			85					90					95		
Glu	Lys	Asp	Arg	Phe	Ala	Ser	Ala	Val	Pro	His	Thr	Thr	Arg	Ser	Arg
			100					105					110		
Arg	Asp	Gln	Glu	Val	Ala	Gly	Arg	Asp	Tyr	His	Phe	Val	Ser	Arg	Gln
		115					120					125			
Ala	Phe	Glu	Ala	Asp	Ile	Ala	Ala	Gly	Lys	Phe	Ile	Glu	His	Gly	Glu
		130				135					140				
Phe	Glu	Lys	Asn	Leu	Tyr	Gly	Thr	Ser	Ile	Asp	Ser	Val	Arg	Gln	Val
145				150					155					160	
Ile	Asn	Ser	Gly	Lys	Ile	Cys	Leu	Leu	Ser	Leu	Arg	Thr	Gln	Ser	Leu
			165					170					175		
Lys	Thr	Leu	Arg	Asn	Ser	Asp	Leu	Lys	Pro	Tyr	Ile	Ile	Phe	Ile	Ala
			180				185						190		
Pro	Pro	Ser	Gln	Glu	Arg	Leu	Arg	Ala	Leu	Leu	Ala	Lys	Glu	Gly	Lys
		195				200						205			
Asn	Pro	Lys	Pro	Glu	Glu	Leu	Arg	Glu	Ile	Ile	Glu	Lys	Thr	Arg	Glu
	210					215					220				
Met	Glu	Gln	Asn	Asn	Gly	His	Tyr	Phe	Asp	Thr	Ala	Ile	Val	Asn	Ser

<400> 3372

Gly	Thr	Ala	Val	Arg	Val	Val	Leu	Val	Pro	Ala	Phe	Ala	Leu	Ala	Lys
1				5					10					15	
Glu	Ala	Pro	Arg	Glu	His	Leu	Asp	His	Gln	Ala	Ala	His	Gln	Pro	Phe
			20					25					30		
Pro	Arg	Pro	Arg	Phe	Arg	Gln	Glu	Thr	Gly	His	Pro	Ser	Leu	Gln	Arg
		35					40					45			
Asp	Phe	Pro	Arg	Ser	Phe	Leu	Leu	Asp	Leu	Pro	Asn	Phe	Pro	Asp	Leu

```

      50              55              60
Ser Lys Ala Asp Ile Asn Gly Gln Asn Pro Asn Ile Gln Val Thr Ile
65              70              75              80
Glu Val Val Asp Gly Pro Asp Ser Glu Ala Asp Lys Asp Gln His Pro
      85              90              95
Glu Asn Lys Pro Ser Trp Ser Val Pro Ser Pro Asp Trp Arg Ala Trp
      100             105             110
Trp Gln Arg Ser Leu Ser Leu Ala Arg Ala Asn Ser Gly Asp Gln Asp
      115             120             125
Tyr Lys Tyr Asp Ser Thr Ser Asp Asp Ser Asn Phe Leu Asn Pro Pro
      130             135             140
Arg Gly Trp Asp His Thr Ala Pro Gly His Arg Thr Phe Glu Thr Lys
      145             150             155             160
Asp Gln Pro Glu Tyr Asp Ser Thr Asp Gly Glu Gly Asp Trp Ser Leu
      165             170             175
Trp Ser Val Cys Ser Val Thr Cys Gly Asn Gly Asn Gln Lys Arg Thr
      180             185             190
Arg Ser Cys Gly Tyr Ala
      195

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<210> 3373

<211> 726

<212> DNA

<213> Homo sapiens

<400> 3373

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tgtacatggt ttctctgggc tgacaggggc cctgcccttg gggcactgag ccctccctgt
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gggtcctcga acagaagcca gggctctgtgc ggcacccacc agctgctggg ccatggcgga
120
gtgttctggt gcgggccagc gcctgaccgg tgcgggcggc ctcaggagag gagagcttgc
180
tcagtgcgtc acgtatgcag ggctcaggct ggggcccggc tccagagcct ggtcacattc
240
ccaagcttca ttctcttcac ctgtgaattg caggcttccc tgggtgtgccc tgcacatgag
300
ggaagacaca cctgaagcac tgggtccctc catggccttg ggccgcagga accgtgggag
360
cagcagcttg ggaaggacat gtcggaggcc ggcgcctgtg cgggcagaag ctgtgtcctc
420
cagcccttcc accaccagca tggtctcatt tccaggtttc tctgtttaa aaacaaaagt
480
agcgcacatcgg tggctctcac gacgtacacc cagaagcacc cgtccatcga ggacgggcct
540
ccgtttgtgg agccgctgct taacttcac tggttcctgc tgctggctgt ggacgggtgc
600
gtcttgggat cctgcagggg gagggggctg tgaatgtgcg ggttgtgtgt agacgtgggt
660
tggatagctg tgtgggtgtg tgtgcaagt tagccatggt gtgggtagcc gtgtgggtat
720
atgcat
726

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<210> 3374

<211> 84
 <212> PRT
 <213> Homo sapiens

<400> 3374
 Met Ser Glu Ala Gly Ala Cys Ala Gly Arg Ser Cys Val Leu Gln Pro
 1 5 10 15
 Phe His His Gln His Val Leu Ile Ser Arg Phe Leu Cys Leu Lys Asn
 20 25 30
 Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro
 35 40 45
 Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile
 50 55 60
 Trp Phe Leu Leu Leu Ala Val Asp Gly Cys Val Leu Gly Ser Cys Arg
 65 70 75 80
 Gly Arg Gly Leu

<210> 3375
 <211> 393
 <212> DNA
 <213> Homo sapiens

<400> 3375
 acgcgtgcat acgtgatctc atgtttgcac acatgtgtcc atgcagatgc atgctctcac
 60
 gcacatgtgc ccacacactc agcactcaca ccccgctctg caggctcagc cccactcctg
 120
 agccacctgc ctgggctttg ggggcccagc cggcatgggg agccccaggc tccagctggc
 180
 ctgccttggc tctgaaatct aggccaggat gcagagcccg cagtgcggcc agtggagccc
 240
 ctggtactgt gcgcagcccc cacctggcag ccccttttcc tgtcaaagcc cctcccagcg
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 360
 cttgcccagc atccccggcc tgcattctcac cag
 393

<210> 3376
 <211> 103
 <212> PRT
 <213> Homo sapiens

<400> 3376
 Met Phe Ala His Met Cys Pro Cys Arg Cys Met Leu Ser Arg Thr Cys
 1 5 10 15
 Ala His Thr Leu Ser Thr His Thr Pro Ser Cys Arg Leu Ser Pro Thr
 20 25 30
 Pro Glu Pro Pro Ala Trp Ala Leu Gly Ala Gln Pro Ala Trp Gly Ala
 35 40 45
 Pro Gly Ser Ser Trp Pro Arg Leu Ala Leu Lys Ser Arg Pro Gly Cys
 50 55 60
 Arg Ala Arg Ser Ala Ala Ser Gly Ala Pro Gly Thr Val Arg Ser Pro

65 70 75 80
 His Leu Ala Ala Pro Phe Pro Val Lys Ala Pro Pro Ser Val Leu Ser
 85 90 95
 Pro Pro Gly Lys Leu Pro Ala
 100

<210> 3377

<211> 5235

<212> DNA

<213> Homo sapiens

<400> 3377

ngtcgacatc ttggtctccg gtcttgggcc tgtttaagaa tcctggcatc acgtgtggcg
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 aggacatggc tgatcagttt tctgacagaa gtgggtaaat ttccgcgttg gtaaatttcc
 120
 tgacaggaaa ttctggggaa ctaaaaaggc tggaagaaca tgaagatgga gcagtcataa
 180
 accaccact caaggacat ctccttcacg accatccaca cgagactcag attgtctgaa
 240
 ttgagctatc gcaacttaat gctaaaagct ccttaaagct acagatttat gacatagttc
 300
 cttccaaaat attacatcat aaatcattga gaagattaaa aaaaaacact tgaagaaatt
 360
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<210> 3378

<211> 970

<212> PRT

<213> Homo sapiens

<400> 3378

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Thr	Gln	Ile	Gly	Gln	Tyr	Gly	Asn	Gly	Leu	Lys	Ser	Gly	Ser	Met	Arg
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Ile	Gly	Lys	Asp	Phe	Ile	Leu	Phe	Thr	Lys	Lys	Glu	Asp	Thr	Met	Thr
	50				55						60				
Cys	Leu	Phe	Leu	Ser	Arg	Thr	Phe	His	Glu	Glu	Glu	Gly	Ile	Asp	Glu
65				70					75					80	
Val	Ile	Val	Pro	Leu	Pro	Thr	Trp	Asn	Ala	Arg	Thr	Arg	Glu	Pro	Val
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Thr	Asp	Asn	Val	Glu	Lys	Phe	Ala	Ile	Glu	Thr	Glu	Leu	Ile	Tyr	Lys
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Tyr	Ser	Pro	Phe	Arg	Thr	Glu	Glu	Glu	Val	Met	Thr	Gln	Phe	Met	Lys
	115					120					125				
Ile	Pro	Gly	Asp	Ser	Gly	Thr	Leu	Val	Ile	Ile	Phe	Asn	Leu	Lys	Leu
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Met	Asp	Asn	Gly	Glu	Pro	Glu	Leu	Asp	Ile	Ile	Ser	Asn	Pro	Arg	Asp
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Ile	Gln	Met	Ala	Glu	Thr	Ser	Pro	Glu	Gly	Thr	Lys	Pro	Glu	Arg	Arg

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Ser Phe Arg Ala Tyr Ala Ala Val Leu Tyr Ile Asp Pro Arg Met Arg
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Ile Phe Ile His Gly His Lys Val Gln Thr Lys Arg Leu Ser Cys Cys
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Leu Tyr Lys Pro Arg Met Tyr Lys Tyr Thr Ser Ser Arg Phe Lys Thr
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Arg Ala Glu Gln Glu Val Arg Ile Ala Val His Val Ala Arg Ile Ala
225      230      235
Glu Glu Lys Ala Arg Glu Ala Glu Ser Lys Ala Arg Thr Leu Glu Val
245      250      255
Arg Leu Gly Gly Asp Leu Thr Arg Asp Ser Arg Val Met Leu Arg Gln
260      265      270
Val Gln Asn Arg Ala Ile Thr Leu Arg Arg Glu Ala Asp Val Lys Lys
275      280      285
Arg Ile Lys Glu Ala Lys Gln Arg Ala Leu Lys Glu Pro Lys Glu Leu
290      295      300
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305      310      315
Phe Ile Tyr Asn Cys Ser Arg Leu Ile Lys Met Tyr Glu Lys Val Gly
325      330      335
Pro Gln Leu Glu Gly Gly Met Ala Cys Gly Gly Val Val Gly Val Val
340      345      350
Asp Val Pro Tyr Leu Val Leu Glu Pro Thr His Asn Lys Gln Asp Phe
355      360      365
Ala Asp Ala Lys Glu Tyr Arg His Leu Leu Arg Ala Met Gly Glu His
370      375      380
Leu Ala Gln Tyr Trp Lys Asp Ile Ala Ile Ala Gln Arg Gly Ile Ile
385      390      395
Lys Phe Trp Asp Glu Phe Gly Tyr Leu Ser Ala Asn Trp Asn Gln Pro
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Pro Ser Ser Glu Leu Arg Tyr Lys Arg Arg Arg Ala Met Glu Ile Pro
420      425      430
Thr Thr Ile Gln Cys Asp Leu Cys Leu Lys Trp Arg Thr Leu Pro Phe
435      440      445
Gln Leu Ser Ser Val Glu Lys Asp Tyr Pro Asp Thr Trp Val Cys Ser
450      455      460
Met Asn Pro Asp Pro Glu Gln Asp Arg Cys Glu Ala Ser Glu Gln Lys
465      470      475
Gln Lys Val Pro Leu Gly Thr Phe Arg Lys Asp Met Lys Thr Gln Glu
485      490      495
Glu Lys Gln Lys Gln Leu Thr Glu Lys Ile Arg Gln Gln Gln Glu Lys
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Leu Glu Ala Leu Gln Lys Thr Thr Pro Ile Arg Ser Gln Ala Asp Leu
515      520      525
Lys Lys Leu Pro Leu Glu Val Thr Thr Arg Pro Ser Thr Glu Glu Pro
530      535      540
Val Arg Arg Pro Gln Arg Pro Arg Ser Pro Pro Leu Pro Ala Val Ile
545      550      555
Arg Asn Ala Pro Ser Arg Pro Pro Ser Leu Pro Thr Pro Arg Pro Ala
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Ser Gln Pro Arg Lys Ala Pro Val Ile Ser Ser Thr Pro Lys Leu Pro
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Ala Leu Ala Ala Arg Glu Glu Ala Ser Thr Ser Arg Leu Leu Gln Pro

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Pro Glu Ala Pro Arg Lys Pro Ala Asn Thr Leu Val Lys Thr Ala Ser
  610              615              620
Arg Pro Ala Pro Leu Val Gln Gln Leu Ser Pro Ser Leu Leu Pro Asn
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Ser Lys Ser Pro Arg Glu Val Pro Ser Pro Lys Val Ile Lys Thr Pro
      645              650              655
Val Val Lys Lys Thr Glu Ser Pro Ile Lys Leu Ser Pro Ala Thr Pro
      660              665              670
Ser Arg Lys Arg Ser Val Ala Val Ser Asp Glu Glu Glu Val Glu Glu
      675              680              685
Glu Ala Glu Arg Arg Lys Glu Arg Cys Lys Arg Gly Arg Phe Val Val
      690              695              700
Lys Glu Glu Lys Lys Asp Ser Asn Glu Leu Ser Asp Ser Ala Gly Gly
  705              710              715              720
Glu Asp Ser Ala Asp Leu Lys Arg Ala Gln Lys Asp Lys Gly Leu His
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Val Glu Val Arg Val Asn Arg Glu Trp Tyr Thr Gly Arg Val Thr Ala
      740              745              750
Val Glu Val Gly Lys His Val Val Arg Trp Lys Val Lys Phe Asp Tyr
      755              760              765
Val Pro Thr Asp Thr Thr Pro Arg Asp Arg Trp Val Glu Lys Gly Ser
      770              775              780
Glu Asp Val Arg Leu Met Lys Pro Pro Ser Pro Glu His Gln Ser Leu
  785              790              795              800
Asp Thr Gln Gln Glu Gly Gly Glu Glu Glu Val Gly Pro Val Ala Gln
      805              810              815
Gln Ala Ile Ala Val Ala Glu Pro Ser Thr Ser Glu Cys Leu Arg Ile
      820              825              830
Glu Pro Asp Thr Thr Ala Leu Ser Thr Asn His Glu Thr Ile Asp Leu
      835              840              845
Leu Val Gln Ile Leu Arg Asn Cys Leu Arg Tyr Phe Leu Pro Pro Ser
      850              855              860
Phe Pro Ile Ser Lys Lys Gln Leu Ser Ala Met Asn Ser Asp Glu Leu
  865              870              875              880
Ile Ser Phe Pro Leu Lys Glu Tyr Phe Lys Gln Tyr Glu Val Gly Leu
      885              890              895
Gln Asn Leu Cys Asn Ser Tyr Gln Ser Arg Ala Asp Ser Arg Ala Lys
      900              905              910
Ala Ser Glu Glu Ser Leu Arg Thr Ser Glu Arg Lys Leu Arg Glu Thr
      915              920              925
Glu Glu Lys Leu Gln Lys Leu Arg Thr Asn Ile Val Ala Leu Leu Gln
      930              935              940
Lys Val Gln Glu Asp Ile Asp Ile Asn Thr Asp Asp Glu Leu Asp Ala
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Tyr Ile Glu Asp Leu Ile Thr Lys Gly Asp
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<210> 3379

<211> 898

<212> DNA

<213> Homo sapiens

<400> 3379

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<211> 299

<212> PRT

<213> Homo sapiens

<400> 3380

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 20 25 30
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 35 40 45
 Ser Glu Asp Ala Leu Leu Gly Ser Glu Ile Ala Gln Val Thr Gly Asn
 50 55 60
 Asp Val Asp Ser Gly Pro Val Leu Trp Tyr Val Leu Ser Pro Ser Gly
 65 70 75 80
 Pro Gln Asp Pro Phe Ser Val Gly Arg Tyr Gly Gly Arg Val Ser Leu
 85 90 95
 Thr Gly Pro Leu Asp Phe Glu Gln Cys Asp Arg Tyr Gln Leu Gln Leu
 100 105 110
 Leu Ala His Asp Gly Pro His Glu Gly Arg Ala Xaa Leu Thr Val Leu
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 Val Glu Asp Val Asn Asp Asn Ala Pro Ala Phe Ser Gln Ser Leu Tyr


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Gln Val Met Leu Leu Glu His Thr Pro Pro Gly Ser Ala Ile Leu Ser
145              150              155              160
Val Ser Ala Thr Asp Arg Asp Ser Gly Ala Asn Gly His Ile Ser Tyr
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His Leu Ala Ser Pro Ala Asp Gly Phe Ser Val Asp Pro Asn Asn Gly
      180              185              190
Thr Leu Phe Thr Ile Val Gly Thr Leu Ala Leu Gly His Asp Gly Ser
      195              200              205
Gly Ala Val Asp Val Val Leu Glu Ala Arg Asp His Gly Ala Pro Val
      210              215              220
Arg Ala Ala Arg Ala Thr Val Asn Val Gln Leu Arg Asp Gln Asn Asp
225              230              235              240
His Ala Pro Ser Phe Thr Leu Phe His Tyr Arg Val Ala Val Thr Glu
      245              250              255
Asp Leu Pro Pro Gly Ser Thr Leu Leu Thr Leu Glu Ala Thr Asp Ala
      260              265              270
Asp Gly Ser Arg Ser His Ala Ala Val Asp Tyr Ser Ile Ile Ser Gly
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<210> 3381

<211> 1379

<212> DNA

<213> Homo sapiens

<400> 3381

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<210> 3382

<211> 279

<212> PRT

<213> Homo sapiens

<400> 3382

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Glu	Glu	Glu	Gln	Glu	Glu	Ser	Glu	Glu	Ala	Ala	Cys	Gly	Ser	Lys	Lys
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Arg	Val	Val	Pro	Gly	Ile	Val	Tyr	Leu	Gly	His	Ile	Pro	Pro	Arg	Phe
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Arg	Pro	Leu	His	Val	Arg	Asn	Leu	Leu	Ser	Ala	Tyr	Gly	Glu	Val	Gly
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Arg	Val	Phe	Phe	Gln	Ala	Glu	Asp	Arg	Phe	Val	Arg	Arg	Lys	Lys	Lys
				85					90					95	
Ala	Ala	Ala	Ala	Ala	Gly	Gly	Lys	Lys	Arg	Ser	Tyr	Thr	Lys	Asp	Tyr
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Phe	Arg	Tyr	Asp	Leu	Trp	Asn	Leu	Lys	Tyr	Leu	His	Arg	Phe	Thr	Trp
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			180					185					190		
Leu	Gln	Ser	Val	Glu	Arg	Gly	Gln	Arg	Phe	Leu	Ala	Ala	Asp	Gly	Asp
	195						200					205			
Pro	Ala	Arg	Pro	Asp	Gly	Ser	Trp	Thr	Phe	Ala	Gln	Arg	Pro	Thr	Glu

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225              230              235              240
Ala Arg Leu Ala Thr Ala Gln Asp Lys Ala Arg Ser Asn Lys Gly Leu
      245              250              255
Leu Ala Arg Ile Phe Gly Ala Pro Pro Pro Ser Glu Ser Met Glu Gly
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<210> 3383
<211> 309
<212> DNA
<213> Homo sapiens

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120
aaatgctcac ttcttaacct cttttgtcct ggagcataga attactgcaa atgctcaccc
180
ctgggagctg tcctgcccc gatctccac acaaacactc cagcatgaaa gagcgagact
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caatctcaaa aaaaaaagt ttcgggcacc tgaacaggaa ctggtttcca tcatcaactc
300
agaaagccc
309

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<210> 3384
<211> 94
<212> PRT
<213> Homo sapiens

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<400> 3384
Met Leu Ala His His Gly Ser Arg Glu Lys Cys Gln Cys Cys Leu His
1              5              10              15
Thr Asn Phe Val Ala Gly Val Ser Ile Val Val Ile Cys Val Ile Gly
      20              25              30
Asn Ala His Phe Leu Thr Ser Phe Val Leu Glu His Arg Ile Thr Ala
      35              40              45
Asn Ala His Pro Trp Glu Leu Ser Cys Pro Arg Ser Pro Thr Gln Thr
      50              55              60
Leu Gln His Glu Arg Ala Arg Leu Asn Leu Lys Lys Lys Lys Phe Arg
65              70              75              80
Ala Pro Glu Gln Glu Leu Val Ser Ile Ile Asn Ser Glu Ser
      85              90

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<210> 3385
<211> 720
<212> DNA
<213> Homo sapiens

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<400> 3385

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 120
 gtgaaaacag tgacgggtgcg ggggtgggga gcactgcggt ccacttcttc agccccccac
 180
 tatcctggaa gcttcagggt gggcccagg cagcctccag ctccagcgac caccctgtt
 240
 cctcttgcca ggttctttgt gaacttcccc tcggccaagc agtacttcag ccagttcaag
 300
 cacatggagg atccccctga gatggagcgg agccccagc tcggaagca cgccctgccga
 360
 gtcagggggg ccctcaacac tgctgtggag aacctgcag accccgacaa ggtgtctct
 420
 gtgctcgccc ttgtggggaa agcccacgcc ctcaagcaca aggtggaacc ggtgtacttc
 480
 aagatcctct ctggggtcac tctggagggtg gtcgcccagg aatttgccag tgacttccca
 540
 cctgagacgc agagagcctg ggccaagctg cgtggcctca tctacagcca cgtgaccgct
 600
 gcctacaagg aagtgggctg ggtgcagcag gtccccaacg ccaccacccc accggccaca
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 720

<210> 3386

<211> 188

<212> PRT

<213> Homo sapiens

<400> 3386

Met	Val	Val	Lys	Thr	Val	Thr	Val	Arg	Gly	Trp	Gly	Ala	Leu	Arg	Ser
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Thr	Ser	Ser	Ala	Pro	His	Tyr	Pro	Gly	Ser	Phe	Arg	Val	Gly	Pro	Arg
			20					25					30		
Gln	Pro	Pro	Ala	Ser	Ala	Thr	Thr	Pro	Val	Pro	Leu	Ala	Arg	Phe	Phe
			35				40					45			
Val	Asn	Phe	Pro	Ser	Ala	Lys	Gln	Tyr	Phe	Ser	Gln	Phe	Lys	His	Met
	50					55				60					
Glu	Asp	Pro	Leu	Glu	Met	Glu	Arg	Ser	Pro	Gln	Leu	Arg	Lys	His	Ala
65					70					75				80	
Cys	Arg	Val	Met	Gly	Ala	Leu	Asn	Thr	Val	Val	Glu	Asn	Leu	His	Asp
			85					90						95	
Pro	Asp	Lys	Val	Ser	Ser	Val	Leu	Ala	Leu	Val	Gly	Lys	Ala	His	Ala
			100					105					110		
Leu	Lys	His	Lys	Val	Glu	Pro	Val	Tyr	Phe	Lys	Ile	Leu	Ser	Gly	Val
			115				120					125			
Ile	Leu	Glu	Val	Val	Ala	Glu	Glu	Phe	Ala	Ser	Asp	Phe	Pro	Pro	Glu
	130					135					140				
Thr	Gln	Arg	Ala	Trp	Ala	Lys	Leu	Arg	Gly	Leu	Ile	Tyr	Ser	His	Val
145					150					155				160	
Thr	Ala	Ala	Tyr	Lys	Glu	Val	Gly	Trp	Val	Gln	Gln	Val	Pro	Asn	Ala
			165					170						175	
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180

185

<210> 3387

<211> 3299

<212> DNA

<213> Homo sapiens

<400> 3387

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120
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180
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240
cgagaagaag taagtgcgc cggctgcggc gggccgagga tcaccattaa caaggacacc
300
aaggtaccca atgcctgttt attcaccatc aacaaagaag accacacact gggaaacatc
360
attaaatcac aactcctaaa agaccgcga gtgctatttg ctggctacaa agtccccac
420
cccttgaggc acaagatcat catccgagtg cagaccacgc cggactacag cccccaggaa
480
gcctttacca acgcatcac cgacctcgc agtgagctgt ccctgctgga ggagcgcttt
540
cgggtggcca taaaagacaa gcaggaagga attgagtagg ggccagaggg ggctctgctc
600
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660
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720
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840
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1020
cctgggcctg cctgtcagtc aaagcaggaa cacttcttcc tgcataactc gaaacacctt
1080
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1140
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1200
tgtgaggcta catcctcccc cagatggcta cgatgttga gtccgtcagg gcggtgaggt
1260
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1320
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1380

2565

ggggtggctg cttcaggatg ttgctgacgt cgtagagcca cacgttgccc tcctcatccc
1440
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1500
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1560
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1680
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1920
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1980
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2040
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2160
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2580
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2760
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2940
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3000

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 3120
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 3180
 gtcggccacc ccggcgtgtg gcgtcgccct gcgtctcctg gagcccgga ctggcgctccg
 3240
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 3299

<210> 3388

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3388

Ser Gly Arg Gly Leu Leu Gly Leu Trp Trp Arg Arg Arg Arg Thr
 1 5 10 15
 Leu Gly Val Trp Thr Gln Arg Arg Arg Glu His Glu Arg Pro Ser Ser
 20 25 30
 Leu Arg Val Val Leu Ala Leu Arg Gly Arg Glu Glu Val Ser Asp Ala
 35 40 45
 Gly Cys Gly Gly Pro Arg Ile Thr Ile Asn Lys Asp Thr Lys Val Pro
 50 55 60
 Asn Ala Cys Leu Phe Thr Ile Asn Lys Glu Asp His Thr Leu Gly Asn
 65 70 75 80
 Ile Ile Lys Ser Gln Leu Leu Lys Asp Pro Gln Val Leu Phe Ala Gly
 85 90 95
 Tyr Lys Val Pro His Pro Leu Glu His Lys Ile Ile Ile Arg Val Gln
 100 105 110
 Thr Thr Pro Asp Tyr Ser Pro Gln Glu Ala Phe Thr Asn Ala Ile Thr
 115 120 125
 Asp Leu Ile Ser Glu Leu Ser Leu Leu Glu Glu Arg Phe Arg Val Ala
 130 135 140
 Ile Lys Asp Lys Gln Glu Gly Ile Glu
 145 150

<210> 3389

<211> 308

<212> DNA

<213> Homo sapiens

<400> 3389

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 120
 gacgggcctc cgtttgtgga gccgctgctt aacttcattt ggttcctgct gctggctgtg
 180
 gacggggaac cttctgacca gcctcatggg ctctcagag caggaggatg gggaggagag
 240
 ccccagcgac ggcagcccca tcgagctgga ctgaactggc caggccacgt ggagacacca
 300

cggtcgac

308

<210> 3390

<211> 102

<212> PRT

<213> Homo sapiens

<400> 3390

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Xaa Val Ser Lys Pro Phe His His Gln His Val Leu Ile Ser Arg Phe
 1           5           10           15
Leu Cys Leu Lys Asn Lys Ser Ser Ala Ser Val Val Phe Thr Thr Tyr
      20           25           30
Thr Gln Lys His Pro Ser Ile Glu Asp Gly Pro Pro Phe Val Glu Pro
      35           40           45
Leu Leu Asn Phe Ile Trp Phe Leu Leu Leu Ala Val Asp Gly Glu Pro
      50           55           60
Ser Asp Gln Pro His Gly Leu Leu Arg Ala Gly Gly Trp Gly Gly Glu
65           70           75           80
Pro Gln Arg Arg Gln Pro His Arg Ala Gly Leu Asn Trp Pro Gly His
      85           90           95
Val Glu Thr Pro Arg Ser
      100

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<210> 3391

<211> 1295

<212> DNA

<213> Homo sapiens

<400> 3391

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gaagccctaa gtgacagttc agagcgtctt ttctcctttg gcgtcatcgc agatgttcaa
120
tttgcagact tagaagatgg ctttaatttc caaggaacca ggcggcgata ctacagacat
180
agtcttcttc acttacaggg tgccattgaa gactggaata atgaaagcag catgccctgt
240
tgtgtccttc agcttggaga tatcatcgat ggatataatg cacagtataa tgcattccaa
300
aagtccttag aacttggtat ggacatgttc aagaggctta aagttccagt tcatcataca
360
tggggaaacc atgaattcta taacttcagt agagagtatt taacacactc taaacttaac
420
actaagtttc tagaagatca gattgtacat catcctgaga ccatgccttc agaagattat
480
tatgcttata attttgtacc attccctaaa ttccggttca ttttacttga tgcatatgac
540
ttgagtgtct tgggcgtgga tcagtcttct ccaaatacag agcagtgtat gaagatattg
600
agggagcaca atccaaatac ggaactgaat agtcctcaag gactttctga gccccagttt
660
gtccagttta atggaggatt cagccaagaa cagctaaact ggttgaatga agtgctaaca
720

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ttctctgaca caaaccaaga aaaggtggtg attgtgagcc atcttcccat ttaccggac
 780
 gcctctgaca atgtgtgcct ggcttgaac tacagagatg cctggcagt catttggct
 840
 catgagtgtg tgggtgtgtt ctttctggt cacacccatg atgggtggcta ctctgaggat
 900
 ccttttgggtg tataccacgt caacctagaa ggagttattg aaacagctcc agacagccaa
 960
 gcctttggca cagttcatgt ctatcctgac aaaatgatgt tgaaaggag aggcagagtt
 1020
 ccagatagaa ttatgaatta caagaaagaa agagccttcc attgttagtc taatttattt
 1080
 taacttgata gaaaatgagc tttgtgtttg tccctcctaa acaaaaaaat aaaaatcctc
 1140
 tgtctcattg tttagtattc agcttgcata acaaaatgta tttatagttt cagtgtgtga
 1200
 tggttgataa aatactcaga aatgttattt tggatcatgt atccattgta agttagaaac
 1260
 aaaccaggga ggaaactgag gcaggggtgt atagt
 1295

<210> 3392

<211> 355

<212> PRT

<213> Homo sapiens

<400> 3392

Ile	Val	Phe	Leu	Leu	Tyr	Leu	Glu	Thr	Cys	Leu	Glu	Val	Met	Asp	Asp
1			5					10					15		
Lys	Pro	Asn	Pro	Glu	Ala	Leu	Ser	Asp	Ser	Ser	Glu	Arg	Leu	Phe	Ser
		20					25					30			
Phe	Gly	Val	Ile	Ala	Asp	Val	Gln	Phe	Ala	Asp	Leu	Glu	Asp	Gly	Phe
	35					40					45				
Asn	Phe	Gln	Gly	Thr	Arg	Arg	Tyr	Tyr	Arg	His	Ser	Leu	Leu	His	
	50			55					60						
Leu	Gln	Gly	Ala	Ile	Glu	Asp	Trp	Asn	Asn	Glu	Ser	Ser	Met	Pro	Cys
65			70					75					80		
Cys	Val	Leu	Gln	Leu	Gly	Asp	Ile	Ile	Asp	Gly	Tyr	Asn	Ala	Gln	Tyr
		85				90						95			
Asn	Ala	Ser	Lys	Lys	Ser	Leu	Glu	Leu	Val	Met	Asp	Met	Phe	Lys	Arg
	100					105					110				
Leu	Lys	Val	Pro	Val	His	His	Thr	Trp	Gly	Asn	His	Glu	Phe	Tyr	Asn
	115					120					125				
Phe	Ser	Arg	Glu	Tyr	Leu	Thr	His	Ser	Lys	Leu	Asn	Thr	Lys	Phe	Leu
	130				135					140					
Glu	Asp	Gln	Ile	Val	His	His	Pro	Glu	Thr	Met	Pro	Ser	Glu	Asp	Tyr
145			150					155					160		
Tyr	Ala	Tyr	His	Phe	Val	Pro	Phe	Pro	Lys	Phe	Arg	Phe	Ile	Leu	Leu
		165				170							175		
Asp	Ala	Tyr	Asp	Leu	Ser	Val	Leu	Gly	Val	Asp	Gln	Ser	Ser	Pro	Lys
	180					185					190				
Tyr	Glu	Gln	Cys	Met	Lys	Ile	Leu	Arg	Glu	His	Asn	Pro	Asn	Thr	Glu
	195					200					205				
Leu	Asn	Ser	Pro	Gln	Gly	Leu	Ser	Glu	Pro	Gln	Phe	Val	Gln	Phe	Asn

```

      210              215              220
Gly Gly Phe Ser Gln Glu Gln Leu Asn Trp Leu Asn Glu Val Leu Thr
225              230              235              240
Phe Ser Asp Thr Asn Gln Glu Lys Val Val Ile Val Ser His Leu Pro
      245              250              255
Ile Tyr Pro Asp Ala Ser Asp Asn Val Cys Leu Ala Trp Asn Tyr Arg
      260              265              270
Asp Ala Leu Ala Val Ile Trp Ser His Glu Cys Val Val Cys Phe Phe
      275              280              285
Ala Gly His Thr His Asp Gly Gly Tyr Ser Glu Asp Pro Phe Gly Val
      290              295              300
Tyr His Val Asn Leu Glu Gly Val Ile Glu Thr Ala Pro Asp Ser Gln
305              310              315              320
Ala Phe Gly Thr Val His Val Tyr Pro Asp Lys Met Met Leu Lys Gly
      325              330              335
Arg Gly Arg Val Pro Asp Arg Ile Met Asn Tyr Lys Lys Glu Arg Ala
      340              345              350
Phe His Cys
      355

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<210> 3393
 <211> 510
 <212> DNA
 <213> Homo sapiens

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<400> 3393
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120
agtcggggcg ggtcaactt cgagtacttg aaacgggagc actcgctgtc gaagccctac
180
caggggtgtg gcacaggcag ttctcactg tggaaatctga tgggcaatng catggtgatg
240
accagatata tccgccttac ccagatatg caaagtaaac aggggtgcctt gtggaaccgg
300
gtgccatgtt tcctgagaga ctgggagttg caggtgcact tcaaaatcca tggacaagga
360
aagaagaatc tgcattggga tggcttgga atctgtgaca caaaggatcg gatgcagcca
420
gggcctgtgt ttggaacat ggacaaattt gtggggctgg gagtatttgt agacacctac
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cccaatgagg agaagcagcc cttcacgcgt
510

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<210> 3394
 <211> 170
 <212> PRT
 <213> Homo sapiens

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<400> 3394
Xaa Arg Leu Trp Asp Pro Leu Gly Arg Gly Ser Ser Gly Gly Asp Val
1          5          10          15
Cys Arg Leu Gly Met Gly Pro Gly Xaa Val Thr Pro Ser Ser Phe Val

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<210> 3395
<211> 807
<212> DNA
<213> Homo sapiens
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2571

<210> 3396
 <211> 205
 <212> PRT
 <213> Homo sapiens

<400> 3396
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 Ser Ser Ser Leu Ser Ala Arg Met Met Ser Gly Ser Arg Gly Ser Ser
 20 25 30
 Leu Asn Asp Thr Tyr His Ser Arg Asp Ser Ser Phe Arg Leu Asp Ser
 35 40 45
 Glu Tyr Gln Ser Thr Ser Ala Ser Ala Ser Ala Ser Pro Phe Gln Ser
 50 55 60
 Ala Trp Tyr Ser Glu Ser Glu Ile Thr Gln Gly Ala Arg Ser Arg Ser
 65 70 75 80
 Gln Asn Gln Gln Arg Asp His Asp Ser Lys Arg Pro Lys Leu Ser Cys
 85 90 95
 Thr Asn Cys Thr Thr Ser Ala Gly Arg Asn Val Gly Asn Gly Leu Asn
 100 105 110
 Thr Leu Ser Asp Ser Ser Trp Arg His Ser Gln Val Pro Arg Ser Ser
 115 120 125
 Ser Met Val Leu Gly Ser Phe Gly Thr Asp Leu Met Arg Glu Arg Arg
 130 135 140
 Asp Leu Glu Arg Arg Thr Asp Ser Ser Ile Ser Asn Leu Met Asp Tyr
 145 150 155 160
 Ser His Arg Ser Gly Asp Phe Thr Thr Ser Ser Tyr Val Gln Asp Arg
 165 170 175
 Val Pro Ser Tyr Ser Gln Gly Ala Arg Pro Lys Glu Asn Ser Met Ser
 180 185 190
 Thr Leu Gln Leu Asn Thr Ser Ser Thr Asn His Gln Leu
 195 200 205

<210> 3397
 <211> 492
 <212> DNA
 <213> Homo sapiens

<400> 3397
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 120
 ccacagagag acagtggcac ctacgagcag cccagccccc tgatccatga ccgagactct
 180
 gtgggctccc agccccctct gcctccgggc ctaccccccg gccactatga ctcacccaag
 240
 aacagccaca tccctggaca ttatgacttg cctccagtac ggcacccccc atcacctcan
 300
 cttcgacgcc aggatcggtg aggagccagg atggtatggc agaggcagca anacctggct
 360
 gttgctgctc aaggctgggg acagagcata gtgtaccctt gccaggagca gggagtggac
 420

cggcaggctg tgaacatgaa caacgcttaa cagagcaagt gatgggagaa taattcatgg
 480
 cttctaccat gg
 492

<210> 3398
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 3398
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 Cys Ser Cys Ser Gln Pro Ala Gly Pro Leu Pro Ala Pro Gly Arg Gly
 20 25 30
 Thr Leu Cys Ser Val Pro Ser Leu Glu Gln Gln Gln Pro Gly Xaa Ala
 35 40 45
 Ala Ser Ala Ile Pro Ser Trp Leu Leu Asn Asp Pro Gly Val Glu Xaa
 50 55 60
 Glu Val Met Gly Asp Ala Val Leu Glu Ala Ser His Asn Val Gln Gly
 65 70 75 80
 Cys Gly Cys Ser Trp Val Ser His Ser Gly Arg Gly Val Gly Pro Glu
 85 90 95
 Ala Glu Gly Ala Gly Ser Pro Gln Ser Leu Gly His Gly Ser Gly Gly
 100 105 110
 Trp Ala Ala Arg Arg Cys His Cys Leu Ser Val Ala Gly Val Ala Ala
 115 120 125
 Ala Ser Gly Cys Pro Arg Thr Glu Glu Ala Ala Trp Gly Glu Ile Leu
 130 135 140
 Arg Glu Gly Leu Ser Ser Pro Cys Ser Cys Ser Pro Gly Pro Pro Gly
 145 150 155 160
 Lys Leu Gly

<210> 3399
 <211> 5784
 <212> DNA
 <213> Homo sapiens

<400> 3399
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 120
 cattacatca accctgcaca cgccatttct ctcctaagtg ccctgaatga ggagcgtctc
 180
 aaaggacagc tgtgtgatgt gctgctgatt gttggagacc aaaagttccg agctcataaa
 240
 aacgtcttgg ctgccagcag cgaatacttt cagagtttat tcacaaataa ggaaaatgag
 300
 tcacaaactg tatttcagct tgacttctgt gagccagatg cttttgataa tgttttaaac
 360
 tacatttatt cttcctctct atttggtgag aagagcagcc ttgctgctgt gcaagaactt
 420

ggctatagtc ttgggatttc ctttctgact aacatcgttt ctaaaacacc tcaagcccc
480
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<210> 3400

<211> 1069

<212> PRT

<213> Homo sapiens

<400> 3400

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Cys	Asp	Val	Leu	Leu	Ile	Val	Gly	Asp	Gln	Lys	Phe	Arg	Ala	His	Lys
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Asn	Val	Leu	Ala	Ala	Ser	Ser	Glu	Tyr	Phe	Gln	Ser	Leu	Phe	Thr	Asn
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Lys	Glu	Asn	Glu	Ser	Gln	Thr	Val	Phe	Gln	Leu	Asp	Phe	Cys	Glu	Pro
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Asp	Ala	Phe	Asp	Asn	Val	Leu	Asn	Tyr	Ile	Tyr	Ser	Ser	Ser	Leu	Phe
			85					90						95	
Val	Glu	Lys	Ser	Ser	Leu	Ala	Ala	Val	Gln	Glu	Leu	Gly	Tyr	Ser	Leu
		100					105						110		
Gly	Ile	Ser	Phe	Leu	Thr	Asn	Ile	Val	Ser	Lys	Thr	Pro	Gln	Ala	Pro
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Phe	Pro	Thr	Cys	Pro	Asn	Arg	Lys	Lys	Val	Phe	Val	Glu	Asp	Asp	Glu
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Lys	Ser	Trp	Pro	Lys	Asp	Ser	Ser	Val	Val	Tyr	Ala	Lys	Ser	Leu	Glu
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Ser Glu Thr Pro Tyr Leu Leu Lys Glu Thr Asn Lys Gly Asn Gly Gln
          290          295          300
Gly Glu Asp Arg Asn Leu Leu Tyr Tyr Ser Lys Leu Gly Leu Val Ile
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Pro Leu Val Lys Ser Leu Leu Arg Arg Ser Leu Ser Met Asp Ser Gln
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Val Pro Val Tyr Ser Pro Ser Ile Asp Leu Lys Ser Ser Gln Gly Ser
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Ser Ser Val Ser Ser Asp Ala Pro Gly Asn Val Leu Cys Ala Leu Ser
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Gln Lys Ser Ser Leu Lys Asp Cys Ser Glu Lys Thr Ala Leu Asp Asp
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Gln Ser Thr Asp Arg Glu Gly Ala Ser Pro Val Thr Glu Val Arg Ile
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Lys Thr Glu Pro Ser Ser Pro Leu Ser Asp Pro Ser Asp Ile Ile Arg
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Val Thr Val Gly Asp Ala Ala Thr Thr Ala Ala Ala Ser Ser Ser Ser
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Pro Asn Lys Lys Phe Lys Cys Lys His Cys Leu Lys Ile Phe Arg Ser
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Thr Ala Gly Leu His Arg His Val Asn Met Tyr His Asn Pro Glu Lys
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Pro Tyr Ala Cys Asp Ile Cys His Lys Arg Phe His Thr Asn Phe Lys
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Val Trp Thr His Cys Gln Thr Gln His Gly Ile Val Lys Asn Pro Ser
          595          600          605
Pro Ala Ser Ser Ser His Ala Val Leu Asp Glu Lys Phe Gln Arg Lys
          610          615          620
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625          630          635          640
Lys Leu Arg Arg Gly Lys Pro Gly Phe Gln Gly Gln Ser Ser Ser Gln
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Ala Gln Gln Val Ile Lys Arg Asn Leu Arg Ser Arg Ala Lys Gly Ala

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Cys Pro Tyr Cys Ser Leu Arg Phe Phe Ser Pro Glu Leu Lys Gln Glu
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His Glu Ser Lys Cys Glu Tyr Lys Lys Leu Thr Cys Leu Glu Cys Met
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Arg Thr Phe Lys Ser Ser Phe Ser Ile Trp Arg His Gln Val Glu Val
785                790                795                800
His Asn Gln Asn Asn Met Ala Pro Thr Glu Asn Phe Ser Leu Pro Val
        805                810                815
Leu Asp His Asn Gly Asp Val Thr Gly Ser Ser Arg Pro Gln Ser Gln
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Pro Glu Pro Asn Lys Val Asn His Ile Val Thr Thr Lys Asp Asp Asn
        835                840                845
Val Phe Ser Asp Ser Ser Glu Gln Val Asn Phe Asp Ser Glu Asp Ser
        850                855                860
Ser Cys Leu Pro Glu Asp Leu Ser Leu Ser Lys Gln Leu Lys Ile Gln
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Val Lys Glu Glu Pro Val Glu Glu Ala Glu Glu Glu Ala Pro Glu Ala
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Ser Thr Ala Pro Lys Glu Ala Gly Pro Ser Lys Glu Ala Ser Leu Trp
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Pro Cys Glu Lys Cys Gly Lys Met Phe Thr Val His Lys Gln Leu Glu
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Cys Asn Lys Ala Phe Arg Thr Asn Phe Arg Leu Trp Ser His Phe Gln
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Ser His Met Ser Gln Ala Ser Glu Glu Ser Ala His Lys Glu Ser Glu
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Pro Pro Pro Leu Pro Lys Ile Gln Pro Leu Glu Pro Asp Ser Pro Thr
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1010                1015                1020
Gln Glu Ser Asp Thr Leu Phe Tyr His Ala Pro Pro Leu Ser Ala Ile
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Thr Phe Lys Arg Gln Phe Met Cys Lys Leu Cys His Arg Thr Phe Lys
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<211> 579

<212> DNA

<213> Homo sapiens

<400> 3401

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<210> 3402

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3402

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			20					25					30		
Val	Tyr	Thr	Arg	Leu	Gly	Glu	Met	Asn	Asn	Ala	Val	Arg	Asn	Leu	Gln
			35				40					45			
Glu	Leu	Leu	Glu	Leu	Asp	Ser	Ser	Ser	Ser	Leu	Cys	Val	Leu	Val	Ser
			50			55					60				
Thr	Val	Gly	Lys	Leu	Cys	Arg	Leu	Ile	Asn	Glu	Asp	Val	Asn	Glu	Gln
65				70					75				80		
Val	Met	Gln	Val	Leu	Gly	Pro	Glu	Asp	Leu	Gln	Ser	Ile	Ile	Tyr	Lys
			85					90					95		
Leu	Glu	Glu	His	Glu	Glu	Phe	Phe	Pro	Ala	Phe	Gln	Ala	Phe	Thr	Asn
			100					105				110			
Asp	Leu	Leu	Glu	Ile	Leu	Glu	Ile	Asp	Asp	Ser	Gly	Cys	His	Cys	Thr
			115				120					125			
Cys	Ser	Lys	Glu	Ile	Lys	Ser	Thr	Phe	Ile	Leu	Lys	Thr	Asn	Gln	Ile
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<210> 3403

<211> 1696

<212> DNA

<213> Homo sapiens

<400> 3403

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<210> 3404

<211> 286

<212> PRT

<213> Homo sapiens

<400> 3404

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Leu	Gly	Glu	Phe	Arg	Ile	Arg	Asp	Leu	Asn	Asp	Glu	Ile	Asn	Lys	Leu
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Leu	Arg	Glu	Lys	Gly	His	Trp	Glu	Val	Arg	Ile	Lys	Glu	Leu	Gly	Gly
			85					90					95		
Pro	Asp	Tyr	Gly	Lys	Val	Gly	Pro	Lys	Met	Leu	Asp	His	Glu	Gly	Lys
		100					105					110			
Glu	Val	Pro	Gly	Asn	Arg	Gly	Tyr	Lys	Tyr	Phe	Gly	Ala	Ala	Lys	Asp
		115				120					125				
Leu	Pro	Gly	Val	Arg	Glu	Leu	Phe	Glu	Lys	Xaa	Thr	Ser	Ser	Ser	Ser
	130				135						140				
Gln	Xaa	Lys	Thr	Arg	Ala	Glu	Leu	Met	Lys	Ala	Ile	Asp	Phe	Glu	Tyr
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Tyr	Gly	Tyr	Leu	Asp	Glu	Asp	Asp	Gly	Val	Ile	Val	Pro	Leu	Glu	Gln
			165					170					175		
Glu	Tyr	Glu	Lys	Lys	Leu	Arg	Ala	Glu	Leu	Val	Glu	Lys	Trp	Lys	Ala
		180					185						190		
Glu	Arg	Glu	Ala	Arg	Leu	Ala	Arg	Gly	Glu	Lys	Glu	Glu	Glu	Glu	Glu
	195					200					205				
Glu	Glu	Glu	Glu	Ile	Asn	Ile	Tyr	Ala	Val	Thr	Glu	Glu	Glu	Ser	Asp
	210				215						220				
Glu	Glu	Gly	Ser	Gln	Glu	Lys	Gly	Gly	Asp	Asp	Ser	Gln	Gln	Lys	Phe
225				230					235					240	
Ile	Ala	His	Val	Pro	Val	Pro	Ser	Gln	Gln	Glu	Ile	Glu	Glu	Ala	Leu
			245					250						255	
Val	Arg	Arg	Lys	Lys	Met	Glu	Leu	Leu	Gln	Lys	Tyr	Ala	Ser	Glu	Thr
			260				265					270			
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<210> 3405

<211> 402

<212> DNA

<213> Homo sapiens

<400> 3405

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180
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240
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300
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<210> 3406

<211> 134

<212> PRT

<213> Homo sapiens

<400> 3406

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Asp Arg Gly Leu Lys Thr Leu Glu Asn Leu Leu Ala Ser Ile Arg Lys
35     40     45
Gly Asn Ala Ile Asp Glu Ala Asp Ile Pro Pro Pro Val Ala Ile Gly
50     55     60
Lys Gly Pro Ala Ser Thr Pro Thr Tyr Ser Pro Ala Pro Thr Gln Pro
65     70     75     80
Ala Pro Arg Ile Ala Ser Ala Pro Glu Pro Arg Val Thr Leu Glu Gly
85     90     95
Pro Ser Ala Thr Ala Pro Ala Ser Ser Pro Gly Leu Ala Lys Pro Gln
100    105    110
Met Pro Pro Gly Pro Cys Ser Pro Pro Ser Gly Pro Val Ala Glu Pro
115    120    125
Pro Ala Arg Leu Gln Ala
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<210> 3407

<211> 535

<212> DNA

<213> Homo sapiens

<400> 3407

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120

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 180
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 240
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 300
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 420
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<210> 3408

<211> 131

<212> PRT

<213> Homo sapiens

<400> 3408

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Ser	Ala	Gly	Thr	Phe	Pro	Gly	His	His	Ala	Phe	Ser	Ala	Val	Arg	Gln
			20					25					30		
Val	Ala	Ala	Pro	Thr	Gly	Pro	Gly	Gly	Thr	Phe	Pro	Gly	His	Pro	Thr
		35				40					45				
Ser	Ser	Val	Ala	Arg	Gln	Val	Ala	Ala	Pro	Thr	Gly	Pro	Ala	Gly	Thr
	50				55						60				
Phe	Pro	Gly	Xaa	Pro	Gly	Leu	Leu	Gly	Lys	Gln	Val	Ala	Ala	Pro	Thr
65					70				75					80	
Gly	Pro	Gly	Gly	Thr	Phe	Pro	Gly	His	Leu	Ala	Ser	Ser	Ala	Arg	Gln
				85				90					95		
Val	Ala	Glu	Leu	Val	Pro	Arg	Leu	Ile	Phe	Leu	Arg	Gln	Thr	Cys	Leu
			100				105					110			
Gln	Arg	Lys	Leu	Cys	Ser	Thr	Gly	Glu	Thr	Gly	Lys	Cys	Thr	Arg	Tyr
		115					120					125			
Trp	Leu	Ile													
			130												

<210> 3409

<211> 959

<212> DNA

<213> Homo sapiens

<400> 3409

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 120
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 180
 cctcggccca gcgcggcccc caccgccatg gaggtgctgg agagcgggga gcagggcggtg
 240

ctgcagtggg accgcaagct gagcgagctg tcagagcccc gggacggcga ggcctcatg
 300
 taccacacgc atttctcaga atttctggat gagttttccc agaacgtctt gggtcagctc
 360
 ctgaatgatc ctttctcttc agagaagagt gtgtcaatgg aggtggaacc ttccccgacg
 420
 tccccggcgc ctctcatcca ggctgagcac agctactccc tgtgcgagga gcctcggggc
 480
 cagtcgcctt tcaccacat taccaccagt gacagcttca atgacgatga ggtggaaagt
 540
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 660
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 720
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 780
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 840
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<210> 3410

<211> 144

<212> PRT

<213> Homo sapiens

<400> 3410

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Lys	Leu	Ser	Glu	Leu	Ser	Glu	Pro	Gly	Asp	Gly	Glu	Ala	Leu	Met	Tyr
			20					25					30		
His	Thr	His	Phe	Ser	Glu	Leu	Leu	Asp	Glu	Phe	Ser	Gln	Asn	Val	Leu
			35				40					45			
Gly	Gln	Leu	Leu	Asn	Asp	Pro	Phe	Leu	Ser	Glu	Lys	Ser	Val	Ser	Met
		50			55					60					
Glu	Val	Glu	Pro	Ser	Pro	Thr	Ser	Pro	Ala	Pro	Leu	Ile	Gln	Ala	Glu
65				70					75					80	
His	Ser	Tyr	Ser	Leu	Cys	Glu	Glu	Pro	Arg	Ala	Gln	Ser	Pro	Phe	Thr
			85				90						95		
His	Ile	Thr	Thr	Ser	Asp	Ser	Phe	Asn	Asp	Asp	Glu	Val	Glu	Ser	Xaa
			100				105						110		
Arg	Asn	Gly	Thr	Cys	Leu	Gln	Thr	Ser	Leu	Gln	His	Pro	Ser	Arg	Gln
		115				120					125				
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<210> 3411

<211> 958

<212> DNA

<213> Homo sapiens

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 240
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 480
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 780
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 840
 ccacaagcac aaactgacca agcacagagt caccagtttc catatgtaat gcaaggaaat
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 958

<210> 3412
 <211> 185
 <212> PRT
 <213> Homo sapiens

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 Thr Val Gly Lys Leu Lys Thr His Leu Ser Asn Val Tyr Pro Ser Lys
 35 40 45
 Pro Leu Thr Lys Asp Gln Arg Leu Val Tyr Ser Gly Arg Leu Leu Pro
 50 55 60
 Asp His Leu Gln Leu Lys Asp Ile Leu Arg Lys Gln Asp Glu Tyr His
 65 70 75 80
 Met Val His Leu Val Cys Thr Ser Arg Thr Pro Pro Ser Ser Pro Lys
 85 90 95
 Ser Ser Thr Asn Arg Glu Ser His Glu Ala Leu Ala Ser Ser Ser Asn

	100		105		110
Ser	Ser Ser Asp His Ser Gly Ser Thr Thr Pro Ser Ser Gly Gln Glu				
	115		120		125
Thr	Leu Ser Leu Ala Val Gly Ser Ser Ser Glu Gly Leu Arg Gln Arg				
	130		135		140
Thr	Leu Pro Gln Ala Gln Thr Asp Gln Ala Gln Ser His Gln Phe Pro				
145		150		155	160
Tyr	Val Met Gln Gly Asn Val Asp Asn Gln Phe Pro Gly Gln Ala Ala				
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Pro	Pro Gly Phe Pro Val Tyr Pro Ala				
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<210> 3413

<211> 3344

<212> DNA

<213> Homo sapiens

<400> 3413

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360
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420
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480
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540
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780
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1080

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<211> 723

<212> PRT

<213> Homo sapiens

<400> 3414

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		20						25				30			
Tyr	Gly	Cys	Val	Gln	Gln	Pro	Lys	Thr	Gln	Glu	Ser	Lys	Leu	Lys	Ile
		35					40					45			
Gly	Gly	Val	Ser	Ser	Val	Asn	Glu	Arg	Pro	Ile	Ala	Gln	Gln	Leu	Asn
		50				55					60				
Pro	Gly	Phe	Gln	Leu	Ser	Phe	Ala	Ser	Ser	Gly	Pro	Ser	Val	Leu	Leu
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Pro	Ser	Val	Pro	Ala	Val	Ala	Ile	Lys	Val	Phe	Cys	Ser	Gly	Cys	Lys
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Lys	Met	Leu	Tyr	Lys	Gly	Gln	Thr	Ala	Tyr	His	Lys	Thr	Gly	Ser	Thr
		100						105					110		
Gln	Leu	Phe	Cys	Ser	Thr	Arg	Cys	Ile	Thr	Arg	His	Ser	Ser	Pro	Ala
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Cys	Leu	Pro	Pro	Pro	Pro	Lys	Lys	Thr	Cys	Thr	Asn	Cys	Ser	Lys	Asp
		130					135					140			
Ile	Leu	Asn	Pro	Lys	Asp	Val	Ile	Thr	Thr	Arg	Phe	Glu	Asn	Ser	Tyr
145				150						155				160	
Pro	Ser	Lys	Asp	Phe	Cys	Ser	Gln	Ser	Cys	Leu	Ser	Ser	Tyr	Glu	Leu
			165						170					175	
Lys	Lys	Lys	Pro	Val	Val	Thr	Ile	Tyr	Thr	Lys	Ser	Ile	Ser	Thr	Lys
			180					185					190		
Cys	Ser	Met	Cys	Gln	Lys	Asn	Ala	Asp	Thr	Arg	Phe	Glu	Val	Lys	Tyr

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  225      230      235      240
Tyr Cys Tyr Ser Ser Ser Gly Pro Cys Gln Ser Gln Lys Val Phe Ser
      245      250      255
Ser Thr Ser Val Thr Ala Tyr Lys Gln Asn Ser Ala Gln Ile Pro Pro
      260      265      270
Tyr Ala Leu Gly Lys Ser Leu Arg Ser Ser Ala Glu Met Ile Glu Asn
      275      280      285
Thr Asn Ser Leu Gly Lys Thr Glu Leu Phe Cys Ser Ile Asn Cys Leu
      290      295      300
Ser Ala Tyr Arg Val Lys Thr Val Thr Ser Ala Gly Val Gln Val Ser
  305      310      315      320
Cys His Ser Cys Lys Thr Ser Ala Ile Pro Gln Tyr His Leu Ala Met
      325      330      335
Ser Asp Gly Thr Ile Tyr Ser Phe Cys Ser Ser Ser Cys Val Val Ala
      340      345      350
Phe Gln Asn Val Phe Ser Lys Pro Lys Gly Thr Asn Ser Ser Ala Val
      355      360      365
Pro Leu Ser Gln Gly Gln Val Val Ser Pro Pro Ser Ser Arg Ser
      370      375      380
Ala Val Ser Ile Gly Gly Gly Asn Thr Ser Ala Val Ser Pro Ser Ser
  385      390      395      400
Ile Arg Gly Ser Ala Ala Ala Ser Leu Gln Pro Leu Gly Glu Gln Ser
      405      410      415
Gln Gln Val Ala Leu Thr His Thr Val Val Lys Leu Lys Cys Gln His
      420      425      430
Cys Asn His Leu Phe Ala Thr Lys Pro Glu Leu Leu Phe Tyr Lys Gly
      435      440      445
Lys Met Phe Leu Phe Cys Gly Lys Asn Cys Ser Asp Glu Tyr Lys Lys
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Lys Asn Lys Val Val Ala Met Cys Glu Tyr Cys Lys Ile Glu Lys Ile
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Val Lys Glu Thr Val Arg Phe Ser Gly Ala Asp Lys Ser Phe Cys Ser
      485      490      495
Glu Gly Cys Lys Leu Leu Tyr Lys His Asp Leu Ala Lys Arg Trp Gly
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Asn His Cys Lys Met Cys Ser Tyr Cys Ser Gln Thr Ser Pro Asn Leu
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Val Gln Asn Arg Leu Glu Gly Lys Leu Glu Glu Phe Cys Cys Glu Asp
      530      535      540
Cys Met Ser Lys Phe Thr Val Leu Phe Tyr Gln Met Ala Lys Cys Asp
  545      550      555      560
Gly Cys Lys Arg Gln Gly Lys Leu Ser Glu Ser Ile Lys Trp Arg Gly
      565      570      575
Asn Ile Lys His Phe Cys Asn Leu Phe Cys Val Leu Glu Phe Cys His
      580      585      590
Gln Gln Ile Met Asn Asp Cys Leu Pro Gln Asn Lys Val Asn Ile Ser
      595      600      605
Lys Ala Lys Thr Ala Val Thr Glu Leu Pro Ser Ala Arg Thr Asp Thr
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<211> 259

<212> PRT

<213> Homo sapiens

<400> 3416

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<211> 405

<212> DNA

<213> Homo sapiens

<400> 3417

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<212> PRT

<213> Homo sapiens

<400> 3418

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<211> 418

<212> PRT

<213> Homo sapiens

<400> 3422

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<211> 1851
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<212> DNA

<213> Homo sapiens

<400> 3423

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<212> PRT

<213> Homo sapiens

<400> 3424

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<211> 1416

<212> DNA

<213> Homo sapiens

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<211> 410

<212> PRT

<213> Homo sapiens

<400> 3426

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				245					250					255	
Gln	Glu	Asp	Arg	Gln	Leu	Ile	Cys	Val	Leu	Cys	Pro	Val	Ile	Gly	Ala
				260					265					270	
His	Gln	Gly	His	Gln	Leu	Ser	Thr	Leu	Asp	Glu	Ala	Phe	Glu	Glu	Leu
				275				280					285		
Arg	Ser	Lys	Asp	Ser	Gly	Gly	Leu	Lys	Ala	Ala	Met	Ile	Glu	Leu	Val
				290			295					300			
Glu	Arg	Leu	Lys	Phe	Lys	Ser	Ser	Asp	Pro	Lys	Val	Thr	Arg	Asp	Gln
					310					315					320
Met	Lys	Met	Phe	Ile	Gln	Gln	Glu	Phe	Lys	Lys	Val	Gln	Lys	Val	Ile
				325					330					335	
Ala	Asp	Glu	Glu	Gln	Lys	Ala	Leu	His	Leu	Val	Asp	Ile	Gln	Glu	Ala
				340					345					350	
Met	Ala	Thr	Ala	His	Val	Thr	Glu	Ile	Leu	Ala	Asp	Ile	Gln	Ser	His
				355				360					365		
Met	Asp	Arg	Leu	Met	Thr	Gln	Met	Ala	Gln	Ala	Lys	Glu	Gln	Leu	Asp
				370			375					380			
Thr	Ser	Asn	Glu	Ser	Ala	Glu	Pro	Lys	Ala	Glu	Gly	Asp	Glu	Glu	Gly
					390					395					400
Pro	Ser	Gly	Ala	Ser	Glu	Glu	Glu	Asp	Thr						
				405					410						

<210> 3427

<211> 580

<212> DNA

<213> Homo sapiens

<400> 3427

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60

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120

gggctctggat tgagacttgg accttctgag cactggcaga tgtactggct tctcttcagg
 180
 caggattttc tctggacaca actctgaact tagactcttt aaggactctg cactcctgtg
 240
 cagcatggaa gaggttcaaag ttcccatatt gctcatcttc tcacaatctt ctgtttccat
 300
 ctcttcaaaa ttttgcagag aatacaatga tggccttggc ttgttttctc catccaccga
 360
 agcccctgtg atattggaca atgccaaga atccatcgaa tcccgaacac ttgctctgg
 420
 tttcaggtct gacagacact ccagggaatc ttcataccac tgtgtttcat catgattata
 480
 ccctgaagcc ccatgggtcca gttccaattc ctgaagcctt ctactgcttg cagggcctgg
 540
 gtggctgcca taagcagaat cgcccagtcc atcttgtgac
 580

<210> 3428

<211> 132

<212> PRT

<213> Homo sapiens

<400> 3428

Met	Asp	Ser	Leu	Ala	Leu	Ser	Asn	Ile	Thr	Gly	Ala	Ser	Val	Asp	Gly
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Glu	Asn	Lys	Pro	Arg	Pro	Ser	Leu	Tyr	Ser	Leu	Gln	Asn	Phe	Glu	Glu
			20					25					30		
Met	Glu	Thr	Glu	Asp	Cys	Glu	Lys	Met	Ser	Asn	Met	Gly	Thr	Leu	Asn
			35				40					45			
Ser	Ser	Met	Leu	His	Arg	Ser	Ala	Glu	Ser	Leu	Lys	Ser	Leu	Ser	Ser
			50				55				60				
Glu	Leu	Cys	Pro	Glu	Lys	Ile	Leu	Pro	Glu	Glu	Lys	Pro	Val	His	Leu
65					70					75				80	
Pro	Val	Leu	Arg	Arg	Ser	Lys	Ser	Gln	Ser	Arg	Pro	Gln	Gln	Val	Lys
			85					90						95	
Phe	Ser	Asp	Asp	Val	Ile	Asp	Asn	Gly	Asn	Tyr	Asp	Ile	Glu	Ile	Arg
			100					105					110		
Gln	Pro	Pro	Met	Ser	Glu	Arg	Thr	Arg	Arg	Arg	Val	Tyr	Asn	Phe	Glu
			115				120					125			
Glu	Arg	Gly	Ser												
			130												

<210> 3429

<211> 634

<212> DNA

<213> Homo sapiens

<400> 3429

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 120
 gtcagcttcc ttttcatact ttcccgcggt tctctccacg agcaggtgca ccagggacct
 180

gtccctctgt cctacacggt caccacagtg acgacccaag gcttcccctt gcctacaggc
 240
 cagcacatcc ctggctgcag tgcccagcag ctcccagcat gctccgtgat gttcagtggg
 300
 cagcattacc cctctgctg cctccccccc ccgcttatcc aggcgtgcac catgcagcag
 360
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 420
 cccccaccac cgggcacaca cccagcagct ccagggtctg tataagaaac cctgtggaag
 480
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 ttgaaacact ctattacaa atgtgaacac gcgt
 634

<210> 3430

<211> 122

<212> PRT

<213> Homo sapiens

<400> 3430

Phe	Leu	Leu	Arg	Val	Ala	Leu	Ala	Val	Ser	Phe	Leu	Phe	Ile	Leu	Ser
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Arg	Arg	Ser	Leu	His	Glu	Gln	Val	His	Gln	Gly	Pro	Val	Pro	Leu	Ser
			20					25					30		
Tyr	Thr	Val	Thr	Thr	Val	Thr	Thr	Gln	Gly	Phe	Pro	Leu	Pro	Thr	Gly
		35					40					45			
Gln	His	Ile	Pro	Gly	Cys	Ser	Ala	Gln	Gln	Leu	Pro	Ala	Cys	Ser	Val
	50					55					60				
Met	Phe	Ser	Gly	Gln	His	Tyr	Pro	Leu	Cys	Cys	Leu	Pro	Pro	Pro	Leu
65					70					75					80
Ile	Gln	Ala	Cys	Thr	Met	Gln	Gln	Leu	Pro	Val	Pro	Tyr	Gln	Ala	Tyr
				85				90					95		
Pro	His	Leu	Ile	Ser	Ser	Asp	His	Tyr	Ile	Leu	His	Pro	Pro	Pro	Pro
			100					105					110		
Gly	Thr	His	Pro	Ala	Ala	Pro	Gly	Ser	Val						
			115				120								

<210> 3431

<211> 1396

<212> DNA

<213> Homo sapiens

<400> 3431

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 120
 ctgcgtggga gcagcgtccc aatgccagcg cgtcacgtcg ccagcgctgc cctagcacgc
 180
 agcgccgcca gccgtgtcgc caacagtacc aaatcgctcg gcagcggtt cgccccgccg
 240

gacttcaacc attgcctcaa ggattgggac tataatggcc ttctgtgct caccaccaac
 300
 gccatcgccc agtgggatct ggtgtgtgac ctgggctggc aggtgatcct ggagcagatc
 360
 ctcttcatct tgggctttgc ctccggctac ctgttcctgg gttaccccgc agacagattt
 420
 ggccgtcgcg ggattgtgct gctgaccttg gggctgggtg gccctgtgg agtaggaggg
 480
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 540
 gccggtgttg acctgggtgt ctacctgatg cgctggagc tgtgcgacct aaccagagg
 600
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 660
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 960
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 1020
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 1080
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 1140
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 1200
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 1260
 gatctgaacg aggtgccat caccacttcc tctgtccttg ggctcttctc ctcccaagct
 1320
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 1380
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 1396

<210> 3432

<211> 296

<212> PRT

<213> Homo sapiens

<400> 3432

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 Arg Val Ala Leu Ala Gly Glu Leu Val Gly Val Gly Gly His Phe Leu
 35 40 45
 Phe Leu Gly Leu Ala Leu Val Ser Lys Asp Trp Arg Phe Leu Gln Arg

50	55	60
Met Ile Thr Ala Pro Cys Ile Leu Phe Leu Phe Tyr Gly Trp Pro Gly		
65	70	75
Leu Phe Leu Glu Ser Ala Arg Trp Leu Ile Val Lys Arg Gln Ile Glu		80
	85	90
Glu Ala Gln Ser Val Leu Arg Ile Leu Ala Glu Arg Asn Arg Pro His		95
	100	105
Gly Gln Met Leu Gly Glu Glu Ala Gln Glu Ala Leu Gln Asp Leu Glu		110
	115	120
Asn Thr Cys Pro Leu Pro Ala Thr Ser Ser Phe Ser Phe Ala Ser Leu		125
	130	135
Leu Asn Tyr Arg Asn Ile Trp Lys Asn Leu Leu Ile Leu Gly Phe Thr		140
	145	150
Asn Phe Ile Ala His Ala Ile Arg His Cys Tyr Gln Pro Val Gly Gly		155
	165	170
Gly Gly Ser Pro Ser Asp Phe Tyr Leu Cys Ser Leu Leu Ala Ser Gly		175
	180	185
Thr Ala Ala Leu Ala Cys Val Phe Leu Gly Val Thr Val Asp Arg Phe		190
	195	200
Gly Arg Arg Gly Ile Leu Leu Ser Met Thr Leu Thr Gly Ile Ala		205
	210	215
Ser Leu Val Leu Leu Gly Leu Trp Asp Cys Glu His Pro Ile Phe Pro		220
	225	230
Thr Val Trp Ala Gln Gln Gly Asn Pro Asn Arg Asp Leu Asn Glu Ala		235
	245	250
Ala Ile Thr Thr Phe Ser Val Leu Gly Leu Phe Ser Ser Gln Ala Ala		255
	260	265
Ala Ile Leu Ser Thr Leu Leu Ala Ala Glu Val Ile Pro Thr Thr Val		270
	275	280
Arg Gly Arg Gly Leu Gly Leu Ile		285
	290	295

<210> 3433

<211> 1257

<212> DNA

<213> Homo sapiens

<400> 3433

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 240
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 360
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 420
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 480

agctgcggtg agcacgtgcc caggagaggg ggttcccatg gtcgccgtgt ggggtacacc
 540
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 600
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 660
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 720
 ctataccacc accctgtcta cacaatccac ccatctacac catcacctct cctctgtcta
 780
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 840
 aatccacccg tgtacaccac aatgtcccct tcgtctgcac cgtcctcctg tctacactgg
 900
 caccactgcc ccagctatac caccaccccg tctacataat ccacccatct gtctacacca
 960
 tcgctctctc tctgtctaca ccatccttct gtcaacacccg gcaccactgc cgtatctata
 1020
 tccacccatc tacaccatca cctcccctgt gtctacacca tcctcccatc cacaccagca
 1080
 ccaccacccc acctacacca tcccaccatc tacgccattg ccaaactctac acagacgacc
 1140
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 1257

<210> 3434

<211> 311

<212> PRT

<213> Homo sapiens

<400> 3434

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Arg	Pro	Ser	Ser	Val	Pro	Pro	Ser	Pro	Ser	Pro	Arg	Pro	Leu	Pro	Gly
			20					25					30		
Gly	Arg	Gln	Arg	Pro	Gln	Arg	Pro	Ser	His	Ser	Arg	Ser	His	Thr	Arg
			35				40					45			
Ser	Asn	Leu	Lys	Arg	Asp	Val	Ala	His	Leu	Tyr	Arg	Gly	Val	Gly	Ser
50						55				60					
Arg	Tyr	Ile	Met	Gly	Ser	Gly	Glu	Ser	Phe	Met	Gln	Leu	Gln	Gln	Arg
65					70				75					80	
Leu	Leu	Arg	Glu	Lys	Glu	Ala	Lys	Ile	Arg	Lys	Ala	Leu	Asp	Arg	Leu
				85					90					95	
Arg	Lys	Lys	Arg	His	Leu	Leu	Arg	Arg	Gln	Arg	Thr	Arg	Arg	Glu	Phe
			100					105					110		
Pro	Val	Ile	Ser	Val	Val	Gly	Tyr	Thr	Asn	Cys	Gly	Glu	His	Ala	Pro
		115				120						125			
Arg	Gly	Gly	Ala	Phe	Arg	Gly	Leu	Arg	Val	Thr	Gly	Glu	Asp	Ser	Pro
130						135					140				
Gly	Gly	Gly	Gln	Gly	Val	Pro	Val	Val	Ser	Val	Val	Pro	Tyr	Asp	Ser
145					150				155					160	
Cys	Gly	Glu	His	Val	Pro	Arg	Arg	Gly	Gly	Ser	His	Gly	Arg	Arg	Val

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<210> 3435
<211> 1225
<212> DNA
<213> Homo sapiens
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<400> 3435
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120
gacagcaatg ccgataccta ctgggagagc gatgggtccc agtgccaaca ctgggtacgg
180
cttactatga agaagggcac cattgtcaag aagctgctac tcgcagtgga taccacagat
240
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300
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420
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720
gactctgaga gcagcaagcc cagcttcatg ccacgcctat acatcaaccg ccgtcttgcc
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840

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 1140
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<210> 3436

<211> 408

<212> PRT

<213> Homo sapiens

<400> 3436

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 20 25 30
 Glu Phe Asn Val Ser Cys Leu Thr Asp Ser Asn Ala Asp Thr Tyr Trp
 35 40 45
 Glu Ser Asp Gly Ser Gln Cys Gln His Trp Val Arg Leu Thr Met Lys
 50 55 60
 Lys Gly Thr Ile Val Lys Lys Leu Leu Leu Ala Val Asp Thr Thr Asp
 65 70 75 80
 Asp Asn Phe Met Pro Lys Arg Val Val Val Tyr Gly Gly Glu Gly Asp
 85 90 95
 Asn Leu Lys Lys Leu Ser Asp Val Ser Ile Asp Xaa Arg Pro Ser Ser
 100 105 110
 Gly Xaa Val Cys Val Leu Glu Asp Met Thr Val His Leu Pro Ile Ile
 115 120 125
 Glu Ile Arg Ile Val Glu Cys Arg Asp Asp Gly Ile Asp Val Arg Leu
 130 135 140
 Arg Gly Val Lys Ile Lys Ser Ser Arg Gln Arg Glu Leu Gly Leu Asn
 145 150 155 160
 Ala Asp Leu Phe Gln Pro Thr Ser Leu Val Arg Tyr Pro Arg Leu Glu
 165 170 175
 Gly Thr Asp Pro Glu Val Leu Tyr Arg Arg Ala Val Leu Leu Gln Arg
 180 185 190
 Phe Ile Lys Ile Leu Asp Ser Val Leu His His Leu Val Pro Ala Trp
 195 200 205
 Asp His Thr Leu Gly Thr Phe Ser Glu Ile Lys Gln Val Lys Gln Phe
 210 215 220
 Leu Leu Leu Ser Arg Gln Arg Pro Gly Leu Val Ala Gln Cys Leu Arg
 225 230 235 240
 Asp Ser Glu Ser Ser Lys Pro Ser Phe Met Pro Arg Leu Tyr Ile Asn
 245 250 255
 Arg Arg Leu Ala Met Glu His Arg Ala Cys Pro Ser Arg Asp Pro Ala

	260		265		270										
Cys	Lys	Asn	Ala	Val	Phe	Thr	Gln	Val	Tyr	Glu	Gly	Leu	Lys	Pro	Ser
	275						280					285			
Asp	Lys	Tyr	Glu	Lys	Pro	Leu	Asp	Tyr	Arg	Trp	Pro	Met	Arg	Tyr	Asp
	290					295					300				
Gln	Trp	Trp	Glu	Cys	Lys	Phe	Ile	Ala	Glu	Gly	Ile	Ile	Asp	Gln	Gly
305					310				315					320	
Gly	Gly	Phe	Arg	Asp	Ser	Leu	Ala	Asp	Met	Ser	Glu	Glu	Leu	Cys	Pro
			325					330					335		
Ser	Ser	Ala	Asp	Thr	Pro	Val	Pro	Leu	Pro	Phe	Phe	Val	Arg	Thr	Ala
		340					345					350			
Asn	Gln	Gly	Asn	Gly	Thr	Gly	Glu	Ala	Arg	Asp	Met	Tyr	Val	Pro	Asn
	355					360				365					
Pro	Ser	Cys	Arg	Asp	Phe	Ala	Lys	Tyr	Glu	Trp	Ile	Gly	Gln	Leu	Met
	370				375				380						
Gly	Ala	Ala	Leu	Arg	Gly	Lys	Glu	Phe	Leu	Val	Leu	Ala	Leu	Pro	Gly
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Phe	Val	Trp	Lys	Gln	Leu	Ser	Ala								
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<210> 3437

<211> 2081

<212> DNA

<213> Homo sapiens

<400> 3437

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240
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360
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420
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780
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840

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 1920
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 1980
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<210> 3438

<211> 105

<212> PRT

<213> Homo sapiens

<400> 3438

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Arg	Pro	Pro	Lys	Arg	Asp	Phe	Gln	Val	Glu	Ala	Thr	Thr	Ala	Glu	Asp
			20					25					30		
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<400> 3439
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1140

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<210> 3440

<211> 287

<212> PRT

<213> Homo sapiens

<400> 3440

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			20					25				30			
Val	Ala	Ala	Ala	Ala	Arg	Trp	Pro	Arg	Gln	Pro	Arg	His	Pro	Arg	His
		35					40				45				
Thr	Ser	Pro	Met	Pro	Pro	Pro	Ala	Ala	Leu	Arg	Pro	Pro	Ala	Gly	Pro
	50					55				60					
Arg	Arg	Pro	Arg	Xaa	Pro	Gly	Gly	Pro	Gln	His	His	Gln	Pro	Gln	Pro
65					70			75						80	
Pro	Leu	Trp	Thr	Pro	Thr	Pro	Pro	Ser	Pro	Ala	Ser	Asp	Trp	Pro	Pro
			85					90					95		
Leu	Pro	Pro	Asn	Arg	Pro	Pro	Gln	Asn	Pro	Gly	Pro	Thr	Leu	Pro	Trp
			100				105					110			
Arg	Gln	Arg	Asp	Lys	Gly	Gly	Pro	Ser	Pro	Leu	Pro	Glu	Ala	Arg	Thr
	115						120				125				
Pro	Trp	Gly	Gly	Gly	Glu	Asp	Val	Ser	Ala	Gly	Pro	Leu	Xaa	Thr	Pro
	130				135						140				
Phe	Leu	Ser	Ala	Pro	Leu	Val	Pro	Arg	Ser	Pro	Gly	Gly	Glu	Ser	Ala
145				150				155						160	
Asp	Ser	Ser	Gln	Ala	Gly	Thr	Arg	Leu	Val	Pro	Glu	His	Ala	Ala	Ala
			165				170						175		
His	Thr	Gln	Gly	His	Gly	Pro	Ser	Gly	Pro	Gly	Thr	Trp	Ser	Gly	Ser
	180						185					190			
Glu	Arg	Pro	Gly	Cys	Leu	Ala	Asp	Arg	Thr	Ser	Glu	Thr	Thr	Gln	Pro
	195					200					205				
Ser	Phe	Glu	Asp	Ala	Pro	Ala	Gln	Pro	Ser	Pro	Gly	Val	Pro	Trp	Arg
	210				215						220				
Thr	Thr	Leu	Ala	Glu	Thr	Leu	Leu	Ile	Pro	Gly	Leu	Glu	Leu	Leu	Gly
225				230				235						240	
Gly	Arg	Gln	Ala	Ser	Thr	Pro	Thr	Leu	Gly	Asn	Ala	Glu	Pro	Leu	Arg
			245				250						255		
Met	Cys	Ala	Arg	Gly	Arg	Val	Cys	Val	Phe	Leu	Arg	Val	Ser	Leu	Phe

	260		265		270									
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<210> 3441

<211> 2074

<212> DNA

<213> Homo sapiens

<400> 3441

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180
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1320

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<210> 3442

<211> 374

<212> PRT

<213> Homo sapiens

<400> 3442

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		20					25					30			
Ala	Glu	Leu	Leu	Met	Ser	Leu	His	Asp	Leu	Asp	Val	Gly	Glu	Ile	Cys
		35				40					45				
Thr	Val	Asp	Pro	Cys	His	Lys	Phe	Thr	Trp	Cys	Leu	Asp	Ala	Cys	Ile
	50				55					60					
Arg	Glu	Arg	Phe	Val	Asp	Ser	Lys	Arg	Ala	Arg	Glu	Leu	Gln	Gly	Phe
65			70					75					80		
Leu	Asp	Asp	Val	Lys	Lys	Gly	Gln	Glu	Gln	Val	Leu	Gly	Asp	Leu	Ser
		85					90					95			
Met	Ile	Leu	Cys	Asp	Pro	Phe	Ala	Ile	Asn	Thr	Leu	Ala	Leu	Ser	Thr
		100					105					110			
Val	Arg	His	Leu	Gln	Glu	Leu	Val	Gly	Gln	Glu	Thr	Leu	Pro	Arg	Asp
	115					120					125				
Ser	Pro	Asp	Leu	Leu	Leu	Leu	Arg	Leu	Leu	Ala	Leu	Gly	Gln	Gly	
	130				135				140						
Ala	Trp	Asp	Met	Ile	Asp	Ser	Gln	Val	Phe	Lys	Glu	Pro	Lys	Met	Glu
145			150					155					160		
Val	Glu	Leu	Ile	Thr	Arg	Phe	Leu	Pro	Met	Leu	Met	Ser	Phe	Leu	Val

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Asp Asp Tyr Thr Phe Asn Val Asp Gln Lys Leu Pro Ala Glu Glu Lys
                180                185                190
Ala Pro Val Ser Tyr Pro Asn Thr Leu Pro Glu Ser Phe Thr Lys Phe
                195                200                205
Leu Gln Glu Gln Arg Met Ala Cys Glu Val Gly Leu Tyr Tyr Val Leu
                210                215                220
His Ile Thr Lys Gln Arg Asn Lys Asn Ala Leu Leu Arg Leu Leu Pro
225                230                235                240
Gly Leu Val Glu Thr Phe Gly Asp Leu Ala Phe Gly Asp Ile Phe Leu
                245                250                255
His Leu Leu Thr Gly Asn Leu Ala Leu Leu Ala Asp Glu Phe Ala Leu
                260                265                270
Glu Asp Phe Cys Ser Ser Leu Phe Asp Gly Phe Phe Leu Thr Ala Ser
                275                280                285
Pro Arg Lys Glu Asn Val His Arg His Ala Leu Arg Leu Leu Ile His
                290                295                300
Leu His Pro Arg Val Ala Pro Ser Lys Leu Glu Ala Leu Gln Lys Ala
305                310                315                320
Leu Glu Pro Thr Gly Gln Ser Gly Glu Ala Val Lys Glu Leu Tyr Ser
                325                330                335
Gln Leu Gly Glu Lys Leu Glu Gln Leu Asp His Arg Lys Pro Ser Pro
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Ala Gln Ala Ala Glu Thr Pro Ala Leu Glu Leu Pro Leu Pro Ser Val
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Pro Ala Pro Ala Pro Leu
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<210> 3443

<211> 2070

<212> DNA

<213> Homo sapiens

<400> 3443

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720
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780
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<210> 3444

<211> 579

<212> PRT

<213> Homo sapiens

<400> 3444

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          20           25           30
Ser Glu Asn Val Glu Lys Ser Lys Ala Tyr Lys Leu Asn Pro Lys Phe
          35           40           45
Cys Ser Leu Ser Phe Gln Ala Thr Lys Cys Lys Leu Ala Gly Leu Glu
          50           55           60
Val Leu Ser Asp Asp Pro Asp Leu Val Lys Val Val Glu Ser Leu Thr
          65           70           75           80
Cys Gly Lys Ile Phe Ala Val Glu Ile Leu Asp Lys Ala Asp Ile Pro
          85           90           95
Leu Val Val Leu Tyr Asp Thr Ser Gly Glu Asp Asp Ile Asn Ile Asn
          100          105          110
Ala Thr Cys Leu Lys Ala Ile Cys Asp Lys Ser Leu Glu Val His Leu
          115          120          125
Gln Val Asp Ala Met Tyr Thr Asn Val Lys Ile Thr Asn Ile Cys Ser
          130          135          140
Asp Gly Thr Leu Tyr Cys Gln Val Pro Cys Lys Gly Leu Asn Lys Leu
          145          150          155          160
Ser Asp Leu Leu Arg Lys Ile Glu Asp Tyr Phe His Cys Lys His Met
          165          170          175
Thr Ser Glu Cys Phe Val Ser Leu Pro Phe Cys Gly Lys Ile Cys Leu
          180          185          190
Phe His Cys Lys Gly Lys Trp Leu Arg Val Glu Ile Thr Asn Val His
          195          200          205
Ser Ser Arg Ala Leu Asp Val Gln Phe Leu Asp Ser Gly Thr Val Thr
          210          215          220
Ser Val Lys Val Ser Glu Leu Arg Glu Ile Pro Pro Arg Phe Leu Gln
          225          230          235          240
Glu Met Ile Ala Ile Pro Pro Gln Ala Ile Lys Cys Cys Leu Ala Asp
          245          250          255
Leu Pro Gln Ser Ile Gly Met Trp Thr Pro Asp Ala Val Leu Trp Leu
          260          265          270
Arg Asp Ser Val Leu Asn Cys Ser Asp Cys Ser Ile Lys Val Thr Lys
          275          280          285
Val Asp Glu Thr Arg Gly Ile Ala His Val Tyr Leu Phe Thr Pro Lys
          290          295          300
Asn Phe Pro Asp Pro His Arg Ser Ile Asn Arg Gln Ile Thr Asn Ala
          305          310          315          320
Asp Leu Trp Lys His Gln Lys Asp Val Phe Leu Ser Ala Ile Ser Ser
          325          330          335
Gly Ala Asp Ser Pro Asn Ser Lys Asn Gly Asn Met Pro Met Ser Gly
          340          345          350
Asn Thr Gly Glu Asn Phe Arg Lys Asn Leu Thr Asp Val Ile Lys Lys
          355          360          365
Ser Met Val Asp His Thr Ser Ala Phe Ser Thr Glu Glu Leu Pro Pro
          370          375          380
Pro Val His Leu Ser Lys Pro Gly Glu His Met Asp Val Tyr Val Pro
          385          390          395          400
Val Ala Cys His Pro Gly Tyr Phe Val Ile Gln Pro Trp Gln Glu Ile

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His Lys Leu Glu Val Leu Met Glu Glu Met Ile Leu Tyr Tyr Ser Val
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Lys Val Glu Asn Lys Trp His Arg Val Leu Leu Lys Gly Ile Leu Thr
              450              455              460
Asn Gly Leu Val Ser Val Tyr Glu Leu Asp Tyr Gly Lys His Glu Leu
465              470              475              480
Val Asn Ile Arg Lys Val Gln Pro Leu Val Asp Met Phe Arg Lys Leu
              485              490              495
Pro Phe Gln Ala Val Thr Ala Gln Leu Ala Gly Val Lys Cys Asn Gln
              500              505              510
Trp Ser Glu Glu Ala Ser Met Val Phe Arg Asn His Val Glu Lys Lys
              515              520              525
Pro Leu Val Ala Leu Val Gln Thr Val Ile Glu Asn Ala Asn Pro Trp
              530              535              540
Asp Arg Lys Val Val Val Tyr Leu Val Asp Thr Ser Leu Pro Asp Thr
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Lys Val Asn

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<210> 3445

<211> 2086

<212> DNA

<213> Homo sapiens

<400> 3445

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720

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1980
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2086

<210> 3446

<211> 169

<212> PRT

<213> Homo sapiens

<400> 3446

Met Asp Ala Leu Glu Gly Glu Ser Phe Ala Leu Ser Phe Ser Ser Ala

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      20           25           30
Met Asp Asp Glu Phe Gln Leu Leu Gln Arg Asn Phe Met Asp Lys Tyr
      35           40           45
Tyr Leu Glu Phe Glu Asp Thr Glu Glu Asn Lys Leu Ile Tyr Thr Pro
      50           55           60
Ile Phe Asn Glu Tyr Ile Ser Leu Val Glu Lys Tyr Ile Glu Glu Gln
      65           70           75           80
Leu Leu Gln Arg Ile Pro Glu Phe Asn Met Ala Ala Phe Thr Thr Thr
      85           90           95
Leu His His Leu Phe Arg Leu Arg His His Lys Asp Glu Val Ala Gly
      100          105          110
Asp Ile Phe Asp Met Leu Leu Thr Phe Thr Asp Phe Leu Ala Phe Lys
      115          120          125
Glu Met Phe Leu Asp Tyr Arg Ala Glu Lys Glu Gly Arg Gly Leu Asp
      130          135          140
Leu Ser Ser Gly Leu Val Thr Ser Leu Cys Lys Ser Ser Ser Leu
      145          150          155          160
Pro Ala Ser Gln Asn Asn Leu Arg His
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<210> 3447

<211> 936

<212> DNA

<213> Homo sapiens

<400> 3447

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120
ggggtgcgct ttgaccgcga gagggcgcgc cgcctgtggg aagccgtgtc cggtgcccag
180
ccggtgggta gagaggaagt ggagcacatg atccagaaga accaatgtct cttaccaaac
240
acccagtgtg aggtttgtct cgccttgett atttctgagt ccagaagct ggcacattac
300
cagagcaaaa aacatgccaa caaagtgaag agatacctag caatccatgg aatggagaca
360
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420
aaccagtgtc gcccacatct taacatgacc ttttctctcc ctgtcgtggc ccagtcgcac
480
tacctgggga agaccacgc aaagaactta aagctgaagc agcagtccac taagtgga
540
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600
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780

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cagtaccaag ctcatgtcag cggcttcaaa cacaagaacc agtcacacaaa aacagtggca
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 936

<210> 3448

<211> 302

<212> PRT

<213> Homo sapiens

<400> 3448

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Val	Gln	Ala	Ala	Asp	Gly	Gly	Ala	Ala	Gly	Pro	Tyr	Ser	Ser	Ser	Glu
		20					25					30			
Leu	Leu	Glu	Gly	Gln	Glu	Pro	Asp	Gly	Val	Arg	Phe	Asp	Arg	Glu	Arg
	35					40					45				
Ala	Arg	Arg	Leu	Trp	Glu	Ala	Val	Ser	Gly	Ala	Gln	Pro	Val	Gly	Arg
50					55				60						
Glu	Glu	Val	Glu	His	Met	Ile	Gln	Lys	Asn	Gln	Cys	Leu	Phe	Thr	Asn
65				70					75					80	
Thr	Gln	Cys	Lys	Val	Cys	Cys	Ala	Leu	Leu	Ile	Ser	Glu	Ser	Gln	Lys
		85						90					95		
Leu	Ala	His	Tyr	Gln	Ser	Lys	Lys	His	Ala	Asn	Lys	Val	Lys	Arg	Tyr
		100					105					110			
Leu	Ala	Ile	His	Gly	Met	Glu	Thr	Leu	Lys	Gly	Glu	Thr	Lys	Lys	Leu
	115					120					125				
Asp	Ser	Asp	Gln	Lys	Ser	Ser	Arg	Ser	Lys	Asp	Lys	Asn	Gln	Cys	Cys
130					135				140						
Pro	Ile	Cys	Asn	Met	Thr	Phe	Ser	Ser	Pro	Val	Val	Ala	Gln	Ser	His
145				150					155					160	
Tyr	Leu	Gly	Lys	Thr	His	Ala	Lys	Asn	Leu	Lys	Leu	Lys	Gln	Gln	Ser
		165						170					175		
Thr	Lys	Val	Glu	Ala	Leu	His	Gln	Asn	Arg	Glu	Met	Ile	Asp	Pro	Asp
	180						185					190			
Lys	Phe	Cys	Ser	Leu	Cys	His	Ala	Thr	Phe	Asn	Asp	Pro	Val	Met	Ala
	195					200						205			
Gln	Gln	His	Tyr	Val	Gly	Lys	Lys	His	Arg	Lys	Gln	Glu	Thr	Lys	Leu
210					215						220				
Lys	Leu	Met	Ala	Arg	Tyr	Gly	Arg	Leu	Ala	Asp	Pro	Ala	Val	Thr	Asp
225				230					235					240	
Phe	Pro	Ala	Gly	Lys	Gly	Tyr	Pro	Cys	Lys	Thr	Cys	Lys	Ile	Val	Leu
		245						250					255		
Asn	Ser	Ile	Glu	Gln	Tyr	Gln	Ala	His	Val	Ser	Gly	Phe	Lys	His	Lys
		260					265					270			
Asn	Gln	Ser	Pro	Lys	Thr	Val	Ala	Ser	Ser	Leu	Gly	Gln	Ile	Pro	Met
	275					280						285			
Gln	Arg	Gln	Pro	Ile	Gln	Lys	Asp	Ser	Thr	Thr	Leu	Glu	Asp		
290					295						300				

<210> 3449

<211> 877

<212> DNA

<213> Homo sapiens

<400> 3449

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 120
 ccggcccttc tggccggcac caaccocgtt gctgtcgtcg cggatggagg cagttgcccc
 180
 gcacactacc cgggtgcacga gtgcgtcttc aagggggatg tgaggagact ctcctctctc
 240
 atccgcacgc acaatatcgg gcagaaagat aatcacggaa atactccttt acaccttget
 300
 gtgatgttag gaaataaaga atgtgccccat ttacttttgg ctcacaatgc tccagtcaag
 360
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 480
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 540
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 600
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 720
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 780
 ggaatcagag atggaaacag aagaagaggt ggatatttta atgagcagtg atatttactc
 840
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 877

<210> 3450

<211> 276

<212> PRT

<213> Homo sapiens

<400> 3450

Xaa Ile Phe Ser Asn His His Arg Leu Gln Leu Lys Ala Ala Pro
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 Ala Ser Ser Asn Pro Pro Gly Ala Pro Ala Leu Pro Leu His Asn Ser
 20 25 30
 Ser Val Thr Ala Asn Ser Gln Ser Pro Ala Leu Leu Ala Gly Thr Asn
 35 40 45
 Pro Val Ala Val Val Ala Asp Gly Gly Ser Cys Pro Ala His Tyr Pro
 50 55 60
 Val His Glu Cys Val Phe Lys Gly Asp Val Arg Arg Leu Ser Ser Leu
 65 70 75 80
 Ile Arg Thr His Asn Ile Gly Gln Lys Asp Asn His Gly Asn Thr Pro
 85 90 95
 Leu His Leu Ala Val Met Leu Gly Asn Lys Glu Cys Ala His Leu Leu

```

      100      105      110
Leu Ala His Asn Ala Pro Val Lys Val Lys Asn Ala Gln Gly Trp Ser
      115      120      125
Pro Leu Ala Glu Ala Ile Ser Tyr Gly Asp Arg Gln Met Ile Thr Ala
      130      135      140
Leu Leu Arg Lys Leu Lys Gln Gln Ser Arg Glu Ser Val Glu Glu Lys
145      150      155      160
Arg Pro Arg Leu Leu Lys Ala Leu Lys Glu Leu Gly Asp Phe Tyr Leu
      165      170      175
Glu Leu His Trp Asp Phe Gln Ser Trp Val Pro Leu Leu Ser Arg Ile
      180      185      190
Leu Pro Ser Asp Ala Cys Lys Ile Tyr Lys Gln Gly Ile Asn Ile Arg
      195      200      205
Leu Asp Thr Thr Leu Ile Asp Phe Thr Asp Met Lys Cys Gln Arg Gly
      210      215      220
Asp Leu Ser Phe Ile Phe Asn Gly Asp Ala Ala Pro Ser Glu Ser Phe
225      230      235      240
Val Val Leu Asp Asn Glu Gln Lys Val Tyr Gln Arg Ile His His Glu
      245      250      255
Ala His Ile Pro Gly Ile Arg Asp Gly Asn Arg Arg Arg Gly Gly Tyr
      260      265      270
Phe Asn Glu Gln
      275

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<210> 3451

<211> 595

<212> DNA

<213> Homo sapiens

<400> 3451

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120
gaaatattca gtaagtagtg ccctgccatt gcaggtttgg atgtccttct gccagcaaaa
180
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240
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300
gtctgaagga tctgatcttg ggttgcttta cttagtcctt cgtgggtattg gtgtgtgtca
360
atgctggagt ccctcagctc cttagctgaa aagagctgaa ggggccttgg aacctggggg
420
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480
tcattaactt cctctctggg gctattttct gttgtgttgg tagctatgag cgctcccatc
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cccccttctt cttttgcagg caggggaacc gcttccattt caactttggg gagag
595

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<210> 3452

<211> 192

<212> PRT

<213> Homo sapiens

<400> 3452

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Met Glu Ala Val Pro Leu Pro Ala Lys Glu Glu Arg Gly Met Gly Ala
 1           5           10           15
Leu Ile Ala Thr Asn Thr Thr Glu Asn Ser Thr Arg Glu Glu Val Asn
          20           25           30
Glu Arg Gln Ser His Pro Ala Thr Gln Gln Gln Leu Gly Lys Thr Leu
          35           40           45
Gln Ser Lys Gln Leu Pro Gln Val Pro Arg Pro Leu Gln Leu Phe Ser
          50           55           60
Ala Lys Glu Leu Arg Asp Ser Ser Ile Asp Thr His Gln Tyr His Glu
65           70           75           80
Gly Leu Ser Lys Ala Thr Gln Asp Gln Ile Leu Gln Thr Leu Ile Gln
          85           90           95
Arg Val Arg Arg Gln Asn Leu Leu Ser Val Val Pro Pro Ser Gln Phe
          100          105          110
Asn Phe Ala His Ser Gly Phe Gln Leu Glu Asp Ile Ser Thr Ser Gln
          115          120          125
Arg Phe Met Leu Gly Phe Ala Gly Arg Arg Thr Ser Lys Pro Ala Met
          130          135          140
Ala Gly His Tyr Leu Leu Asn Ile Ser Thr Tyr Gly Arg Gly Ser Glu
145          150          155          160
Ser Phe Arg Arg Thr His Ser Val Asn Pro Glu Asp Arg Phe Cys Leu
          165          170          175
Ser Ser Pro Thr Glu Ala Leu Lys Met Gly Tyr Thr Asn Cys Lys Asn
          180          185          190

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<210> 3453

<211> 477

<212> DNA

<213> Homo sapiens

<400> 3453

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120
gcgttagtg atacgctcac cgggataccta tccccagtac aggaggtgcg ggcggctgct
180
gaagaacaga ttaaggtgct ggaggtgacg gaggaatttg gtgttcactt ggcagaactg
240
actgtagatc cccagggggc actggcaatc cgtcagctgg catcagtcac cttgaaacaa
300
tatgtggaga ctactggtg tgcccaatca gagaaattta ggccctcctga aactacagaa
360
agggcaaaaa ttgttatccg ggagctattg cctaattggg tgagagaatc gataagcaaa
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477

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<210> 3454

<211> 159

<212> PRT

<213> Homo sapiens

<400> 3454

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Lys Met Ala Ala Ala Ala Ala Gly Ala Ala Ser Gly Leu Pro Gly
 20           25           30
Pro Val Ala Gln Gly Leu Lys Glu Ala Leu Val Asp Thr Leu Thr Gly
 35           40           45
Ile Leu Ser Pro Val Gln Glu Val Arg Ala Ala Ala Glu Glu Gln Ile
 50           55           60
Lys Val Leu Glu Val Thr Glu Glu Phe Gly Val His Leu Ala Glu Leu
 65           70           75           80
Thr Val Asp Pro Gln Gly Ala Leu Ala Ile Arg Gln Leu Ala Ser Val
 85           90           95
Ile Leu Lys Gln Tyr Val Glu Thr His Trp Cys Ala Gln Ser Glu Lys
100          105          110
Phe Arg Pro Pro Glu Thr Thr Glu Arg Ala Lys Ile Val Ile Arg Glu
115          120          125
Leu Leu Pro Asn Gly Leu Arg Glu Ser Ile Ser Lys Val Arg Ser Ser
130          135          140
Val Ala Tyr Ala Val Ser Ala Ile Ala His Trp Asp Trp Pro Glu
145          150          155

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<210> 3455

<211> 4886

<212> DNA

<213> Homo sapiens

<400> 3455

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120
cttgctcggag actgagctat tggcagtgcc ttcagctctg agctcaggca cctcgaacat
180
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240
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480
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540
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600
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660
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720

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gaggggtgta ggctggcaca gcacctcgtc caaaagctca gcccagaaaa tgacaacgat
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 4886

<210> 3456

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3456

Glu	Ile	Glu	Lys	Lys	Gly	Lys	Gly	Lys	Lys	Arg	Arg	Gly	Arg	Arg	Ser
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Lys	Lys	Gln	Arg	Arg	Gly	Arg	Lys	Glu	Gly	Glu	Glu	Asp	Gln	Asn	
		20					25					30			
Pro	Pro	Cys	Pro	Arg	Leu	Asn	Gly	Val	Leu	Met	Glu	Val	Glu	Glu	Pro
		35					40					45			
Glu	Val	Leu	Gln	Asp	Ser	Leu	Asp	Arg	Cys	Tyr	Ser	Thr	Pro	Ser	Met
	50					55					60				
Tyr	Phe	Glu	Leu	Pro	Asp	Ser	Phe	Gln	His	Tyr	Arg	Ser	Val	Phe	Tyr
65					70					75				80	
Ser	Phe	Glu	Glu	Glu	His	Ile	Ser	Phe	Ala	Leu	Tyr	Val	Asp	Asn	Arg
			85						90					95	
Phe	Phe	Thr	Leu	Thr	Val	Thr	Ser	Leu	His	Leu	Val	Phe	Gln	Met	Gly
			100					105					110		
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115

<210> 3457
 <211> 646
 <212> DNA
 <213> Homo sapiens

<400> 3457
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 120
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 180
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 360
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 420
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 480
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 540
 aaccctccag gccttctcct gccacaggct ctgtctctgt cccgtcgctg tgcctcctgc
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 646

<210> 3458
 <211> 61
 <212> PRT
 <213> Homo sapiens

<400> 3458
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 20 25 30
 Ile Cys Ala Cys Leu Phe Thr His Arg Trp Glu Cys Arg Val Cys Ile
 35 40 45
 Leu Cys Xaa Cys Thr Cys Thr Gln Ala Xaa Ala Gly Lys
 50 55 60

<210> 3459
 <211> 592
 <212> DNA
 <213> Homo sapiens

<400> 3459
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 120
 gacctactt cactgcaggg ggctcagccc agtctgcctc aggcagaaca agggctctggg
 180
 ggtggctgtg gggggtgtg gatgggtccc agtgggcctg ctgccactcc caccacatgg
 240
 gacctgcctt ccggccctgc caggattcca gtccctgcctt gtcaccccca gcttcaggc
 300
 ccttcctgt gtgcagcctc agtttgctg ctgcagaata agcaccacgc tccctcgtgg
 360
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 420
 ggccccggcc acgtccctgc ccccgagct ggccttcagc ggggacagt gtcagcactg
 480
 aagacagtca tacctgccc gcccggcactg ccctgctcag cacggggaca atttgaactt
 540
 aagctttaac ttaattaaaa tgaactaaaa ttaaaaaaaaa aaaaaaaaaa aa
 592

<210> 3460

<211> 115

<212> PRT

<213> Homo sapiens

<400> 3460

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Ser	Gly	Pro	Ala	Arg	Ile	Pro	Val	Leu	Pro	Cys	Ser	Pro	Gln	Leu	Pro
			20					25					30		
Gly	Pro	Ser	Leu	Cys	Ala	Ala	Ser	Val	Cys	Leu	Leu	Gln	Asn	Lys	His
			35				40					45			
His	Ala	Pro	Ser	Trp	Ala	Glu	Ala	Pro	Ala	Asp	Ser	Pro	Arg	Ala	Leu
	50					55				60					
Gln	Ala	Cys	Pro	Val	Leu	Cys	Gln	Ala	Gly	Pro	Gly	His	Val	Pro	Ala
65					70					75				80	
Pro	Gly	Ala	Gly	Leu	Gln	Arg	Gly	Gln	Trp	Ser	Ala	Leu	Lys	Thr	Val
			85					90					95		
Ile	Pro	Ala	Arg	Pro	Ala	Leu	Pro	Cys	Ser	Ala	Arg	Gly	Gln	Phe	Glu
			100					105					110		
Leu	Lys	Leu													
			115												

<210> 3461

<211> 474

<212> DNA

<213> Homo sapiens

<400> 3461

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 180

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 300
 ctctatgcag ctttctgctt tggtagagacc ttaaaggagc caaagtccac ccggtcttc
 360
 acgttccgtc accaccgatc cattgtccag ctctatgtgg ctcccgcccc agagaagtcc
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 474

<210> 3462

<211> 101

<212> PRT

<213> Homo sapiens

<400> 3462

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Leu	Leu	Gly	Gly	His	Trp	Leu	Arg	Ala	Gln	Gly	Tyr	Ala	Asn	Pro	Phe
		20					25					30			
Trp	Leu	Ala	Leu	Ala	Leu	Leu	Ile	Ala	Met	Thr	Leu	Tyr	Ala	Ala	Phe
		35					40				45				
Cys	Phe	Gly	Glu	Thr	Leu	Lys	Glu	Pro	Lys	Ser	Thr	Arg	Leu	Phe	Thr
	50					55				60					
Phe	Arg	His	His	Arg	Ser	Ile	Val	Gln	Leu	Tyr	Val	Ala	Pro	Ala	Pro
65					70				75					80	
Glu	Lys	Ser	Arg	Lys	His	Leu	Ala	Leu	Tyr	Ser	Leu	Ala	Ile	Phe	Val
			85					90					95		
Val	Ile	Thr	Val	His											
			100												

<210> 3463

<211> 1734

<212> DNA

<213> Homo sapiens

<400> 3463

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 cagcagcggc agggcaagca ccatcctaata tatctcatgg ctaatgaacg catgaacctc
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 360
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 420
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caaaagaaac tttcagaata tatgaaagct ttgatcaata agaaagaact tctcagtga
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 780
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 1734

<210> 3464

<211> 434

<212> PRT

<213> Homo sapiens

<400> 3464

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 Leu Glu Asp Pro Ala Val Pro Arg Leu Thr Ala Ala Leu Pro Ala Ala
 20 25 30
 Glu Leu Pro Glu Arg Arg Arg Arg Gln Gln Arg Gln Gly Lys His His

35	40	45
Pro Asn Tyr Leu Met Ala	Asn Glu Arg Met Asn Leu Met Asn Met Ala	
50	55	60
Lys Leu Ser Ile Lys Gly Leu Ile Glu Ser Ala Leu Asn Leu Gly Arg		
65	70	75
Thr Leu Asp Ser Asp Tyr Ala Pro Leu Gln Gln Phe Phe Val Val Met		
85	90	95
Glu His Cys Leu Lys His Gly Leu Lys Ala Lys Lys Thr Phe Leu Gly		
100	105	110
Gln Asn Lys Ser Phe Trp Gly Pro Leu Glu Leu Val Glu Lys Leu Val		
115	120	125
Pro Glu Ala Ala Glu Ile Thr Ala Ser Val Lys Asp Leu Pro Gly Leu		
130	135	140
Lys Thr Pro Val Gly Arg Gly Arg Ala Trp Leu Arg Leu Ala Leu Met		
145	150	155
Gln Lys Lys Leu Ser Glu Tyr Met Lys Ala Leu Ile Asn Lys Lys Glu		
165	170	175
Leu Leu Ser Glu Phe Tyr Glu Pro Asn Ala Leu Met Met Glu Glu Glu		
180	185	190
Gly Ala Ile Ile Ala Gly Leu Leu Val Gly Leu Asn Val Ile Asp Ala		
195	200	205
Asn Phe Cys Met Lys Gly Glu Asp Leu Asp Ser Gln Val Gly Val Ile		
210	215	220
Asp Phe Ser Met Tyr Leu Lys Asp Gly Asn Ser Ser Lys Gly Thr Glu		
225	230	235
Gly Asp Gly Gln Ile Thr Ala Ile Leu Asp Gln Lys Asn Tyr Val Glu		
245	250	255
Glu Leu Asn Arg His Leu Asn Ala Thr Val Asn Asn Leu Gln Ala Lys		
260	265	270
Val Asp Ala Leu Glu Lys Ser Asn Thr Lys Leu Thr Glu Glu Leu Ala		
275	280	285
Val Ala Asn Asn Arg Ile Ile Thr Leu Gln Glu Glu Met Glu Arg Val		
290	295	300
Lys Glu Glu Ser Ser Tyr Ile Leu Glu Ser Asn Arg Lys Gly Pro Lys		
305	310	315
Gln Asp Arg Thr Ala Glu Gly Gln Ala Leu Ser Glu Ala Arg Lys His		
325	330	335
Leu Lys Glu Glu Thr Gln Leu Arg Leu Asp Val Glu Lys Glu Leu Glu		
340	345	350
Met Gln Ile Ser Met Arg Gln Glu Met Glu Leu Ala Met Lys Met Leu		
355	360	365
Glu Lys Asp Val Cys Glu Lys Gln Asp Ala Leu Val Ser Leu Arg Gln		
370	375	380
Gln Leu Asp Asp Leu Arg Ala Leu Lys His Glu Leu Ala Phe Lys Leu		
385	390	395
Gln Ser Ser Asp Leu Gly Val Lys Gln Lys Ser Glu Leu Asn Ser Arg		
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420	425	430
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<210> 3465

<211> 2904

<212> DNA

<213> Homo sapiens

<400> 3465

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720
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<210> 3466

<211> 315

<212> PRT

<213> Homo sapiens

<400> 3466

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Gly Arg His Arg Lys Leu Pro Glu Asn Trp Thr Asp Thr Arg Glu Thr
          35           40           45
Leu Leu Glu Gly Met Leu Phe Ser Leu Lys Tyr Leu Gly Met Thr Leu
          50           55           60
Val Glu Gln Pro Lys Gly Glu Glu Leu Ser Ala Ala Ala Ile Lys Arg
          65           70           75           80
Ile Val Ala Thr Ala Lys Ala Ser Gly Lys Lys Leu Gln Lys Val Thr
          85           90           95
Leu Lys Val Ser Pro Arg Gly Ile Ile Leu Thr Asp Asn Leu Thr Asn
          100          105          110
Gln Leu Ile Glu Asn Val Ser Ile Tyr Arg Ile Ser Tyr Cys Thr Ala
          115          120          125
Asp Lys Met His Asp Lys Val Phe Ala Tyr Ile Ala Gln Ser Gln His
          130          135          140
Asn Gln Ser Leu Glu Cys His Ala Phe Leu Cys Thr Lys Arg Lys Met
          145          150          155          160
Ala Gln Ala Val Thr Leu Thr Val Ala Gln Ala Phe Lys Val Ala Phe
          165          170          175
Glu Phe Trp Gln Val Ser Lys Glu Glu Lys Glu Lys Arg Asp Lys Ala
          180          185          190
Ser Gln Glu Gly Gly Asp Val Leu Gly Ala Arg Gln Asp Cys Thr Pro
          195          200          205
Pro Leu Lys Ser Leu Val Ala Thr Gly Asn Leu Leu Asp Leu Glu Glu
          210          215          220
Thr Ala Lys Ala Pro Leu Ser Thr Val Ser Ala Asn Thr Thr Asn Met
          225          230          235          240
Asp Glu Val Pro Arg Pro Gln Ala Leu Ser Gly Ser Ser Val Val Trp
          245          250          255
Glu Leu Asp Asp Gly Leu Asp Glu Ala Phe Ser Arg Leu Ala Gln Ser
          260          265          270
Arg Thr Asn Pro Gln Val Leu Asp Thr Gly Leu Thr Ala Gln Asp Met
          275          280          285
His Tyr Ala Gln Cys Leu Ser Pro Val Asp Trp Asp Lys Pro Asp Ser
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<210> 3467

<211> 638

<212> DNA

<213> Homo sapiens

<400> 3467

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180

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 420
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 480
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 540
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 638

<210> 3468

<211> 88

<212> PRT

<213> Homo sapiens

<400> 3468

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Tyr	Asp	Phe	Pro	Pro	Leu	Cys	Met	Ser	Gly	Leu	His	Asp	Phe	Gln	Phe
			20					25					30		
Trp	Leu	Cys	Tyr	Thr	Ser	Cys	Tyr	Gln	Gln	Asn	Arg	Val	Ser	Leu	Gly
		35				40						45			
Gln	Ser	Cys	Gly	Tyr	Thr	Ser	Val	Ser	Gln	Asp	Phe	Leu	Cys	Gln	Arg
		50				55				60					
Ala	Val	Lys	Leu	Arg	Thr	Lys	Val	Ile	Lys	Ile	Gln	Leu	Tyr	Tyr	Trp
65					70				75					80	
Ile	Val	Leu	Asp	Cys	Phe	Ser	Ser								
					85										

<210> 3469

<211> 1710

<212> DNA

<213> Homo sapiens

<400> 3469

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 aacaaagaac cgccggcgcc ggcccagcag ctgcagccgc agcctgtggc tgtgcagggc
 180
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 240
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780
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<210> 3470

<211> 322

<212> PRT

<213> Homo sapiens

<400> 3470

Ala Ala Ala Pro Gly Asn Gly Arg Ala Ser Ala Pro Arg Leu Leu Leu

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      20           25           30
Pro Asp Glu Asp Leu Ser His Arg Asn Lys Glu Pro Pro Ala Pro Ala
      35           40           45
Gln Gln Leu Gln Pro Gln Pro Val Ala Val Gln Gly Pro Glu Pro Ala
      50           55           60
Arg Val Glu Lys Ile Phe Thr Pro Ala Ala Pro Val His Thr Asn Lys
      65           70           75           80
Glu Asp Pro Ala Thr Gln Thr Asn Leu Gly Phe Ile His Ala Phe Val
      85           90           95
Ala Ala Ile Ser Val Ile Ile Val Ser Glu Leu Gly Asp Lys Thr Phe
      100          105          110
Phe Ile Ala Ala Ile Met Ala Met Arg Tyr Asn Arg Leu Thr Val Leu
      115          120          125
Ala Gly Ala Met Leu Ala Leu Gly Leu Met Thr Cys Leu Ser Val Leu
      130          135          140
Phe Gly Tyr Ala Thr Thr Val Ile Pro Arg Val Tyr Thr Tyr Tyr Val
      145          150          155          160
Ser Thr Val Leu Phe Ala Ile Phe Gly Ile Arg Met Leu Arg Glu Gly
      165          170          175
Leu Lys Met Ser Pro Asp Glu Gly Gln Glu Glu Leu Glu Glu Val Gln
      180          185          190
Ala Glu Leu Lys Lys Lys Asp Glu Glu Phe Gln Arg Thr Lys Leu Leu
      195          200          205
Asn Gly Pro Gly Asp Val Glu Thr Gly Thr Ser Ile Thr Val Pro Gln
      210          215          220
Lys Lys Trp Leu His Phe Ile Ser Pro Ile Phe Val Gln Ala Leu Thr
      225          230          235          240
Leu Thr Phe Leu Ala Glu Trp Gly Asp Arg Ser Gln Leu Thr Thr Ile
      245          250          255
Val Leu Ala Ala Arg Glu Asp Pro Tyr Gly Val Ala Val Gly Gly Thr
      260          265          270
Val Gly His Cys Leu Cys Thr Gly Leu Ala Val Ile Gly Gly Arg Met
      275          280          285
Ile Ala Gln Lys Ile Ser Val Arg Thr Val Thr Ile Ile Gly Gly Ile
      290          295          300
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<210> 3471

<211> 2335

<212> DNA

<213> Homo sapiens

<400> 3471

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gagaagtgcc gtagcgacac ggagatcctg ccctccctgt tcatgcgctg caccaccgac
180

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<210> 3472

<211> 631

<212> PRT

<213> Homo sapiens

<400> 3472

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Val	Val	Ala	Thr	Ala	Asp	Gly	Ser	Ser	Ala	Ser	Pro	Val	Gln	Phe	Tyr
			20					25					30		
Lys	Val	Cys	Val	Ser	Val	Val	Ser	Glu	Lys	Cys	Arg	Ile	Asp	Thr	Glu
		35					40					45			
Ile	Leu	Pro	Ser	Leu	Phe	Met	Arg	Cys	Thr	Thr	Asp	Leu	Asn	Arg	Lys
	50					55					60				
Asp	Lys	Phe	Pro	Ala	Ile	Thr	His	Leu	Lys	Phe	Leu	Ala	Arg	Asp	Met
65				70						75				80	
Ser	Glu	Gln	Val	Leu	Leu	Cys	Ala	Ser	Ser	Gln	Thr	Ser	Ser	Ile	Val
				85					90					95	
Glu	Cys	Trp	Ser	Leu	Arg	Lys	Glu	Gly	Leu	Pro	Val	Asn	Asn	Ile	Phe
			100					105					110		
Gln	Gln	Ile	Ser	Pro	Val	Val	Gly	Asp	Lys	Gln	Pro	Thr	Ile	Leu	Lys
		115					120					125			
Trp	Arg	Ile	Leu	Ser	Ala	Thr	Asn	Asp	Leu	Asp	Arg	Val	Ser	Ala	Val
	130					135					140				
Ala	Leu	Pro	Lys	Leu	Pro	Ile	Ser	Leu	Thr	Asn	Thr	Asp	Leu	Lys	Val
145				150						155				160	
Ala	Ser	Asp	Thr	Gln	Phe	Tyr	Pro	Gly	Leu	Gly	Leu	Ala	Leu	Ala	Phe
				165					170					175	
His	Asp	Gly	Ser	Val	His	Ile	Val	His	Arg	Leu	Ser	Leu	Gln	Thr	Met
		180						185					190		
Ala	Val	Phe	Tyr	Ser	Ser	Ala	Ala	Pro	Arg	Pro	Val	Asp	Glu	Pro	Ala
		195					200					205			
Met	Lys	Arg	Pro	Arg	Thr	Ala	Gly	Pro	Ala	Val	His	Leu	Lys	Ala	Met
	210					215					220				
Gln	Leu	Ser	Trp	Thr	Ser	Leu	Ala	Leu	Val	Gly	Ile	Asp	Ser	His	Gly

<210> 3473
<211> 1660

<212> DNA

<213> Homo sapiens

<400> 3473

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240
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420
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540
gagtttggcg ttctcagcgc caagaaggag cccatccaac cttcgggtgct cagacggacc
600
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660
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1500

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 1560
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<210> 3474

<211> 474

<212> PRT

<213> Homo sapiens

<400> 3474

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Ile	Ser	Gly	Leu	Leu	Leu	Cys	Arg	Trp	Thr	Cys	Arg	His	Cys	Cys	Gln
			20				25						30		
Lys	Cys	Tyr	Glu	Ser	Ser	Cys	Cys	Gln	Ser	Ser	Glu	Asp	Glu	Val	Glu
			35				40					45			
Ile	Leu	Gly	Pro	Phe	Pro	Ala	Gln	Thr	Pro	Pro	Trp	Leu	Met	Ala	Ser
	50					55					60				
Arg	Ser	Ser	Asp	Lys	Asp	Gly	Asp	Ser	Val	His	Thr	Ala	Ser	Glu	Val
65					70					75				80	
Pro	Leu	Thr	Pro	Arg	Thr	Asn	Ser	Pro	Asp	Gly	Arg	Arg	Ser	Ser	Ser
				85					90					95	
Asp	Thr	Ser	Lys	Ser	Thr	Tyr	Ser	Leu	Thr	Arg	Arg	Ile	Ser	Ser	Leu
			100					105					110		
Glu	Ser	Arg	Arg	Pro	Ser	Ser	Pro	Leu	Ile	Asp	Ile	Lys	Pro	Ile	Glu
			115				120					125			
Phe	Gly	Val	Leu	Ser	Ala	Lys	Lys	Glu	Pro	Ile	Gln	Pro	Ser	Val	Leu
	130					135					140				
Arg	Arg	Thr	Tyr	Asn	Pro	Asp	Asp	Tyr	Phe	Arg	Lys	Phe	Glu	Pro	His
145					150					155					160
Leu	Tyr	Ser	Leu	Asp	Ser	Asn	Ser	Asp	Asp	Val	Asp	Ser	Leu	Thr	Asp
			165						170					175	
Glu	Glu	Ile	Leu	Ser	Lys	Tyr	Gln	Leu	Gly	Met	Leu	His	Phe	Ser	Thr
			180					185					190		
Gln	Tyr	Asp	Leu	Leu	His	Asn	His	Leu	Thr	Val	Arg	Val	Ile	Glu	Ala
			195				200					205			
Arg	Asp	Leu	Pro	Pro	Pro	Ile	Ser	His	Asp	Gly	Ser	Arg	Gln	Asp	Met
	210					215					220				
Ala	His	Ser	Asn	Pro	Tyr	Val	Lys	Ile	Cys	Leu	Leu	Pro	Asp	Gln	Lys
225					230					235					240
Asn	Ser	Lys	Gln	Thr	Gly	Val	Lys	Arg	Lys	Thr	Gln	Lys	Pro	Val	Phe
			245						250					255	
Glu	Glu	Arg	Tyr	Thr	Phe	Glu	Ile	Pro	Phe	Leu	Glu	Ala	Gln	Arg	Arg
			260					265					270		
Thr	Leu	Leu	Leu	Thr	Val	Val	Asp	Phe	Asp	Lys	Phe	Ser	Arg	His	Cys
			275				280					285			
Val	Ile	Gly	Lys	Val	Ser	Val	Pro	Leu	Cys	Glu	Val	Asp	Leu	Val	Lys
	290					295					300				
Gly	Gly	His	Trp	Trp	Lys	Ala	Leu	Ile	Pro	Ser	Ser	Gln	Asn	Glu	Val
305					310					315					320
Glu	Leu	Gly	Glu	Leu	Leu	Leu	Ser	Leu	Asn	Tyr	Leu	Pro	Ser	Ala	Gly

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          325          330          335
Arg Leu Asn Val Asp Val Ile Arg Ala Lys Gln Leu Leu Gln Thr Asp
          340          345          350
Val Ser Gln Gly Ser Asp Pro Phe Val Lys Ile Gln Leu Val His Gly
          355          360          365
Leu Lys Leu Val Lys Thr Lys Lys Thr Ser Phe Leu Arg Gly Thr Ile
          370          375          380
Asp Pro Phe Tyr Asn Glu Ser Phe Ser Phe Lys Val Pro Gln Glu Glu
          385          390          395          400
Leu Glu Asn Ala Ser Leu Val Phe Thr Val Phe Gly His Asn Met Lys
          405          410          415
Ser Ser Asn Asp Phe Ile Gly Arg Ile Val Ile Gly Gln Tyr Ser Ser
          420          425          430
Gly Pro Ser Glu Thr Asn His Trp Arg Arg Met Leu Asn Thr His Arg
          435          440          445
Thr Ala Val Glu Gln Trp His Ser Leu Arg Ser Arg Ala Glu Cys Asp
          450          455          460
Arg Val Ser Pro Ala Ser Leu Glu Val Thr
          465          470

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<210> 3475

<211> 514

<212> DNA

<213> Homo sapiens

<400> 3475

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120
gaggtgctcaacacgctggtgcagctggcgccgacctggccatctttgcccctttggggg
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240
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<210> 3476

<211> 171

<212> PRT

<213> Homo sapiens

<400> 3476

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Trp Leu Val Leu Gln Pro Phe Phe Tyr Ser Leu Arg Pro Leu Cys Val

```

```

                20                25                30
His Pro Lys Ala Val Thr Arg Met Glu Val Leu Asn Thr Leu Val Gln
      35                40                45
Leu Ala Ala Asp Leu Ala Ile Phe Ala Leu Trp Gly Leu Lys Pro Val
      50                55                60
Val Tyr Leu Leu Ala Ser Ser Phe Leu Gly Leu Gly Leu His Pro Ile
      65                70                75                80
Ser Gly His Phe Val Ala Glu His Tyr Met Phe Leu Lys Gly His Glu
      85                90                95
Thr Tyr Ser Tyr Tyr Gly Pro Leu Asn Trp Ile Thr Phe Asn Val Gly
      100                105                110
Tyr His Val Glu His His Asp Phe Pro Ser Ile Pro Gly Tyr Asn Leu
      115                120                125
Pro Leu Val Arg Lys Ile Ala Pro Glu Tyr Tyr Asp His Leu Pro Gln
      130                135                140
His His Ser Trp Val Lys Val Leu Trp Asp Phe Val Phe Glu Asp Ser
      145                150                155                160
Leu Gly Pro Tyr Ala Arg Val Lys Arg Val Tyr
      165                170

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<210> 3477

<211> 356

<212> DNA

<213> Homo sapiens

<400> 3477

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180
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240
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356

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<210> 3478

<211> 116

<212> PRT

<213> Homo sapiens

<400> 3478

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Met Ile Arg Met Pro Ser Arg Lys Asn His Pro Leu Pro Val Phe Ser
  1                5                10                15
Leu Ala Val Arg Val Gly Lys Trp Arg Arg His Leu Thr Ile Thr Leu
      20                25                30
Ser Gly Asp Lys Asp Lys Gly Leu Pro Glu Thr Ser Val Val Arg Thr
      35                40                45
Ser Lys His Lys Lys Asn Ala Tyr Leu Leu Val Pro Leu Cys His Ile
      50                55                60
Trp Ser His Leu Ser Gly Ser Lys Val Lys Gly His Phe Leu Lys Phe

```

```

65              70              75              80
Phe Leu Leu Phe Ile Lys Ser His Gly Arg Val Asp Ala Gly Gly Gln
              85              90              95
Ala Pro Val Ala Gly Leu Asp Glu Asp Pro Glu Thr Ala Gly Gln Ala
              100              105              110
Ala Glu Ala Arg
              115

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<210> 3479

<211> 797

<212> DNA

<213> Homo sapiens

<400> 3479

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120
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660
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797

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<210> 3480

<211> 192

<212> PRT

<213> Homo sapiens

<400> 3480

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Asn Leu Arg Arg Tyr Pro Gly Ser Asp Arg Ile Met Leu Gln Lys Trp
              20              25              30
Gln Lys Arg Asp Ile Ser Asn Phe Glu Tyr Leu Met Tyr Leu Asn Thr

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      35          40          45
Ala Ala Gly Arg Thr Cys Asn Asp Tyr Met Gln Tyr Pro Val Phe Pro
   50          55          60
Trp Val Leu Ala Asp Tyr Thr Ser Glu Thr Leu Asn Leu Ala Asn Pro
  65          70          75          80
Lys Ile Phe Arg Asp Leu Ser Lys Pro Met Gly Ala Gln Thr Lys Glu
      85          90          95
Arg Lys Leu Lys Phe Ile Gln Arg Phe Lys Glu Val Glu Lys Thr Glu
      100          105          110
Gly Asp Met Thr Ala Gln Cys His Tyr Tyr Thr His Tyr Ser Ser Ala
      115          120          125
Ile Ile Val Ala Ser Tyr Leu Val Arg Met Pro Pro Phe Thr Gln Ala
      130          135          140
Phe Cys Ala Leu Gln Val Ser Cys Cys His Ser Leu Tyr Thr His Thr
  145          150          155          160
His Thr His Thr His Thr Tyr Ala Cys Ile Thr Arg Leu Arg Pro Val
      165          170          175
Leu Glu Gln Arg Gln Asp Ala Ser Ala Lys Asn Leu Val Ile Ser Gln
      180          185          190

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<210> 3481

<211> 1794

<212> DNA

<213> Homo sapiens

<400> 3481

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aaaagcccag cacttcccag agccagggac tgacacaaca gaaagtctgc aagcaatgcc
  120
atgaggtcct gaccagaggg tcttctgccca atgcctccaa gtggtcacca cctcagctct
  180
gcagaccctg cgggtgctggg agccaccatg gagagtaggt gctacggctg cgctgtcaag
  240
ttcacctctt tcaagaagga gtacggctgt aagaattgtg gcaggngctt ctgttcaggc
  300
tgcctaagct tcaagtgcagc agtgcctcgg actgggaaca cccaacagaa agtctgcaag
  360
caatgccatg aggtcctgac cagagggctt tctgccaatg cctccaagtg gtcaccacct
  420
cagaactata agaagcgtgt ggcagccttg gaagccaagc aaaagcccag cacttcccag
  480
agccagggac tgacacgaca agaccagatg attgctgagc gcctagcacg actccgccag
  540
gagaacaagc ccaagttagt cccctcacag gcagagatag aggcaagggt ggctgcccta
  600
aaggatgaac gtcagggttc catcccttcc acccaggaaa tggaggcacg acttgacgag
  660
ttgcagggca gagttctacc ttctcaaacc cccagccccg gcacatcaca caccggacac
  720
caggacccaa gcccagcaga cacaggatct gctaacgcag ctggcagctg aggtggctat
  780
cgatgaaagc tggaaggag gagggccagc tgcctctctc cagaatgatc tcaaccaggg
  840

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tggcccagg agcactaatt ccaagaggca ggccacttgg ttcttggaga aggagaagag
 900
 cagactgctg gctgaggcag cacttgagtt gcgggaggag aacacgaggc aggaacggat
 960
 tctggccctg gccaagcgac tagccatgct gcggggacag gaccccgaga gagtgcacct
 1020
 ccaggactat cgctcccag acagtgatga cgacgaggat gaggagacag ccatccaaag
 1080
 agtcctgcag cagctcactg aagaagcttc cctggatgag gcaagtggct ttaacatccc
 1140
 tgcagagcag gcttctcgac cctggacgca accccgcggg gcagagcctg agggccagga
 1200
 tgtggacccc aggcctgagg ctgaggaaga ggagctcccc tgggtgctgca tctgcaatga
 1260
 ggatgccacc ctacgtgcg ctggctgcga tggggacctc ttctgtgccc gctgcttcg
 1320
 agagggccat gatgcctttg agcttaaaga gcaccagaca tctgcctact ctctccacg
 1380
 tgcaggccaa gagcactgaa gacaccctgg tcctcccga agggcagtcc cacaggcagc
 1440
 ggcacccatt tctgggcccc gccacaggac gtccgatggg agagcttgct tggctctact
 1500
 gatgatggat agggcccttc ctgagccttg gtgtccctgg aatgaggaaa gattctccat
 1560
 tcgagagaat gactgggagg gaagaagtcg gggccctcct attagaagcc cagactggaa
 1620
 gtgagaggca tgatggggag agaccagact gaatctacgg gtgagccctg taacctggct
 1680
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 1740
 ggaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa
 1794

<210> 3482

<211> 206

<212> PRT

<213> Homo sapiens

<400> 3482

Met	Pro	Pro	Ser	Gly	His	His	Leu	Ser	Ser	Ala	Asp	Pro	Ala	Val	Leu
1				5				10						15	
Gly	Ala	Thr	Met	Glu	Ser	Arg	Cys	Tyr	Gly	Cys	Ala	Val	Lys	Phe	Thr
			20				25						30		
Leu	Phe	Lys	Lys	Glu	Tyr	Gly	Cys	Lys	Asn	Cys	Gly	Arg	Xaa	Phe	Cys
		35					40					45			
Ser	Gly	Cys	Leu	Ser	Phe	Ser	Ala	Ala	Val	Pro	Arg	Thr	Gly	Asn	Thr
	50					55				60					
Gln	Gln	Lys	Val	Cys	Lys	Gln	Cys	His	Glu	Val	Leu	Thr	Arg	Gly	Ser
65				70					75					80	
Ser	Ala	Asn	Ala	Ser	Lys	Trp	Ser	Pro	Pro	Gln	Asn	Tyr	Lys	Lys	Arg
			85					90					95		
Val	Ala	Ala	Leu	Glu	Ala	Lys	Gln	Lys	Pro	Ser	Thr	Ser	Gln	Ser	Gln
			100					105					110		
Gly	Leu	Thr	Arg	Gln	Asp	Gln	Met	Ile	Ala	Glu	Arg	Leu	Ala	Arg	Leu

```

      115      120      125
Arg  Gln  Glu  Asn  Lys  Pro  Lys  Leu  Val  Pro  Ser  Gln  Ala  Glu  Ile  Glu
      130      135      140
Ala  Arg  Leu  Ala  Ala  Leu  Lys  Asp  Glu  Arg  Gln  Gly  Ser  Ile  Pro  Ser
145      150      155      160
Thr  Gln  Glu  Met  Glu  Ala  Arg  Leu  Ala  Ala  Leu  Gln  Gly  Arg  Val  Leu
      165      170      175
Pro  Ser  Gln  Thr  Pro  Gln  Pro  Gly  Thr  Ser  His  Thr  Gly  His  Gln  Asp
      180      185      190
Pro  Ser  Pro  Ala  Asp  Thr  Gly  Ser  Ala  Asn  Ala  Ala  Gly  Ser
      195      200      205

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<210> 3483

<211> 477

<212> DNA

<213> Homo sapiens

<400> 3483

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nccggccgcgg cgcggaacgg cgccctccgc cccaccatgg gcaacagcgc gagccgcaac
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gacttcgagt gggtctacac cgaccagccg cacacgcagc ggcgcaagga gatactggcc
120
aagtaccggg ccatcaaggc cctgatgcgg ccagaccgcg gcctcaagtg ggcggggctg
180
gtgctggtgc tgggtcagat gctggcctgc tggctggtgc gcgggctggc ctggcgctgg
240
ctgctgttct gggcctacgc ctttggtggc tgcgtgaacc actcgtgac gctggccatc
300
cagacatct cgcacaacgc ggccttcggc acggggccgtg cggcacgcaa ccgctggctg
360
gccgtgttcg ccaacctgcc cgtgggtgtg ccctacgccg cctccttcaa gaagtaccac
420
gtggaccacc accgctacct gggcgggcgac ggactggacg tggacgtgcc cacgcgt
477

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<210> 3484

<211> 147

<212> PRT

<213> Homo sapiens

<400> 3484

```

Met  Gly  Asn  Ser  Ala  Ser  Arg  Asn  Asp  Phe  Glu  Trp  Val  Tyr  Thr  Asp
1      5      10      15
Gln  Pro  His  Thr  Gln  Arg  Arg  Lys  Glu  Ile  Leu  Ala  Lys  Tyr  Pro  Ala
      20      25      30
Ile  Lys  Ala  Leu  Met  Arg  Pro  Asp  Pro  Arg  Leu  Lys  Trp  Ala  Gly  Leu
      35      40      45
Val  Leu  Val  Leu  Val  Gln  Met  Leu  Ala  Cys  Trp  Leu  Val  Arg  Gly  Leu
      50      55      60
Ala  Trp  Arg  Trp  Leu  Leu  Phe  Trp  Ala  Tyr  Ala  Phe  Gly  Gly  Cys  Val
65      70      75      80
Asn  His  Ser  Leu  Thr  Leu  Ala  Ile  His  Asp  Ile  Ser  His  Asn  Ala  Ala
      85      90      95
Phe  Gly  Thr  Gly  Arg  Ala  Ala  Arg  Asn  Arg  Trp  Leu  Ala  Val  Phe  Ala

```

	100		105		110										
Asn	Leu	Pro	Val	Gly	Val	Pro	Tyr	Ala	Ala	Ser	Phe	Lys	Lys	Tyr	His
	115		120		125										
Val	Asp	His	His	Arg	Tyr	Leu	Gly	Gly	Asp	Gly	Leu	Asp	Val	Asp	Val
	130		135		140										
Pro	Thr	Arg													
145															

<210> 3485

<211> 812

<212> DNA

<213> Homo sapiens

<400> 3485

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120
gtctaaaaaa tcttattgtt ctcaggtag cagttagttg agcagagtc attggtgaag
180
caatctagtt attggcaaatt tctaacacat ggtaagggtgt gggggaaagg atttaaaata
240
acagaaaaat gtaagtacaa acatacataa cagcaaaata aaactcactt taacaaaaat
300
ttatttaaaa tgttaccctc atatttcctc aatgaccaac ttgtttcagt tttatctccc
360
cctcatccgg ttattttatg tctttttggg aggaaggagg atgaggggtt ttgtttttta
420
acaaaatcac tggcttttta aaaagtgtta ctgcagtcatt ttataagatg catgttatgt
480
ggaagtgata cctgagttgt ttgcattggc aatggaagag gcagcagctc tgaaaggagt
540
atgagtcagg aaaaaaatcc ttcaggaacc ttcaagattg aagaaagaac ttcttttaac
600
attaaagacc aagtattatt ggccagagtc tcttctgaga ttgtgagttt ttcattaact
660
ccttgtgtaa aagtcagtaa aatatcaatg atatcattct gaattttctg ttcattacta
720
tccaaacgac ctgagagggg gatagagcac aggagcatat gtaaagtaac aagcgctgaa
780
ggaacacgca tgcctttaa ctcaaaggat cc
812

<210> 3486

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3486

Met	Arg	Val	Pro	Ser	Ala	Leu	Val	Thr	Leu	His	Met	Leu	Leu	Cys	Ser
1			5					10					15		
Ile	Pro	Leu	Ser	Gly	Arg	Leu	Asp	Ser	Asp	Glu	Gln	Lys	Ile	Gln	Asn
		20					25					30			
Asp	Ile	Ile	Asp	Ile	Leu	Leu	Thr	Phe	Thr	Gln	Gly	Val	Asn	Glu	Lys

```

          35              40              45
Leu Thr Ile Ser Glu Glu Thr Leu Ala Asn Asn Thr Trp Ser Leu Met
          50              55              60
Leu Lys Glu Val Leu Ser Ser Ile Leu Lys Val Pro Glu Gly Phe Phe
65          70          75          80
Ser Gly Leu Ile Leu Leu Ser Glu Leu Leu Pro Leu Pro Leu Pro Met
          85          90          95
Gln Thr Thr Gln Val Ser Leu Pro His Asn Met His Leu Ile Asn Asp
          100          105          110
Cys Ser Asn Thr Phe
          115

```

<210> 3487

<211> 772

<212> DNA

<213> Homo sapiens

<400> 3487

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nnattgtatc aaaatcctag atttgaataa cttattatct taaataatca gtaactaaaa
60
ccaagcaatc catcacacaa agaggggaaa gggtaatat ctgagttata aattttttac
120
cctgtctgat aaaaatagaa gcctgaaagt ttaaattttt cctggattta aatttaaaga
180
taaatttggt tttcagtga atatcctcaa tagcaatttt accaaagagg ctttcttctg
240
aaggccacct ctgaaataat tagaggataa atgtcaatgg catgatatta agatattact
300
tggccaggcg tggtcgtcac gcgtgtaatc ccagcacttt gggaggccga ggcagggtgga
360
tcacgaggtc aagaaatcga gaccagcctg gctaacacag tgaaaccccg tctcattctg
420
agcttcttga caccttttaa tccagtcact gaaattagca tctgcaccta gaaagaaaaa
480
actgactata acatcactca tctgcacaac ctattaatca gcaaatactt actgaatacc
540
tactacatcc caggcagtgt tctaggcact ggggagtcgg cagcgaacaa aacctgtctt
600
aacagacctt atcaccaact ctactatagt tataaacata ccaatagttt aacatttagt
660
tgttaatcat gaaacatttt gattttttta aaattttaac tacagtcaac ctttaatttca
720
cagatacaaa taatctgcat ttcccccaat cccgctgctc ttagagaagc tt
772

```

<210> 3488

<211> 59

<212> PRT

<213> Homo sapiens

<400> 3488

```

Asp Ile Thr Trp Pro Gly Val Val Val Thr Arg Val Ile Pro Ala Leu
1          5          10          15
Trp Glu Ala Glu Ala Gly Gly Ser Arg Gly Gln Glu Ile Glu Thr Ser

```

```

                20                25                30
Leu Ala Asn Thr Val Lys Pro Arg Leu Ile Leu Ser Phe Leu Thr Pro
                35                40                45
Phe Asn Pro Val Thr Glu Ile Ser Ile Cys Thr
                50                55

```

<210> 3489
 <211> 288
 <212> DNA
 <213> Homo sapiens

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<400> 3489
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60
agggagacca ggtctggccc ccaactctaa ggctcatctt agaggcgaga ttcaggccca
120
gcccaggggtg ccccatgagg cctggtggtt ggaggcagag ggtatccctt gcccaaattc
180
gtgccacatt cacagtcaact gggaaagcta cggggatggg ccgggcgcgg tggctcacac
240
ctgtaatccc agcactttgg agagccccaa gacgacggat cacgagtc
288

```

<210> 3490
 <211> 90
 <212> PRT
 <213> Homo sapiens

```

<400> 3490
Met Gly Ala His Leu Leu Pro Gly Pro Gly Arg Pro Gly Arg Pro Gly
1                5                10                15
Arg Pro Gly Leu Ala Pro Asn Ser Lys Ala His Leu Arg Gly Glu Ile
                20                25                30
Gln Ala Gln Pro Arg Val Pro His Glu Ala Trp Trp Leu Glu Ala Glu
                35                40                45
Gly Ile Pro Cys Pro Asn Ser Cys His Ile His Ser His Trp Glu Ser
                50                55                60
Tyr Gly Asp Gly Pro Gly Ala Val Ala His Thr Cys Asn Pro Ser Thr
65                70                75                80
Leu Glu Ser Pro Lys Thr Thr Asp His Glu
                85                90

```

<210> 3491
 <211> 568
 <212> DNA
 <213> Homo sapiens

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<400> 3491
gggaaccgac gtccctctgt ggtgaaattc cacccttca cgccgtgcat cgccgtagcc
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gacaaggaca gcatctgctt ttgggactgg gagaaagggg agaagctgga ttatttccac
120
aatgggaacc ctcggtacac gagggtcact gccatggagt atctgaatgg ccaggactgc
180

```

```
<400> 3493
nggggggggat atccatgcag cgatcaggat gaaagaggtg attcaggaca accaagtaat
60
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aaggaactgt ttggagatga cagtgaggac gagggagctt cacatcatag tggtagtgat
120
aatcactctg aaagatcaga caatagatca gaagcttctg agcgttctga ccatgaggac
180
aatgaccctt cagatgtaga tcagcacagt ggatcagaag cccctaataga tgatgaagac
240
gaaggtcata gatcggatgg agggagccat cattcagaag cagaaggttc tgaaaaagca
300
cattcagatg atgaaaaatg gggcagagaa gataaaagt accagtcaga tgatgaaaag
360
atacaaaaatt ctgatgatga ggagagggca caaggatctg atgaagataa gctgcagaat
420
tctgacgatg atgagaaaat gcagaacaca gatgatgagg agaggcctca gctttccgat
480
gatgagagac aacagctatc tgaggaggaa aaggctaatt ctgatgatga acggccggta
540
gcttctgata atgatgatga gaaacagaat tctgatgatg aagaacaacc acagctgtct
600
gatgaagaga aaatgcaaaa ttctgatgat gaaaggccac agggcccaga tgaagaacac
660
aggcattcag atgatgaaga ggaacaggat cataaatcag aatccgcaag aggcagtgat
720
agtgaagatg aagttttacg aatgaaacgc aagaatgcga ttgcatctga ttcagaagcg
780
gatagtgaca ctgaggtgcc aaaagataat agtggaacca tggatttatt tggaggtgca
840
gatgatatct cttcagggag tgatggagaa gacaaaccac ctactccagg acagcctgtt
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960
gaagtagaaa taccctaaagt aaacactgat ttaggaaaacg acttatattt tgttaaactg
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cggatagtca agtggtcaga tgggaagcatg tccctgcatt taggcaatga agtgtttgat
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1380
gccacacata gaaagatgac tctgtcactt gcagataggt gttcaaagac acagaagatt
1440
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1620
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1680

cgagaggaac gagccagaat ctattcatca gacagtgatg agggatcaga agaagataaa
 1740
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 1800
 aagagaaaag cagaagatga tgataaagca aataaaaagc ataagaagta tgtgatcagc
 1860
 gatgaagagg aagaagatga tgattgaagt atgaaatatg aaaacatttt atatatttta
 1920
 ttgtacagtt ataaatatgt aaacatgagt tattttgatt gaaatgaatc gatttgcttt
 1980
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 2040
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 2100
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 2220
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 2244

<210> 3494

<211> 628

<212> PRT

<213> Homo sapiens

<400> 3494

Xaa	Gly	Gly	Tyr	Pro	Cys	Ser	Asp	Gln	Asp	Glu	Arg	Gly	Asp	Ser	Gly
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Gln	Pro	Ser	Asn	Lys	Glu	Leu	Phe	Gly	Asp	Asp	Ser	Glu	Asp	Glu	Gly
			20					25					30		
Ala	Ser	His	His	Ser	Gly	Ser	Asp	Asn	His	Ser	Glu	Arg	Ser	Asp	Asn
		35					40					45			
Arg	Ser	Glu	Ala	Ser	Glu	Arg	Ser	Asp	His	Glu	Asp	Asn	Asp	Pro	Ser
	50					55					60				
Asp	Val	Asp	Gln	His	Ser	Gly	Ser	Glu	Ala	Pro	Asn	Asp	Asp	Glu	Asp
65				70						75				80	
Glu	Gly	His	Arg	Ser	Asp	Gly	Gly	Ser	His	His	Ser	Glu	Ala	Glu	Gly
			85					90						95	
Ser	Glu	Lys	Ala	His	Ser	Asp	Asp	Glu	Lys	Trp	Gly	Arg	Glu	Asp	Lys
			100					105					110		
Ser	Asp	Gln	Ser	Asp	Asp	Glu	Lys	Ile	Gln	Asn	Ser	Asp	Asp	Glu	Glu
		115				120						125			
Arg	Ala	Gln	Gly	Ser	Asp	Glu	Asp	Lys	Leu	Gln	Asn	Ser	Asp	Asp	Asp
	130					135					140				
Glu	Lys	Met	Gln	Asn	Thr	Asp	Asp	Glu	Glu	Arg	Pro	Gln	Leu	Ser	Asp
145				150						155				160	
Asp	Glu	Arg	Gln	Gln	Leu	Ser	Glu	Glu	Glu	Lys	Ala	Asn	Ser	Asp	Asp
			165					170					175		
Glu	Arg	Pro	Val	Ala	Ser	Asp	Asn	Asp	Asp	Glu	Lys	Gln	Asn	Ser	Asp
		180						185					190		
Asp	Glu	Glu	Gln	Pro	Gln	Leu	Ser	Asp	Glu	Glu	Lys	Met	Gln	Asn	Ser
	195					200						205			
Asp	Asp	Glu	Arg	Pro	Gln	Ala	Pro	Asp	Glu	Glu	His	Arg	His	Ser	Asp

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      210              215              220
Asp Glu Glu Glu Gln Asp His Lys Ser Glu Ser Ala Arg Gly Ser Asp
225              230              235              240
Ser Glu Asp Glu Val Leu Arg Met Lys Arg Lys Asn Ala Ile Ala Ser
      245              250              255
Asp Ser Glu Ala Asp Ser Asp Thr Glu Val Pro Lys Asp Asn Ser Gly
      260              265              270
Thr Met Asp Leu Phe Gly Gly Ala Asp Asp Ile Ser Ser Gly Ser Asp
      275              280              285
Gly Glu Asp Lys Pro Pro Thr Pro Gly Gln Pro Val Asp Glu Asn Gly
      290              295              300
Leu Pro Gln Asp Gln Gln Glu Glu Glu Pro Ile Pro Glu Thr Arg Ile
305              310              315              320
Glu Val Glu Ile Pro Lys Val Asn Thr Asp Leu Gly Asn Asp Leu Tyr
      325              330              335
Phe Val Lys Leu Pro Asn Phe Leu Ser Val Glu Pro Arg Pro Phe Asp
      340              345              350
Pro Gln Tyr Tyr Glu Asp Glu Phe Glu Asp Glu Glu Met Leu Asp Glu
      355              360              365
Glu Gly Arg Thr Arg Leu Lys Leu Lys Val Glu Asn Thr Ile Arg Trp
      370              375              380
Arg Ile Arg Arg Asp Glu Glu Gly Asn Glu Ile Lys Glu Ser Asn Ala
385              390              395              400
Arg Ile Val Lys Trp Ser Asp Gly Ser Met Ser Leu His Leu Gly Asn
      405              410              415
Glu Val Phe Asp Val Tyr Lys Ala Pro Leu Gln Gly Asp His Asn His
      420              425              430
Leu Phe Ile Arg Gln Gly Thr Gly Leu Gln Gly Gln Ala Val Phe Lys
      435              440              445
Ala Lys Leu Thr Phe Arg Pro His Ser Thr Asp Ser Ala Thr His Arg
      450              455              460
Lys Met Thr Leu Ser Leu Ala Asp Arg Cys Ser Lys Thr Gln Lys Ile
465              470              475              480
Arg Ile Leu Pro Met Ala Gly Arg Asp Pro Glu Cys Gln Arg Thr Glu
      485              490              495
Met Ile Lys Lys Glu Glu Glu Arg Leu Arg Ala Ser Ile Arg Arg Glu
      500              505              510
Ser Gln Gln Arg Arg Met Arg Glu Lys Gln His Gln Arg Gly Leu Ser
      515              520              525
Ala Ser Tyr Leu Glu Pro Asp Arg Tyr Asp Glu Glu Glu Glu Gly Glu
      530              535              540
Glu Ser Ile Ser Leu Ala Ala Ile Lys Asn Arg Tyr Lys Gly Gly Ile
545              550              555              560
Arg Glu Glu Arg Ala Arg Ile Tyr Ser Ser Asp Ser Asp Glu Gly Ser
      565              570              575
Glu Glu Asp Lys Ala Gln Arg Leu Leu Lys Ala Lys Lys Leu Thr Ser
      580              585              590
Asp Glu Glu Gly Glu Pro Ser Gly Lys Arg Lys Ala Glu Asp Asp Asp
      595              600              605
Lys Ala Asn Lys Lys His Lys Lys Tyr Val Ile Ser Asp Glu Glu Glu
      610              615              620
Glu Asp Asp Asp
625

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<210> 3495
 <211> 1085
 <212> DNA
 <213> Homo sapiens

<400> 3495
 cgggggccag ggtgccggca ggggcgtccg gggcgctctg accggcctcg cccgcccccc
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 120
 gcgtccccgg aggagatcaa gaaggcctat cggaagctgg cgctcaagta ccaccggagc
 180
 aagaaccgg atgagggcga gaagtttaaa ctcatatccc aggcataatga agtgctttca
 240
 gatccaaaga aaagggatgt ttatgaccaa ggcggagagc aggcaattaa agaaggagggc
 300
 tcaggcagcc ccagcttctc ttcacccatg gacatctttg acatgttctt tggtggtggt
 360
 ggacggatgg ctagagagag aagaggcaag aatgttgtag accagttatc tgtaactctt
 420
 gaagatctat ataatggagt cacgaagaaa ttggccctcc agaaaaatgt aatttgtag
 480
 aaatgtgaag gtgttggtgg gaagaaggga tcggtggaga agtgcccgt gtgcaagggg
 540
 cgggggatgc agatccacat ccagcagatc gggccgggca tggtagagca gatccagacc
 600
 gtgtgcatcg agtgcaaggg ccagggtgag cgcataacc ccaaggaccg ctgcgagagc
 660
 tgcagcgggg ccaaggtgat ccgtgagaag aagattatcg aggtacatgt tgaaaaaggt
 720
 atgaaagatg ggcaaaagat actatttcat ggagaaggag atcaggagcc tgagctggag
 780
 cctggtgatg tcataattgt gcttgatcag aaggatcata gtgtctttca gagacgagggc
 840
 catgacttga tcatgaaaat gaaaattcag ctttctgaag ctctttgtgg cttcaagaag
 900
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 960
 aagcacgggg acctgagatg cgtgcgcgat gaaggaatgc ccatctacaa agcaccctcg
 1020
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 1080
 ctgga
 1085

<210> 3496
 <211> 337
 <212> PRT
 <213> Homo sapiens

<400> 3496
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 1 5 10 15
 Ala Ser Pro Glu Glu Ile Lys Lys Ala Tyr Arg Lys Leu Ala Leu Lys

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      20      25      30
Tyr His Pro Asp Lys Asn Pro Asp Glu Gly Glu Lys Phe Lys Leu Ile
      35      40      45
Ser Gln Ala Tyr Glu Val Leu Ser Asp Pro Lys Lys Arg Asp Val Tyr
      50      55      60
Asp Gln Gly Gly Glu Gln Ala Ile Lys Glu Gly Gly Ser Gly Ser Pro
65      70      75      80
Ser Phe Ser Ser Pro Met Asp Ile Phe Asp Met Phe Phe Gly Gly Gly
      85      90      95
Gly Arg Met Ala Arg Glu Arg Arg Gly Lys Asn Val Val His Gln Leu
      100      105      110
Ser Val Thr Leu Glu Asp Leu Tyr Asn Gly Val Thr Lys Lys Leu Ala
      115      120      125
Leu Gln Lys Asn Val Ile Cys Glu Lys Cys Glu Gly Val Gly Gly Lys
      130      135      140
Lys Gly Ser Val Glu Lys Cys Pro Leu Cys Lys Gly Arg Gly Met Gln
145      150      155      160
Ile His Ile Gln Gln Ile Gly Pro Gly Met Val Gln Gln Ile Gln Thr
      165      170      175
Val Cys Ile Glu Cys Lys Gly Gln Gly Glu Arg Ile Asn Pro Lys Asp
      180      185      190
Arg Cys Glu Ser Cys Ser Gly Ala Lys Val Ile Arg Glu Lys Lys Ile
      195      200      205
Ile Glu Val His Val Glu Lys Gly Met Lys Asp Gly Gln Lys Ile Leu
      210      215      220
Phe His Gly Glu Gly Asp Gln Glu Pro Glu Leu Glu Pro Gly Asp Val
225      230      235      240
Ile Ile Val Leu Asp Gln Lys Asp His Ser Val Phe Gln Arg Arg Gly
      245      250      255
His Asp Leu Ile Met Lys Met Lys Ile Gln Leu Ser Glu Ala Leu Cys
      260      265      270
Gly Phe Lys Lys Thr Ile Lys Thr Leu Asp Asn Arg Ile Leu Val Ile
      275      280      285
Thr Ser Lys Ala Gly Glu Val Ile Lys His Gly Asp Leu Arg Cys Val
      290      295      300
Arg Asp Glu Gly Met Pro Ile Tyr Lys Ala Pro Leu Glu Lys Gly Ile
305      310      315      320
Leu Ile Ile Gln Phe Leu Val Ile Phe Pro Xaa Lys His Trp Leu Ser
      325      330      335
Leu

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<210> 3497

<211> 1638

<212> DNA

<213> Homo sapiens

<400> 3497

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120
tttttagtat atccttctaa aaagttttcc tgagaatttt tagtttggcc tctcaagttt
180

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ccttatattta cctttttctta aattacctcc ctcccttccct agtgaaatga gccttccttc
 240
 agcatacgca acttatccct attgcttttt tcatacccaa ttttttggtt tatctctttc
 300
 agccaactgg gtcctgaagt agctgaaatg cgaaaaaggc agcagtccca aaatgaagga
 360
 acacctgctg tgtctcaagc tcctggaaac cagaggccca acaacacctg ttgcttttgt
 420
 tgggtgctgtt gttgcagctg ctccctgcctc actgtgagga atgaagaaag aggggaaaat
 480
 gcgggaagac ccacacacac tacaaaaatg gagagtatcc aggtcctaga ggaatgccaa
 540
 aacccactg cagaggaagt cttgtcctgg tctcaaaatt ttgacaagat gatgaaggcc
 600
 ccagcaggaa gaaacctttt cagagagttc ctccgaacag aatacagtga agagaacctt
 660
 cttttctggc ttgcttgtga agacttaaag aaggagcaga aaaaaaagt aattgaagaa
 720
 aaggctagga tgatatatga agattacatt tctatactat caccaaaaga ggtcagttct
 780
 gattctcgag ttagagaggt gatcaataga aatctgttgg atcccaatcc tcacatgtat
 840 aacttcagat atatacttta atgcacagag attcttttcc aaggtttttg 900
 aactctcaaa ttataagtc atttgttgaa agtactgctg gctcttcttc tgaatcttaa
 960
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 1020
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 1080
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 1140
 aaataccaca caaaacaatg aattgccaaa ttgtttggtt tattcaagac tcattctact
 1200
 tgcaagcaaa gtgtatttgt agtcctatga acagtctcct cgtgtatctc cagagactgc
 1260
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 1320
 taacttatat ctgtatttaa ggacttttgt gcaatatggg cttaagaaat aattgccaaa
 1380
 aaaatcggcc atggtttgca ttttttaaca taatctaaga cagaaaaaaa gcaattttta
 1440
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 1500
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 1560
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 1620
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 1638

<210> 3498

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3498

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Gln Ala Pro Gly Asn Gln Arg Pro Asn Asn Thr Cys Cys Phe Cys Trp
          20           25           30
Cys Cys Cys Cys Ser Cys Ser Cys Leu Thr Val Arg Asn Glu Glu Arg
          35           40           45
Gly Glu Asn Ala Gly Arg Pro Thr His Thr Thr Lys Met Glu Ser Ile
          50           55           60
Gln Val Leu Glu Glu Cys Gln Asn Pro Thr Ala Glu Glu Val Leu Ser
65           70           75           80
Trp Ser Gln Asn Phe Asp Lys Met Met Lys Ala Pro Ala Gly Arg Asn
          85           90           95
Leu Phe Arg Glu Phe Leu Arg Thr Glu Tyr Ser Glu Glu Asn Leu Leu
          100          105          110
Phe Trp Leu Ala Cys Glu Asp Leu Lys Lys Glu Gln Asn Lys Lys Val
          115          120          125
Ile Glu Glu Lys Ala Arg Met Ile Tyr Glu Asp Tyr Ile Ser Ile Leu
          130          135          140
Ser Pro Lys Glu Val Ser Leu Asp Ser Arg Val Arg Glu Val Ile Asn
145          150          155          160
Arg Asn Leu Leu Asp Pro Asn Pro His Met Tyr Glu Asp Ala Gln Leu
          165          170          175
Gln Ile Tyr Thr Leu Met His Arg Asp Ser Phe Pro Arg Phe Leu Asn
          180          185          190
Ser Gln Ile Tyr Lys Ser Phe Val Glu Ser Thr Ala Gly Ser Ser Ser
          195          200          205
Glu Ser
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<210> 3499

<211> 732

<212> DNA

<213> Homo sapiens

<400> 3499

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120
tgccacgggc ggcgtcccag cctggcacag aggtattgtg attccanaa tggccaagnc
180
aacagactcn aacctcagga tngttctatt ttgcgccaga agcaataatt ttttttctct
240
tctggaaaagc cttttcaaga tagtgatgtt gatgtggggg cacggcggtc gccgggtaca
300
tggaggtacc ggggtcacag cagcgcaagc accgggaagc agggagcccc tggctctgac
360
tgggcctgta tttttcatgt tgtttctcag ccctctcggc atggtccgga ggcgacggca
420
gtcctcagt cccctccac tctgtctgtt cccctggac atggggcaca cgactcagga
480
ccaggccaga ggcaaaggca aggagcaggc agtacgccag caagagtccc tgtccacggg
540

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agcccatctt cctgccgggc cctccgtccc gccggccgct cctcccgcgc cgcccctaga
 600
 gcatctcccg ccggccaagc ctccctcccg ccanggtccg gggcgatgca cagactcggg
 660
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 720
 gggggcggtg cg
 732

<210> 3500

<211> 168

<212> PRT

<213> Homo sapiens

<400> 3500

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Gly	Ala	Arg	Arg	Ser	Pro	Gly	Thr	Trp	Arg	Tyr	Arg	Gly	His	Ser	Ser
		20						25					30		
Ala	Ser	Thr	Gly	Lys	Gln	Gly	Ala	Pro	Gly	Pro	Asp	Trp	Ala	Cys	Ile
		35					40					45			
Phe	His	Val	Val	Leu	Gln	Pro	Ser	Arg	His	Gly	Pro	Glu	Ala	Thr	Ala
	50					55					60				
Ala	Pro	Gln	Ser	Pro	Pro	Thr	Pro	Ala	Val	Pro	Pro	Gly	His	Gly	Ala
65					70					75				80	
His	Asp	Ser	Gly	Pro	Gly	Gln	Arg	Gln	Arg	Gln	Gly	Ala	Gly	Ser	Thr
			85					90						95	
Pro	Ala	Arg	Val	Pro	Val	His	Gly	Ser	Pro	Ser	Ser	Cys	Arg	Ala	Leu
		100						105					110		
Arg	Pro	Ala	Gly	Arg	Ser	Ser	Arg	Ala	Ala	Pro	Arg	Ala	Ser	Pro	Ala
		115					120					125			
Gly	Gln	Ala	Ser	Ser	Arg	Pro	Xaa	Ser	Gly	Ala	Met	His	Arg	Leu	Gly
	130					135					140				
Glu	Gly	Asn	Arg	Ala	Gly	Glu	Lys	Val	Phe	Arg	Arg	Thr	Ala	Val	Gln
145					150					155					160
Lys	Arg	Arg	Val	Gly	Gly	Gly	Thr								
					165										

<210> 3501

<211> 691

<212> DNA

<213> Homo sapiens

<400> 3501

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 120
 cccctatag agaagatgga tgcattccttg tccatgcttg ctaattgcga gaagctttca
 180
 ctgtctacaa actgcattga aaaaattgcc aacctgaatg gcttaaaaaa cttgaggata
 240
 ttatcttttag gaagaaacaa cataaagaac ttaaattggac tggaggcagt aggggacaca
 300

ttagaagaac tgtggatctc ctacaatttt attgagaagt tgaaagggat ccacataatg
 360
 aagaaattga agattctcta catgtctaata aacctggtaa aagactgggc tgagtttgtg
 420
 aagctggcag aactgccatg cctcgaagac ctggtgtttg taggcaatcc cttggaagag
 480
 aaacattctg ctgagaataa ctggattgaa gaagcaacca agagagtgcc caaactgaaa
 540
 aagctggatg gtactccagt aattaaaggg gatgaggaag aagacaacta atgccacgct
 600
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 660
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 691

<210> 3502

<211> 196

<212> PRT

<213> Homo sapiens

<400> 3502

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Leu	Ala	Arg	Trp	Glu	Glu	Lys	Thr	Gly	Gln	Arg	Pro	Ser	Glu	Ala	Lys
		20						25					30		
Glu	Ile	Lys	Leu	Tyr	Ala	Gln	Ile	Pro	Pro	Ile	Glu	Lys	Met	Asp	Ala
		35					40					45			
Ser	Leu	Ser	Met	Leu	Ala	Asn	Cys	Glu	Lys	Leu	Ser	Leu	Ser	Thr	Asn
		50				55				60					
Cys	Ile	Glu	Lys	Ile	Ala	Asn	Leu	Asn	Gly	Leu	Lys	Asn	Leu	Arg	Ile
65					70				75					80	
Leu	Ser	Leu	Gly	Arg	Asn	Asn	Ile	Lys	Asn	Leu	Asn	Gly	Leu	Glu	Ala
			85					90					95		
Val	Gly	Asp	Thr	Leu	Glu	Glu	Leu	Trp	Ile	Ser	Tyr	Asn	Phe	Ile	Glu
		100						105					110		
Lys	Leu	Lys	Gly	Ile	His	Ile	Met	Lys	Lys	Leu	Lys	Ile	Leu	Tyr	Met
		115					120					125			
Ser	Asn	Asn	Leu	Val	Lys	Asp	Trp	Ala	Glu	Phe	Val	Lys	Leu	Ala	Glu
		130				135					140				
Leu	Pro	Cys	Leu	Glu	Asp	Leu	Val	Phe	Val	Gly	Asn	Pro	Leu	Glu	Glu
145					150				155					160	
Lys	His	Ser	Ala	Glu	Asn	Asn	Trp	Ile	Glu	Glu	Ala	Thr	Lys	Arg	Val
			165					170					175		
Pro	Lys	Leu	Lys	Lys	Leu	Asp	Gly	Thr	Pro	Val	Ile	Lys	Gly	Asp	Glu
		180					185						190		
Glu	Glu	Asp	Asn												
		195													

<210> 3503

<211> 857

<212> DNA

<213> Homo sapiens

<400> 3503

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 120
 aatgcccaaga gattagcgga gaagctccga gcccagaaac gggaacaaga cacaaagaag
 180
 gagccggtgt ccacaaacgc tgttcagcgg agagtgaag aaatagtgcg gttcacacgg
 240
 cagctgcagc gagtccaccc caacgtgctt gctaaggcac tgacccgagg aattctccac
 300
 caggacaaga accttggtgt catcaataag ccctacggtc tccctgtgca tggtgccct
 360
 ggggtccagc tctgcatcac tgatgtacta cctatcctgg caaagatgct tcatggccac
 420
 aaggcagagc ccttgcattt gtgccaccgg ctggacaagg aaaccacagg tgtaatggtg
 480
 ttggcttggg acaaggacat ggcacatcaa gtccaagagt tgtttagaac ccgtcaggtg
 540
 gtgaagaagt actgggcat cactgtgcat gtcccatgc cctcagcagg agtcgtggac
 600
 atccccattg tggagaagga ggggcaaggc cagcagcaac accccagaat gacattgtcc
 660
 ccgagctccc gcatggacga tgggaaaatg gtgaaagtgc ggcgcagccg gaatgcgcaa
 720
 gttgctgtaa ctcagtacca ggtgctcagc agcactctct cctccgcctt cgtggagctc
 780
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 840
 ccaatccttg gtgatca
 857

<210> 3504

<211> 285

<212> PRT

<213> Homo sapiens

<400> 3504

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Gln	Gly	Cys	Gly	Ser	Leu	Phe	Thr	Leu	Val	Ser	Lys	Pro	Phe	Cys	Ala
		20						25				30			
Ala	Ala	Ala	Ala	Ser	Thr	Ala	Ile	Asn	Ala	Gln	Arg	Leu	Ala	Glu	Lys
		35					40				45				
Leu	Arg	Ala	Gln	Lys	Arg	Glu	Gln	Asp	Thr	Lys	Lys	Glu	Pro	Val	Ser
	50				55			60							
Thr	Asn	Ala	Val	Gln	Arg	Arg	Val	Gln	Glu	Ile	Val	Arg	Phe	Thr	Arg
65				70				75				80			
Gln	Leu	Gln	Arg	Val	His	Pro	Asn	Val	Leu	Ala	Lys	Ala	Leu	Thr	Arg
			85				90				95				
Gly	Ile	Leu	His	Gln	Asp	Lys	Asn	Leu	Val	Val	Ile	Asn	Lys	Pro	Tyr
		100					105				110				
Gly	Leu	Pro	Val	His	Gly	Gly	Pro	Gly	Val	Gln	Leu	Cys	Ile	Thr	Asp
		115					120				125				
Val	Leu	Pro	Ile	Leu	Ala	Lys	Met	Leu	His	Gly	His	Lys	Ala	Glu	Pro

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      130              135              140
Leu His Leu Cys His Arg Leu Asp Lys Glu Thr Thr Gly Val Met Val
145              150              155              160
Leu Ala Trp Asp Lys Asp Met Ala His Gln Val Gln Glu Leu Phe Arg
      165              170              175
Thr Arg Gln Val Val Lys Lys Tyr Trp Ala Ile Thr Val His Val Pro
      180              185              190
Met Pro Ser Ala Gly Val Val Asp Ile Pro Ile Val Glu Lys Glu Gly
      195              200              205
Gln Gly Gln Gln Gln His Pro Arg Met Thr Leu Ser Pro Ser Ser Arg
      210              215              220
Met Asp Asp Gly Lys Met Val Lys Val Arg Arg Ser Arg Asn Ala Gln
225              230              235              240
Val Ala Val Thr Gln Tyr Gln Val Leu Ser Ser Thr Leu Ser Ser Ala
      245              250              255
Leu Val Glu Leu Gln Pro Ile Thr Gly Ile Lys His Gln Leu Arg Val
      260              265              270
His Leu Ser Phe Gly Leu Asp Cys Pro Ile Leu Gly Asp
      275              280              285

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<210> 3505

<211> 1612

<212> DNA

<213> Homo sapiens

<400> 3505

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120
cttgctgcat ccctgggctc tgcggagaag gaaccgcagc agcccccggc cctgtggagg
180
aaggttggtg acttctctgt gaaggccatc atgcgcacca tgtggttcgc cggcggcttc
240
caccgggtgg ccgtgaaggg gcggcaggcg ctgcccaccg aggcggccat cctcacgctc
300
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atgaagacag agagcagaga catcccgatc tggggaactc tgatccagta tatacggcct
420
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480
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540
aacaggacct gcctaattac cttcaaacct ggtgcattca tccctggagc gccctgccac
600
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660
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720
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780
aacgtgcggc gagtcatggc cgaggccttg ggtgtctccg tgactgacta cacgttcgag
840

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 960
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 1020
 gccgcctccc tggaagtccc cgtttctgac ttgctggaag acatgttttc actgttcgac
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 1200
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 1320
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 1380
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 1440
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 1500
 ctggattagg acccaggggt gcggagagac gcggccctc ccgctggac atcaccgcca
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<210> 3506

<211> 502

<212> PRT

<213> Homo sapiens

<400> 3506

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Met	Thr	Leu	Thr	Leu	Phe	Pro	Val	Arg	Leu	Leu	Val	Ala	Ala	Ala	Met
			20					25				30			
Met	Leu	Leu	Ala	Trp	Pro	Leu	Ala	Leu	Val	Ala	Ser	Leu	Gly	Ser	Ala
			35				40					45			
Glu	Lys	Glu	Pro	Glu	Gln	Pro	Pro	Ala	Leu	Trp	Arg	Lys	Val	Val	Asp
			50			55					60				
Phe	Leu	Leu	Lys	Ala	Ile	Met	Arg	Thr	Met	Trp	Phe	Ala	Gly	Gly	Phe
65					70				75						80
His	Arg	Val	Ala	Val	Lys	Gly	Arg	Gln	Ala	Leu	Pro	Thr	Glu	Ala	Ala
			85					90					95		
Ile	Leu	Thr	Leu	Ala	Pro	His	Ser	Ser	Tyr	Phe	Asp	Ala	Ile	Pro	Val
			100					105					110		
Thr	Met	Thr	Met	Ser	Ser	Ile	Val	Met	Lys	Thr	Glu	Ser	Arg	Asp	Ile
			115				120					125			
Pro	Ile	Trp	Gly	Thr	Leu	Ile	Gln	Tyr	Ile	Arg	Pro	Val	Phe	Val	Ser
			130			135					140				
Arg	Ser	Asp	Gln	Asp	Ser	Arg	Arg	Lys	Thr	Val	Glu	Glu	Ile	Lys	Arg
145				150					155					160	
Arg	Ala	Gln	Ser	Asn	Gly	Lys	Trp	Pro	Gln	Ile	Met	Ile	Phe	Pro	Glu

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      165      170      175
Gly Thr Cys Thr Asn Arg Thr Cys Leu Ile Thr Phe Lys Pro Gly Ala
      180      185      190
Phe Ile Pro Gly Ala Pro Val His Pro Gly Val Leu Arg Tyr Pro Asn
      195      200      205
Lys Leu Asp Thr Ile Thr Trp Thr Trp Gln Gly Pro Gly Ala Leu Glu
      210      215      220
Ile Leu Trp Leu Thr Leu Cys Gln Phe His Asn Gln Val Glu Ile Glu
      225      230      235      240
Phe Leu Pro Val Tyr Ser Pro Ser Glu Glu Glu Lys Arg Asn Pro Ala
      245      250      255
Leu Tyr Ala Ser Asn Val Arg Arg Val Met Ala Glu Ala Leu Gly Val
      260      265      270
Ser Val Thr Asp Tyr Thr Phe Glu Asp Cys Gln Leu Ala Leu Ala Glu
      275      280      285
Gly Gln Leu Arg Leu Pro Ala Asp Thr Cys Leu Leu Glu Phe Ala Arg
      290      295      300
Leu Val Arg Gly Leu Gly Leu Lys Pro Glu Lys Leu Glu Lys Asp Leu
      305      310      315      320
Asp Arg Tyr Ser Glu Arg Ala Arg Met Lys Gly Gly Glu Lys Ile Gly
      325      330      335
Ile Ala Glu Phe Ala Ala Ser Leu Glu Val Pro Val Ser Asp Leu Leu
      340      345      350
Glu Asp Met Phe Ser Leu Phe Asp Glu Ser Gly Ser Gly Glu Val Asp
      355      360      365
Leu Arg Glu Cys Val Val Ala Leu Ser Val Val Cys Trp Pro Ala Arg
      370      375      380
Thr Leu Asp Thr Ile Gln Leu Ala Phe Lys Met Tyr Gly Ala Gln Glu
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Asp Gly Ser Val Gly Glu Gly Asp Leu Ser Cys Ile Leu Lys Thr Ala
      405      410      415
Leu Gly Val Ala Glu Leu Thr Val Thr Asp Leu Phe Arg Ala Ile Asp
      420      425      430
Gln Glu Glu Lys Gly Lys Ile Thr Phe Ala Asp Phe His Arg Phe Ala
      435      440      445
Glu Met Tyr Pro Ala Phe Ala Glu Glu Tyr Leu Tyr Pro Asp Gln Thr
      450      455      460
His Phe Glu Ser Cys Ala Glu Thr Ser Pro Ala Pro Ile Pro Asn Gly
      465      470      475      480
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Val Arg Lys Lys Leu Asp
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<210> 3507

<211> 885

<212> DNA

<213> Homo sapiens

<400> 3507

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<210> 3508

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3508

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 Glu Gly Glu Leu Pro Thr His Glu Gln Val Phe Leu Ser Pro Pro Pro
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 Pro Leu Ser Pro Arg Gly Pro Gly Leu Pro Gln Lys Leu Glu Glu Arg
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 <212> DNA
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<211> 462

<212> PRT

<213> Homo sapiens

<400> 3512

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 Ser Gln Thr Cys Asp Trp Gly Asn Leu Leu Gln Asp Ile Ile Leu Gln
 65 70 75 80
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 Gln Tyr Val Ser Phe Lys Val Asp Ser Ser Lys Glu Ser Ala Glu Ala
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 Gly Leu Ile Ser Thr Ala Arg Pro Ser Phe Met Asp Leu Pro Lys Ser
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 210 215 220
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 225 230 235 240
 Ser Cys Pro His Val Ser Pro Ala Gly Ile Leu Cys Val Ala Asp Gln
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 Val Ser Lys Asp Val Leu Gly Arg Val Gly Met Thr Cys Pro Arg Leu

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385	390	395
Gly Glu Cys Glu Val Ser Cys Ser Ala Phe Val	Glu Phe Val Lys Met	400
405	410	415
Cys Gly Gly Arg Leu Ser Gln Leu Ser Ile Met	Glu Glu Val Leu Ile	
420	425	430
Pro Asp Gln Lys Tyr Ser Leu Glu Gln Ile His	Trp Glu Val Ser Lys	
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<210> 3513

<211> 2103

<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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<211> 547

<212> PRT

<213> Homo sapiens

<400> 3516

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Asp	Gln	Ile	Gln	Thr	Leu	Met	Leu	Gln	Asn	Arg	Thr	Leu	Leu	Glu	Gln
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Asp	Lys	Leu	Asn	Glu	Leu	Arg	Arg	Gln	Lys	Glu	Lys	Leu	Glu	Glu	Lys
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Ile	Met	Asp	Gln	Tyr	Lys	Phe	Tyr	Asp	Pro	Ser	Pro	Pro	Arg	Arg	Arg
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Gly	Asn	Trp	Ile	Thr	Leu	Lys	Met	Arg	Lys	Leu	Ile	Lys	Ser	Lys	Lys
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Asp	Ile	Asn	Arg	Glu	Arg	Gln	Lys	Ser	Leu	Thr	Leu	Thr	Pro	Thr	Arg
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Ser	Asp	Ser	Ser	Glu	Gly	Phe	Leu	Gln	Leu	Pro	His	Gln	Asp	Ser	Gln
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 Tyr Leu Lys Arg Gln Thr Arg Ser Ser Pro Val Leu Gln His Lys Ile
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 Ser Glu Thr Leu Glu Ser Arg His His Lys Ile Lys Thr Gly Ser Pro
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 Gly Ser Glu Val Val Thr Leu Gln Gln Phe Leu Glu Glu Ser Asn Lys
 355 360 365
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 Glu Val Met Lys Ser Leu Ser Val Ser Ser Asp Phe Leu Gly Lys Asp
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 Lys Pro Val Ser Cys Gly Leu Ala Arg Ser Val Ser Gly Lys Thr Pro
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 Gly Pro Arg Lys Thr Glu Asp Thr Tyr Phe Ile Ser Ser Ala Gly Lys
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 Pro Thr Pro Gly Thr Gln Gly Lys Ile Lys Leu Val Lys Glu Ser Ser
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 485 490 495
 Ile His Asp Phe Leu Thr Lys Asp Ser Arg Leu Pro Ile Ser Val Asp
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<211> 342

<212> DNA

<213> Homo sapiens

<400> 3517

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<211> 99

<212> PRT

<213> Homo sapiens

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Ile Val Ala Ser Phe Val Leu Ala Gly Glu Thr Glu Ala Thr Ala Leu
      35           40           45
Gln Arg Met Pro Asp Arg Pro Thr Ser Arg Pro Leu Leu Val Arg Ala
      50           55           60
Ser Leu Ser Pro Ser Gly Leu Gly Ala Cys Asp Thr Ala Leu Arg Pro
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<211> 2207

<212> DNA

<213> Homo sapiens

<400> 3519

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<212> PRT
<213> Homo sapiens
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<400> 3520

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Val Val Asn Leu Pro Pro Ala Gln Leu Ser Ser Ser Asp Glu Glu Thr
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Arg Glu Glu Leu Ala Arg Ile Gly Leu Val Pro Pro Pro Glu Glu Phe
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Pro Thr Thr Val Pro Ser Pro Ala Ser Gly Lys Pro Ser Ser Glu Pro
 85          90          95
Pro Pro Ala Pro Glu Ser Ala Ala Asp Ser Gly Val Glu Glu Ala Asp
100          105          110
Thr Arg Ser Ser Ser Asp Pro His Leu Glu Thr Thr Ser Thr Ile Ser
115          120          125
Thr Val Ser Ser Met Ser Thr Leu Ser Ser Glu Ser Gly Glu Leu Thr
130          135          140
Asp Thr His Thr Ser Phe Ala Asp Gly His Thr Phe Leu Leu Glu Lys
145          150          155          160
Pro Pro Val Pro Pro Lys Pro Lys Leu Lys Ser Pro Leu Gly Lys Gly
165          170          175
Pro Val Thr Phe Arg Asp Pro Leu Leu Lys Gln Ser Ser Asp Ser Glu
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195          200          205
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Trp Gly Asp Pro Val Glu Ser Arg Gly Leu Pro Gly Pro Glu Asp Asp
225          230          235          240
Lys Pro Thr Val Ile Ser Glu Leu Ser Ser Arg Leu Gln Gln Leu Asn
245          250          255
Lys Asp Thr Arg Ser Leu Gly Glu Glu Pro Val Gly Gly Leu Gly Ser
260          265          270
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<211> 638

<212> DNA

<213> Homo sapiens

<400> 3521

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<210> 3522

<211> 181

<212> PRT

<213> Homo sapiens

<400> 3522

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 50 55 60
 Leu Arg Cys Gly Leu Pro Ser Glu Gln Arg Ala Ala Gly Glu Ala Arg
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 Gly Leu His Leu Leu Gln Asp Pro Thr Pro Gly Arg Leu Cys Gln Ala
 85 90 95
 Pro Ala Gly Pro Pro Gly Gly Gly His Gly Pro Ala Gly Arg Gly Gln
 100 105 110
 Pro Ser Arg His Arg Pro Gly Glu Pro Gln Gly Gly Arg Gly Gly Xaa
 115 120 125
 Pro Asp Pro Ser Thr Pro Ser Val Arg Gly Ser Gln Arg Thr Ala Ser
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 Ser Pro Ala Ser Ser
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<210> 3523

<211> 2614

<212> DNA

<213> Homo sapiens

<400> 3523

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<210> 3524

<211> 444

<212> PRT

<213> Homo sapiens

<400> 3524

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Glu	Arg	Trp	Leu	Val	Ile	Asp	Arg	Lys	Val	Tyr	Asn	Ile	Ser	Asp	Phe
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Gln	Pro	Ser	Phe	Glu	Pro	Thr	Lys	Asn	Lys	Glu	Leu	Thr	Asp	Glu	Phe
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His Val Phe Phe Leu Leu Tyr Leu Leu His Ile Leu Leu Leu Asp Gly
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Leu Leu Cys Ala Val Leu Leu Ser Ala Val Gln Ala Gln Ala Gly Trp
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Leu Gln His Asp Phe Gly His Leu Ser Val Phe Ser Thr Ser Lys Trp
      180      185      190
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Ala Ser Trp Trp Asn His Met His Phe Gln His His Ala Lys Pro Asn
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Gln Arg Lys Lys Trp Val Asp Leu Val Trp Met Ile Thr Phe Tyr Val
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Arg Phe Phe Leu Thr Tyr Val Pro Leu Leu Gly Leu Lys Ala Phe Leu
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      325      330      335
Val Thr Gln Met Asn His Ile Pro Met His Ile Asp His Asp Arg Asn
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Met Asp Trp Val Ser Thr Gln Leu Gln Ala Thr Cys Asn Val His Lys
      355      360      365
Ser Ala Phe Asn Asp Trp Phe Ser Gly His Leu Asn Phe Gln Ile Glu
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His His Leu Phe Pro Thr Met Pro Arg His Asn Tyr His Lys Val Ala
385      390      395      400
Pro Leu Val Gln Ser Leu Cys Ala Lys His Gly Ile Glu Tyr Gln Ser
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<210> 3525

<211> 1116

<212> DNA

<213> Homo sapiens

<400> 3525

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<210> 3526

<211> 304

<212> PRT

<213> Homo sapiens

<400> 3526

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Ser Glu Lys Lys Lys Asp Arg Ile Asp Ala Phe Leu Arg Glu Val Asn		
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Gln Arg Val Val Arg Val Pro Ser Val Pro Glu Thr Glu Leu Thr Asp		
180	185	190
Gln Ala Trp Leu Pro Ala Gly Val Arg Val Pro Leu His Gln Val Pro		
195	200	205
Tyr Ala Val Lys Gly Cys Phe Arg Phe Leu Pro Pro Ala Gln Val Thr		
210	215	220
Val Val Gly Ser Tyr Leu Leu Gly Thr Cys Ile Arg Pro Asp Ile Asn		
225	230	235
Val Asp Val Ala Leu Thr Met Pro Arg Glu Ile Leu Gln Asp Lys Asp		
245	250	255
Gly Leu Asn Gln Arg Tyr Phe Arg Lys Arg Ala Leu Tyr Leu Ala His		
260	265	270
Leu Ala His His Leu Ala Gln Asp Pro Leu Phe Gly Ser Val Cys Phe		
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<210> 3527

<211> 2838

<212> DNA

<213> Homo sapiens

<400> 3527

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<211> 281

<212> PRT

<213> Homo sapiens

<400> 3528

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			100					105					110		
Asp	Leu	Met	Asp	Cys	Glu	Gln	Lys	Met	Val	Asp	Gly	Thr	Tyr	Trp	Val
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Asp	Pro	Asn	Leu	Gly	Cys	Ser	Ser	Asp	Thr	Ile	Glu	Val	Ser	Cys	Asn
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Phe	Thr	His	Gly	Gly	Gln	Thr	Cys	Leu	Lys	Pro	Ile	Thr	Ala	Ser	Lys
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Val	Glu	Phe	Ala	Ile	Ser	Arg	Val	Gln	Met	Asn	Phe	Leu	His	Leu	Leu
			165					170						175	
Ser	Ser	Glu	Val	Thr	Gln	His	Ile	Thr	Ile	His	Cys	Leu	Asn	Met	Thr
			180					185					190		
Val	Trp	Gln	Glu	Gly	Thr	Gly	Gln	Thr	Pro	Ala	Lys	Gln	Ala	Val	Arg
			195				200					205			
Phe	Arg	Ala	Trp	Asn	Gly	Gln	Ile	Phe	Glu	Ala	Gly	Gly	Gln	Phe	Arg
			210			215					220				
Pro	Glu	Val	Ser	Met	Asp	Gly	Cys	Lys	Val	Gln	Asp	Gly	Arg	Trp	His

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Gln Thr Leu Phe Thr Phe Arg Thr Gln Asp Pro Gln Gln Leu Pro Ile						
	245		250		255	
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<210> 3529

<211> 3026

<212> DNA

<213> Homo sapiens

<400> 3529

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<211> 206

<212> PRT

<213> Homo sapiens

<400> 3530

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<211> 879

<212> DNA

<213> Homo sapiens

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 420
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 660
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 720
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 780
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<210> 3532

<211> 254

<212> PRT

<213> Homo sapiens

<400> 3532

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Tyr	Ser	His	Asp	Gly	Thr	Asp	Ser	Pro	Pro	Asp	Ala	Asp	Glu	Val	Val
			20				25					30			
Ile	Val	Leu	Asn	Asn	Phe	Lys	Ser	Lys	Ile	Ile	Lys	Val	Lys	Val	Gln
		35				40					45				
Lys	Lys	Ala	Asp	Met	Val	Asn	Glu	Asp	Leu	Leu	Ser	Asp	Gly	Thr	Ser
	50					55					60				
Glu	Asn	Glu	Ser	Gly	Phe	Trp	Asp	Ser	Phe	Lys	Trp	Gly	Phe	Thr	Gly
65				70						75				80	
Gln	Lys	Thr	Glu	Glu	Val	Lys	Gln	Asp	Lys	Asp	Asp	Ile	Ile	Asn	Ile
			85					90						95	
Phe	Ser	Val	Ala	Ser	Gly	His	Leu	Tyr	Glu	Arg	Phe	Leu	Arg	Ile	Met
		100						105					110		
Met	Leu	Ser	Val	Leu	Lys	Asn	Thr	Lys	Thr	Pro	Val	Lys	Phe	Trp	Phe
		115					120					125			
Leu	Lys	Asn	Tyr	Leu	Ser	Pro	Thr	Phe	Lys	Glu	Phe	Ile	Pro	Tyr	Met
	130					135					140				
Ala	Asn	Glu	Tyr	Asn	Phe	Gln	Tyr	Glu	Leu	Val	Gln	Tyr	Lys	Trp	Pro
145				150						155				160	
Arg	Trp	Leu	His	Gln	Gln	Thr	Glu	Lys	Gln	Arg	Ile	Ile	Trp	Gly	Tyr
			165					170						175	
Lys	Ile	Leu	Phe	Leu	Asp	Val	Leu	Phe	Pro	Leu	Val	Val	Asp	Lys	Phe

	180		185		190
Leu Phe Val	Asp Ala Asp Gln Ile Val Arg Thr Asp	Leu Lys Glu Leu			
195	200	205			
Arg Asp Phe Asn Leu Asp Gly Ala Pro Tyr Gly Tyr Thr Pro Phe Cys					
210	215	220			
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225	230	235		240	
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<210> 3533

<211> 1151

<212> DNA

<213> Homo sapiens

<400> 3533

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180
cagtggacgc accccaactc catggataac ttgccagtg ccgcttcccc cctggagcag
240
aaccttagca agcatggtgc tatccctgga ggtctaagca ttgggcctcc aggttaagtcc
300
tccattgatg actcctatgg ccggtacgat ttaatccaga acagtgagtc accagccagt
360
cctcccgtag ctgttcccca tagctggtca cgtgccaaat ctgacagtga taaaatctca
420
aatggctcta gcatcaactg gccccagaa ttccatccgg gagttccatg gaaaggactg
480
cagaatattg accctgagaa tgaccctgac gtcactcctg gcagtgtccc cactgggcct
540
accatcaaca ccaccatcca ggatgtcaac cgctacctcc tcaagagtgg agggtcctcc
600
ccgccatcat ctcagaatgc caagctgcct tcttcgagtg cctggccact cagtgcctcc
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720
gacatcaaat cgacgtggtc ctctggccct acctcccaca cgcaagcctc tctgtctcat
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840
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1020
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1140

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<210> 3534

<211> 313

<212> PRT

<213> Homo sapiens

<400> 3534

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Pro	Ser	Gln	Ser	Gln	Ser	Arg	Leu	Pro	Gln	Trp	Thr	His	Pro	Asn	Ser
		20					25					30			
Met	Asp	Asn	Leu	Pro	Ser	Ala	Ala	Ser	Pro	Leu	Glu	Gln	Asn	Pro	Ser
		35				40					45				
Lys	His	Gly	Ala	Ile	Pro	Gly	Gly	Leu	Ser	Ile	Gly	Pro	Pro	Gly	Lys
	50				55					60					
Ser	Ser	Ile	Asp	Asp	Ser	Tyr	Gly	Arg	Tyr	Asp	Leu	Ile	Gln	Asn	Ser
65					70				75					80	
Glu	Ser	Pro	Ala	Ser	Pro	Pro	Val	Ala	Val	Pro	His	Ser	Trp	Ser	Arg
				85					90					95	
Ala	Lys	Ser	Asp	Ser	Asp	Lys	Ile	Ser	Asn	Gly	Ser	Ser	Ile	Asn	Trp
			100				105						110		
Pro	Pro	Glu	Phe	His	Pro	Gly	Val	Pro	Trp	Lys	Gly	Leu	Gln	Asn	Ile
		115				120					125				
Asp	Pro	Glu	Asn	Asp	Pro	Asp	Val	Thr	Pro	Gly	Ser	Val	Pro	Thr	Gly
	130				135					140					
Pro	Thr	Ile	Asn	Thr	Thr	Ile	Gln	Asp	Val	Asn	Arg	Tyr	Leu	Leu	Lys
145					150					155				160	
Ser	Gly	Gly	Ser	Ser	Pro	Pro	Ser	Ser	Gln	Asn	Ala	Thr	Leu	Pro	Ser
			165						170					175	
Ser	Ser	Ala	Trp	Pro	Leu	Ser	Ala	Ser	Gly	Tyr	Ser	Ser	Ser	Phe	Ser
		180					185						190		
Ser	Ile	Ala	Ser	Ala	Pro	Ser	Val	Ala	Gly	Lys	Leu	Ser	Asp	Ile	Lys
	195						200				205				
Ser	Thr	Trp	Ser	Ser	Gly	Pro	Thr	Ser	His	Thr	Gln	Ala	Ser	Leu	Ser
	210				215						220				
His	Glu	Leu	Trp	Lys	Val	Pro	Arg	Asn	Ser	Thr	Ala	Pro	Thr	Arg	Pro
225					230					235				240	
Pro	Pro	Gly	Leu	Thr	Asn	Pro	Lys	Pro	Ser	Ser	Thr	Trp	Gly	Ala	Ser
			245						250					255	
Pro	Leu	Gly	Trp	Thr	Ser	Ser	Tyr	Ser	Ser	Gly	Ser	Ala	Trp	Ser	Thr
		260					265						270		
Asp	Thr	Ser	Gly	Arg	Thr	Ser	Ser	Trp	Leu	Val	Leu	Arg	Asn	Leu	Thr
	275					280					285				
Pro	Gln	Val	Gln	Tyr	Gly	Ala	Pro	Ala	Ser	Leu	Ser	Met	Ile	Gln	Gly
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<210> 3535

<211> 723

<212> DNA

<213> Homo sapiens

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 120
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 180
 gcctcatcaa aacattgttg gagaaaactg ggtgcccacg gaggagaaac ggaatgcaag
 240
 gagattgcaa tctgtgcttt gaaccagatg cactattact aatagctgga ggaaattttg
 300
 aagatcagct tagagaagaa gtgggtccaga gagtttctct tctccttctc tattacatta
 360
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 420
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 480
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 540
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 600
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 723

<210> 3536
 <211> 163
 <212> PRT
 <213> Homo sapiens

<400> 3536
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 20 25 30
 Arg Val Ser Leu Leu Leu Leu Tyr Ile Ile His Gln Glu Glu Ile
 35 40 45
 Cys Ser Ser Lys Leu Asn Met Ser Asn Lys Glu Tyr Lys Phe Tyr Leu
 50 55 60
 His Ser Leu Leu Ser Leu Arg Gln Asp Glu Asp Ser Ser Phe Leu Ser
 65 70 75 80
 Gln Asn Glu Thr Glu Asp Ile Leu Ala Phe Thr Arg Gln Tyr Phe Asp
 85 90 95
 Thr Ser Gln Ser Gln Cys Met Glu Thr Lys Thr Leu Gln Lys Lys Ser
 100 105 110
 Gly Ile Val Ser Ser Glu Gly Ala Asn Glu Ser Thr Leu Pro Gln Leu
 115 120 125
 Ala Ala Met Ile Ile Thr Leu Ser Leu Gln Gly Val Cys Leu Gly Gln
 130 135 140
 Gly Asn Leu Pro Ser Pro Asp Tyr Phe Thr Glu Tyr Ile Phe Ser Ser

WO 00/58473

PCT/US00/08621

145
Leu Asn Arg

150

155

160

<210> 3537

<211> 714

<212> DNA

<213> Homo sapiens

<400> 3537

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120
cataaggcca agagtaagtg cgtgaatgca cttaagacaa agtcaggaca cgagcttcac
180
atgacaggcc ccgcgtgggc gaccagccag ccctggggac gggcacgcca cgccacacac
240
acactcacca ctgtacagcc tgggactccc attgcatatt cacaggcccc gccgggcagg
300
gcacctcaag gctgggggag gggcaggggc agggaggagc cgtgggggtgt ccctgggtgg
360
gtggagaggg cagcatgtga gaggcaaagt tgcaccaaca ctgggcgtga gacgtgagca
420
gcctcagggtg tacggcatga gatgtgtgtg gttggggggt gtctgctga cccgggaggg
480
gggtgtgtgt gagatgagca cagaggcat gcgtggcacg tgctcgtgtg gtggtcgcgt
540
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600
aagggtcctt cagacgtgcc cctaccagc aggcacagaa atgtttgcat aaggccagc
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<210> 3538

<211> 154

<212> PRT

<213> Homo sapiens

<400> 3538

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20           25           30
Leu Lys Asp Pro Ser Ser Asn Pro Ala Gly Pro Arg Ala Thr Ala Gly
35           40           45
Gln Gly Val Ala Pro Gly Phe Arg His Ala Thr Thr Arg Ala Arg
50           55           60
Ala Thr His Ala Ser Cys Ala His Leu Thr His Thr Pro Leu Pro Gly
65           70           75           80
His Ala Asp Thr Pro Gln Pro His Thr Ser His Ala Val His Leu Arg
85           90           95
Leu Leu Thr Ser His Ala Gln Cys Trp Cys Thr Phe Ala Ser His Met

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100 105 110
 Leu Pro Ser Pro Pro Thr Gln Gly His Pro Thr Ala Pro Pro Cys Pro
 115 120 125
 Cys Pro Ser Pro Ser Leu Glu Val Pro Cys Pro Ala Gly Pro Val Asn
 130 135 140
 Met Gln Trp Glu Ser Gln Ala Val Gln Trp
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<210> 3539

<211> 818

<212> DNA

<213> Homo sapiens

<400> 3539

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 120
 cggggggcg aggttgagc gagccagat cgcgaggta cgctccagtc tgggcgacaa
 180
 gagcgaaact cgatatcaaa aaaaaaaaaa acgtcctgat ccagagcct cttcacgcgt
 240
 cccctaccac agcacttcag agaagcaggt ctttaatcag tgtgtctaga tgcagctgct
 300
 gactgtcacc cctaccccg ctctctccca gtctgaggac ggccagtcac cccattgcc
 360
 cagaatcaga cgaccctcg ttcttcaga gccaagctgg gcaacttccc ctggcaagcc
 420
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 540
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 600
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 660
 gccctcctgg agctgcagca cagcatcccc ctgggcccac acgtcctccc ggtctgtctg
 720
 cccgataatg agaccctcta ccgcagcggc ttgttgggct acgtcagtg gtttggcatg
 780
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 818

<210> 3540

<211> 180

<212> PRT

<213> Homo sapiens

<400> 3540

Ser Val Cys Leu Asp Ala Ala Ala Asp Cys His Pro Tyr Pro Ala Ser
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 Leu Pro Val Cys Gly Arg Pro Val Thr Pro Ile Ala Gln Asn Gln Thr
 20 25 30
 Thr Leu Gly Ser Ser Arg Ala Lys Leu Gly Asn Phe Pro Trp Gln Ala

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      35          40          45
Phe Thr Ser Ile His Gly Arg Gly Gly Gly Ala Leu Leu Gly Asp Arg
      50          55          60
Trp Ile Leu Thr Ala Ala His Thr Val Tyr Pro Lys Asp Ser Val Ser
      65          70          75          80
Leu Arg Lys Asn Gln Ser Val Asn Val Phe Leu Gly His Thr Ala Ile
      85          90          95
Asp Glu Met Leu Lys Leu Gly Asn His Pro Val His Arg Val Val Val
      100          105          110
His Pro Asp Tyr Arg Gln Asn Glu Ser His Asn Phe Ser Gly Asp Ile
      115          120          125
Ala Leu Leu Glu Leu Gln His Ser Ile Pro Leu Gly Pro Asn Val Leu
      130          135          140
Pro Val Cys Leu Pro Asp Asn Glu Thr Leu Tyr Arg Ser Gly Leu Leu
      145          150          155          160
Gly Tyr Val Ser Gly Phe Gly Met Glu Met Gly Trp Leu Thr Thr Glu
      165          170          175
Leu Lys Tyr Ser
      180

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<210> 3541

<211> 722

<212> DNA

<213> Homo sapiens

<400> 3541

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120
acggctgctg cccttggtact actacctcca aatacgttct tgctggtagt ggcggcagca
180
ggaccaatta cctctttttt gctctccctc gagaagctcc agatggcgctc ttccgtgggc
240
aacgtggccg acagcacaga accaacgaaa cgtatgcttt ccttccaagg gttagctgag
300
ttggcacatc gagaatatca ggcaggagat tttagggcag ctgagagaca ctgcatgcag
360
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420
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480
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540
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600
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aa
722

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<210> 3542

<211> 153

<212> PRT

<213> Homo sapiens

<400> 3542

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Met Ala Ser Ser Val Gly Asn Val Ala Asp Ser Thr Glu Pro Thr Lys
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Arg Met Leu Ser Phe Gln Gly Leu Ala Glu Leu Ala His Arg Glu Tyr
      20             25             30
Gln Ala Gly Asp Phe Glu Ala Ala Glu Arg His Cys Met Gln Leu Trp
      35             40             45
Arg Gln Glu Pro Asp Asn Thr Gly Val Leu Leu Leu Leu Ser Ser Ile
      50             55             60
His Phe Gln Cys Arg Arg Leu Asp Arg Ser Ala His Phe Ser Thr Leu
65             70             75             80
Ala Ile Lys Gln Asn Pro Leu Leu Ala Glu Ala Tyr Ser Asn Leu Gly
      85             90             95
Asn Val Tyr Lys Glu Arg Gly Gln Leu Gln Glu Ala Ile Glu His Tyr
      100            105            110
Arg His Ala Leu Arg Leu Lys Pro Asp Phe Ile Asp Gly Tyr Ile Asn
      115            120            125
Ala Ala Ala Ala Leu Val Ala Ala Gly Asp Met Glu Gly Ala Val Gln
      130            135            140
Ala Tyr Val Ser Ala Leu Gln Pro Gly
145            150

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<210> 3543

<211> 1206

<212> DNA

<213> Homo sapiens

<400> 3543

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120
gtttggttgt tgctcaggat gtgtaatagt ttctcttcag ccataagcca cgcttggtag
180
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240
tgatttggag cacttggaag atcactgttt tgtgttctac gacccaattg agaggattat
300
gtggagctaa gttttaccaa tcaggatcat ccttccttgt ggggttagcag gcagttataa
360
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420
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480
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540
atattctgtc tggttgcctt agtgagggcc tccataactg atccaggaag actccctgag
600
aaccccaaga tcccacatgg agaaagggag ttctgggaat tatgtaacaa gtgtaatttg
660

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 720
 catcactgtc catggattaa caattgtgtt ggtgaagata atcattggct ctttctgcag
 780
 ttgtgtttct aactgaact tcttacttgc tacgcactga tgttttcttt ctgccactat
 840
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 960
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 1020
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 1080
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<210> 3544

<211> 273

<212> PRT

<213> Homo sapiens

<400> 3544

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Met	Gly	Leu	Ile	Val	Phe	Val	Trp	Leu	Tyr	Asn	Ile	Val	Leu	Ile	Pro
			20					25					30		
Lys	Ile	Val	Leu	Phe	Pro	His	Tyr	Glu	Glu	Gly	His	Ile	Pro	Gly	Ile
		35					40					45			
Leu	Ile	Ile	Ile	Phe	Tyr	Gly	Ile	Ser	Ile	Phe	Cys	Leu	Val	Ala	Leu
	50					55					60				
Val	Arg	Ala	Ser	Ile	Thr	Asp	Pro	Gly	Arg	Leu	Pro	Glu	Asn	Pro	Lys
65					70				75					80	
Ile	Pro	His	Gly	Glu	Arg	Glu	Phe	Trp	Glu	Leu	Cys	Asn	Lys	Cys	Asn
			85					90					95		
Leu	Met	Arg	Pro	Lys	Arg	Ser	His	His	Cys	Ser	Arg	Cys	Gly	His	Cys
			100					105					110		
Val	Arg	Arg	Met	Asp	His	His	Cys	Pro	Trp	Ile	Asn	Asn	Cys	Val	Gly
			115				120					125			
Glu	Asp	Asn	His	Trp	Leu	Phe	Leu	Gln	Leu	Cys	Phe	Tyr	Thr	Glu	Leu
	130					135					140				
Leu	Thr	Cys	Tyr	Ala	Leu	Met	Phe	Ser	Phe	Cys	His	Tyr	Tyr	Tyr	Phe
145					150					155				160	
Leu	Pro	Leu	Lys	Lys	Arg	Asn	Leu	Asp	Leu	Phe	Val	Phe	Arg	His	Glu
			165					170					175		
Leu	Ala	Ile	Met	Arg	Leu	Ala	Ala	Phe	Met	Gly	Ile	Thr	Met	Leu	Val
			180					185					190		
Gly	Ile	Thr	Gly	Leu	Phe	Tyr	Thr	Gln	Leu	Ile	Gly	Ile	Ile	Thr	Pro
		195					200					205			
Cys	Ser	Leu	Ile	Leu	Leu	Lys	Cys	Gly	Ser	Val	Ser	Asn	Asn	Ser	Leu

210	215	220
Gly Asp Leu Met Lys Ile Ser Glu Thr Phe Ala Leu Arg Ile Pro Ser		
225	230	235
Phe Val Val Met Cys Pro Glu Asn Ser Ser Leu Arg Val Phe Asn Ser		240
	245	250
Val Lys Leu Leu Leu Cys Leu Asp Ser Pro Leu Ile Gln Trp Ser Thr		255
	260	265
		270

Lys

<210> 3545

<211> 3657

<212> DNA

<213> Homo sapiens

<400> 3545

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120
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<212> PRT

<213> Homo sapiens

<400> 3546

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 Val Lys His Leu Arg His Ser Ala Trp Pro Pro Thr Leu Leu Gln Met
 65 70 75 80
 Val His Thr Leu Ala Ser Asn Gly Ala Asn Ser Ile Trp Glu His Ser
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 Leu Leu Asp Pro Ala Gln Val Gln Ser Gly Arg Arg Lys Ala Asn Pro
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 Gln Asp Lys Val His Pro Ile Lys Ser Glu Phe Ile Arg Ala Lys Tyr
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 Gln Met Leu Ala Phe Val His Lys Leu Pro Cys Arg Asp Asp Asp Gly

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Lys Ala Gly Gln Thr Leu Gln Ala Glu Leu Leu Val Val Tyr Gly Ala
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<213> Homo sapiens
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<212> PRT

<213> Homo sapiens

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Glu Cys Pro Leu Met Ser Asp Ser Asn Asn Phe Ile Thr Ile Ala Ile						
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Leu Glu Asn Trp Trp Ser Val Leu Glu Pro Pro Leu Phe Leu Lys Ile						
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<211> 2542

<212> DNA

<213> Homo sapiens

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<211> 500

<212> PRT

<213> Homo sapiens

<400> 3550

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 Tyr Arg Arg Lys Glu Ile Leu Pro Phe Glu Lys Met Lys Glu Gln Arg
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 195 200 205
 Glu Asn Lys Lys Leu Ser Leu Asp Thr Asp Ala Arg Phe Gly His Gly
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 Glu Arg Arg Asp Arg Phe Val Gly Gln Ser Glu Gly Lys Lys Ala Arg
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 Pro Thr Ala Arg Arg Glu Asp Pro Ser Phe Glu Arg Tyr Pro Lys Asn
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<211> 545

<212> DNA

<213> Homo sapiens

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<211> 55

<212> PRT

<213> Homo sapiens

<400> 3552

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				Lys	Lys
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<212> DNA

<213> Homo sapiens

<400> 3553

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 ggaagattta atgaaagggt tattctgtct ctggcctctt gtaagaagtg tctcgtcatt
 120
 gatgaccagc tcaacatcct gcccatctcc tcccacgttg ccaccatgga ggccctgcct
 180
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 300
 gccaaagctg tcttgaaatt tatcgagggc atctctgaaa agaccctgag gagtactgtt
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 420
 gcggtggcat ttgggtactc caatatcttt gttacctccc caagccctga taacctccat
 480
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 540
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 600
 ttctgagaac acaggcagac tattcagtat atacatcctg cagatgctgt gaagctgggc
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 720
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 780
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 840
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 900
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 960
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 1020
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 1080
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 1140
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 1200
 cctcctgtgc cccccacca gaatgccctt ccaaaagtgc ttgctgttat ccaggatatg
 1260

gaacagagggc gtccttgtgg cagtgatttg gggaaccact gaggcacag gaattagtgg
 1320
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 1380
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<210> 3554

<211> 419

<212> PRT

<213> Homo sapiens

<400> 3554

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Gln	Asp	Val	Val	Gly	Arg	Phe	Asn	Glu	Arg	Phe	Ile	Leu	Ser	Leu	Ala
			20					25					30		
Ser	Cys	Lys	Lys	Cys	Leu	Val	Ile	Asp	Asp	Gln	Leu	Asn	Ile	Leu	Pro
	35						40					45			
Ile	Ser	Ser	His	Val	Ala	Thr	Met	Glu	Ala	Leu	Pro	Pro	Gln	Thr	Pro
	50					55					60				
Asp	Glu	Ser	Leu	Gly	Pro	Ser	Asp	Leu	Glu	Leu	Arg	Glu	Leu	Lys	Glu
65				70					75					80	
Ser	Leu	Gln	Asp	Thr	Gln	Pro	Val	Gly	Val	Leu	Val	Asp	Cys	Cys	Lys
			85					90					95		
Thr	Leu	Asp	Gln	Ala	Lys	Ala	Val	Leu	Lys	Phe	Ile	Glu	Gly	Ile	Ser
			100					105					110		
Glu	Lys	Thr	Leu	Arg	Ser	Thr	Val	Ala	Leu	Thr	Ala	Ala	Arg	Gly	Arg
	115						120					125			
Gly	Lys	Ser	Ala	Ala	Leu	Gly	Leu	Ala	Ile	Ala	Gly	Ala	Val	Ala	Phe
	130					135					140				
Gly	Tyr	Ser	Asn	Ile	Phe	Val	Thr	Ser	Pro	Ser	Pro	Asp	Asn	Leu	His
145			150						155					160	
Thr	Leu	Phe	Glu	Phe	Val	Phe	Lys	Gly	Phe	Asp	Ala	Leu	Gln	Tyr	Gln
			165					170					175		
Glu	His	Leu	Asp	Tyr	Glu	Ile	Ile	Gln	Ser	Leu	Asn	Pro	Glu	Phe	Asn
	180							185				190			
Lys	Ala	Val	Ile	Ile	Val	Asn	Val	Phe	Arg	Glu	His	Arg	Gln	Thr	Ile
	195					200					205				
Gln	Tyr	Ile	His	Pro	Ala	Asp	Ala	Val	Lys	Leu	Gly	Gln	Ala	Glu	Leu
	210					215					220				
Val	Val	Ile	Asp	Glu	Ala	Ala	Ala	Ile	Pro	Leu	Pro	Leu	Val	Lys	Ser
225				230					235					240	
Leu	Leu	Gly	Pro	Tyr	Leu	Val	Phe	Met	Ala	Ser	Thr	Ile	Asn	Gly	Tyr
			245					250					255		
Glu	Gly	Thr	Gly	Arg	Ser	Leu	Ser	Leu	Lys	Leu	Ile	Gln	Gln	Leu	Arg
		260					265					270			
Gln	Gln	Ser	Ala	Gln	Ser	Gln	Val	Ser	Thr	Thr	Ala	Glu	Asn	Lys	Thr
	275					280						285			
Thr	Thr	Thr	Ala	Arg	Leu	Ala	Ser	Ala	Arg	Thr	Leu	His	Glu	Val	Ser
	290					295					300				
Leu	Gln	Glu	Ser	Ile	Arg	Tyr	Ala	Pro	Gly	Asp	Ala	Val	Glu	Lys	Trp
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Leu	Asn	Asp	Leu	Leu	Cys	Leu	Asp	Cys	Leu	Asn	Ile	Thr	Arg	Ile	Val

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<400> 3555
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120
atgaaccagg cgttgcagag gcgcttcgcc aagggggtgc agtacaacat gaagatagtg
180
atccggggag acaggaacac gggcaagaca gcgctgtggc accgcctgca gggccggccg
240
ttcgtggagg agtacatccc cacacaggag atccagggtca ccagcatcca ctggagctac
300
aagaccacgg atgacatcgt gaagggtgaa gtctgggatg tagtagacaa aggaaaatgc
360
aaaaagcgag gcgacggctt aaagatggag aacgaccccc aggaggcgga gtctgaaatg
420
gccttggatg ctgagttcct ggacgtgtac aagaactgca acggggtggg catgatgttc
480
gacattacca agcagtggac cttcaattac attctccggg agcttccaaa agtgccacc
540
cacgtgccag tgtgcgtgct ggggaactac cgggacatgg gcgagcacc agtcatcnn
600
tgccggacgn acgtgcgtga cttcatcgac aacctggaca gacctccagg ttctctctac
660
ttccgctatg ctgagcttct catgaagaac agcttcggcc taaagtacct tcataagttc
720
ttcaatatcc catttttgca gcttcagagg gagacgctgt tgcggcagct ggagacgaac
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840
aactacggca tcttctctga gatgatggag gctcgcagcc gtggccatgc gtccccactg
900
gcggccaacg ggcagagccc atccccgggc tcccagtcac cagtggtgcc tgcaggcgct
960
gtgtccacgg ggagctccag ccccggcaca gccagcccc cccacagct gccctcaat
1020

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ggttgccccca ccatacctc
1038

<210> 3556

<211> 333

<212> PRT

<213> Homo sapiens

<400> 3556

Met	Phe	Ser	Ala	Leu	Lys	Lys	Leu	Val	Gly	Ser	Asp	Gln	Ala	Pro	Gly
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Arg	Asp	Lys	Asn	Ile	Pro	Ala	Gly	Leu	Gln	Ser	Met	Asn	Gln	Ala	Leu
			20					25					30		
Gln	Arg	Arg	Phe	Ala	Lys	Gly	Val	Gln	Tyr	Asn	Met	Lys	Ile	Val	Ile
			35				40					45			
Arg	Gly	Asp	Arg	Asn	Thr	Gly	Lys	Thr	Ala	Leu	Trp	His	Arg	Leu	Gln
	50					55					60				
Gly	Arg	Pro	Phe	Val	Glu	Glu	Tyr	Ile	Pro	Thr	Gln	Glu	Ile	Gln	Val
65					70					75				80	
Thr	Ser	Ile	His	Trp	Ser	Tyr	Lys	Thr	Thr	Asp	Asp	Ile	Val	Lys	Val
			85						90					95	
Glu	Val	Trp	Asp	Val	Val	Asp	Lys	Gly	Lys	Cys	Lys	Lys	Arg	Gly	Asp
			100					105					110		
Gly	Leu	Lys	Met	Glu	Asn	Asp	Pro	Gln	Glu	Ala	Glu	Ser	Glu	Met	Ala
		115					120						125		
Leu	Asp	Ala	Glu	Phe	Leu	Asp	Val	Tyr	Lys	Asn	Cys	Asn	Gly	Val	Val
	130					135						140			
Met	Met	Phe	Asp	Ile	Thr	Lys	Gln	Trp	Thr	Phe	Asn	Tyr	Ile	Leu	Arg
145					150					155				160	
Glu	Leu	Pro	Lys	Val	Pro	Thr	His	Val	Pro	Val	Cys	Val	Leu	Gly	Asn
			165						170					175	
Tyr	Arg	Asp	Met	Gly	Glu	His	Arg	Val	Ile	Xaa	Cys	Arg	Thr	Xaa	Val
			180					185					190		
Arg	Asp	Phe	Ile	Asp	Asn	Leu	Asp	Arg	Pro	Pro	Gly	Ser	Ser	Tyr	Phe
		195					200					205			
Arg	Tyr	Ala	Glu	Ser	Ser	Met	Lys	Asn	Ser	Phe	Gly	Leu	Lys	Tyr	Leu
	210					215					220				
His	Lys	Phe	Phe	Asn	Ile	Pro	Phe	Leu	Gln	Leu	Gln	Arg	Glu	Thr	Leu
225				230					235					240	
Leu	Arg	Gln	Leu	Glu	Thr	Asn	Gln	Leu	Asp	Met	Asp	Ala	Thr	Leu	Glu
			245						250					255	
Glu	Leu	Ser	Val	Gln	Gln	Glu	Thr	Glu	Asp	Gln	Asn	Tyr	Gly	Ile	Phe
			260					265					270		
Leu	Glu	Met	Met	Glu	Ala	Arg	Ser	Arg	Gly	His	Ala	Ser	Pro	Leu	Ala
		275					280					285			
Ala	Asn	Gly	Gln	Ser	Pro	Ser	Pro	Gly	Ser	Gln	Ser	Pro	Val	Val	Pro
	290					295					300				
Ala	Gly	Ala	Val	Ser	Thr	Gly	Ser	Ser	Ser	Pro	Gly	Thr	Ala	Gln	Pro
305					310					315				320	
Ala	Pro	Gln	Leu	Pro	Leu	Asn	Gly	Cys	Pro	Thr	Ile	Leu			
			325						330						

<210> 3557

<211> 486

<212> DNA

<213> Homo sapiens

<400> 3557

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 ccggcattga tcaagtccat ctgggctatg gccataagcc aacaccagtt ctatctggac
 120
 agaaagcaga gtaagtccaa aatccatgca gcacgcagcc tgagtgcagat cgccatcgac
 180
 ctgaccgaga cggggacgct gaagacctcg aagctggcca acatgggtag caaggggaag
 240
 atcatcagcg gcagcagcgg cagcctgctg tcttcaggat ctggtgccag gagacactgc
 300
 attctactcc caggtttctca ggaatcagat agctcgcagt cggccaagaa ggacatgctg
 360
 gctgccttga agtccaggca ggaagctctg gaggaacccc tgcgtcagag gctggaggaa
 420
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 480
 ctggat
 486

<210> 3558

<211> 162

<212> PRT

<213> Homo sapiens

<400> 3558

Ser	Val	Thr	Arg	Arg	Thr	Phe	Gly	His	Ser	Gly	Ile	Ala	Val	His	Thr
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Trp	Tyr	Ala	Cys	Pro	Ala	Leu	Ile	Lys	Ser	Ile	Trp	Ala	Met	Ala	Ile
			20					25					30		
Ser	Gln	His	Gln	Phe	Tyr	Leu	Asp	Arg	Lys	Gln	Ser	Lys	Ser	Lys	Ile
		35					40					45			
His	Ala	Ala	Arg	Ser	Leu	Ser	Glu	Ile	Ala	Ile	Asp	Leu	Thr	Glu	Thr
		50					55				60				
Gly	Thr	Leu	Lys	Thr	Ser	Lys	Leu	Ala	Asn	Met	Gly	Ser	Lys	Gly	Lys
65					70					75				80	
Ile	Ile	Ser	Gly	Ser	Ser	Gly	Ser	Leu	Leu	Ser	Ser	Gly	Ser	Gly	Ala
			85					90						95	
Arg	Arg	His	Cys	Ile	Leu	Leu	Pro	Gly	Ser	Gln	Glu	Ser	Asp	Ser	Ser
			100					105					110		
Gln	Ser	Ala	Lys	Lys	Asp	Met	Leu	Ala	Ala	Leu	Lys	Ser	Arg	Gln	Glu
		115					120					125			
Ala	Leu	Glu	Glu	Thr	Leu	Arg	Gln	Arg	Leu	Glu	Glu	Leu	Lys	Lys	Leu
		130				135					140				
Cys	Leu	Arg	Glu	Ala	Glu	Leu	Thr	Gly	Lys	Leu	Pro	Val	Glu	Tyr	Pro
145					150					155					160
Leu	Asp														

<210> 3559

<211> 673

<212> DNA

<213> Homo sapiens

<400> 3559

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ggccgcggct ccccgccacc tgcggccatg gatgaggagc gcgccctcta catcgcccg
120
gccggcgaag caggggctat cgagcgggtc ctgagggatt acagcgacaa gcatagggct
180
actttcaaat ttgaatcaac agatgaagat aaaagaaaga aactctgtga aggcataatt
240
aaagtcccta taaaggacat cccaacaaca tgtcaagtgt cctgcctgga agtactccgc
300
attctctcca gagacaaaaa ggtttttagtt cctgtgacaa ctaaggaaaa tatgcagata
360
ctgctgcgac tagccaagct aaatgagtta gatgattctt tggagaaagt atcagagttc
420
ccagttattg tggagtcatt aaaatgtctg tgtaatatag tgttcaacag tcagatggca
480
cagcagctca gcctggaact taatcttgct gcaaagctct gtaacctcct gagaaagtgc
540
aaggaccgga aatttatcaa tgacattaag tgctttgact tgcgcttgct cttccttctg
600
tcacttttgc acaccgacat caggtcacaa ttgcgctatg agctccaggg actaccgctg
660
ctaacgcaga tcg
673

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<210> 3560

<211> 195

<212> PRT

<213> Homo sapiens

<400> 3560

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Met Asp Glu Glu Arg Ala Leu Tyr Ile Val Arg Ala Gly Glu Ala Gly
 1          5          10          15
Ala Ile Glu Arg Val Leu Arg Asp Tyr Ser Asp Lys His Arg Ala Thr
      20          25          30
Phe Lys Phe Glu Ser Thr Asp Glu Asp Lys Arg Lys Lys Leu Cys Glu
      35          40          45
Gly Ile Phe Lys Val Leu Ile Lys Asp Ile Pro Thr Thr Cys Gln Val
      50          55          60
Ser Cys Leu Glu Val Leu Arg Ile Leu Ser Arg Asp Lys Lys Val Leu
65          70          75          80
Val Pro Val Thr Thr Lys Glu Asn Met Gln Ile Leu Leu Arg Leu Ala
      85          90          95
Lys Leu Asn Glu Leu Asp Asp Ser Leu Glu Lys Val Ser Glu Phe Pro
      100          105          110
Val Ile Val Glu Ser Leu Lys Cys Leu Cys Asn Ile Val Phe Asn Ser
      115          120          125
Gln Met Ala Gln Gln Leu Ser Leu Glu Leu Asn Leu Ala Ala Lys Leu
      130          135          140
Cys Asn Leu Leu Arg Lys Cys Lys Asp Arg Lys Phe Ile Asn Asp Ile

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145             150             155             160
Lys Cys Phe Asp Leu Arg Leu Leu Phe Leu Leu Ser Leu Leu His Thr
             165             170             175
Asp Ile Arg Ser Gln Leu Arg Tyr Glu Leu Gln Gly Leu Pro Leu Leu
             180             185             190
Thr Gln Ile
             195

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<210> 3561

<211> 523

<212> DNA

<213> Homo sapiens

<400> 3561

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acgcgtgcct gtaggcagac gaggggccag tgggcagagc agacatgaat gccccctgaa
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ggctcacaga gctgactcag aagggccatt gtcacacact ggtaagagct gattctgagg
120
ggagggcatg agacgcctat tgcagagctg ctcaccagaa ggtcacagga atttagaaga
180
gaagctccta cctgcccccg atcatgcacg tggccactga ggatgccaga cgaggtgatg
240
ctgggtctcat agagaatgta cccgaaggac tgtccatttc cccattgac tggcaggttc
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360
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420
aagcggaggt ttggtgggtg ttttctactt tgacttctca ttgcactaaa catacaactc
480
tccaggggtga cggggaagag gagtggggca aaggggtgtg cac
523

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<210> 3562

<211> 106

<212> PRT

<213> Homo sapiens

<400> 3562

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Met His Val Ala Thr Glu Asp Ala Arg Arg Gly Asp Ala Gly Leu Ile
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Glu Asn Val Pro Glu Gly Leu Ser Ile Ser Pro Ile Asp Trp Gln Val
             20             25             30
Leu His Val Asp Gly Leu Phe Arg Leu Asp Trp Leu Arg Thr Glu Glu
             35             40             45
Met Glu Gly Trp Ala Gly Ser Gly Gly Val Gly Ser Gln Thr Asp Ser
             50             55             60
Ala Trp Gly Leu Ala His Gly Val Glu Ala Glu Val Trp Trp Val Phe
             65             70             75             80
Ser Thr Leu Thr Ser His Cys Thr Lys His Thr Thr Leu Gln Gly Asp
             85             90             95
Gly Glu Glu Glu Trp Gly Lys Gly Val Cys
             100             105

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<210> 3563
 <211> 359
 <212> DNA
 <213> Homo sapiens

<400> 3563
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 cgaagccagg ggcgcgcggc gatgtgagcc atgagcgcca cgtggacgct gtcgccggag
 120
 cccctgccgc cgtcgacggg gccccagtg ggcgcgggcc tggacgcgga gcagcgcacg
 180
 gtgttcgcct tcgtgctctg cctgctcgtg gtgctggtgc tgttgatggt gcgctgcgtg
 240
 cgcacccctgc tcgacccta cagccgcagtg cccgcctcgt cctggaccga ccacaaggag
 300
 gcgctcgagc gcgggcagtt cgactacgcg ttggtgtgag gggcgcggcg cccctagg
 359

<210> 3564
 <211> 82
 <212> PRT
 <213> Homo sapiens

<400> 3564
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 Gly Pro Pro Val Gly Ala Gly Leu Asp Ala Glu Gln Arg Thr Val Phe
 20 25 30
 Ala Phe Val Leu Cys Leu Leu Val Val Leu Val Leu Leu Met Val Arg
 35 40 45
 Cys Val Arg Ile Leu Leu Asp Pro Tyr Ser Arg Met Pro Ala Ser Ser
 50 55 60
 Trp Thr Asp His Lys Glu Ala Leu Glu Arg Gly Gln Phe Asp Tyr Ala
 65 70 75 80
 Leu Val

<210> 3565
 <211> 580
 <212> DNA
 <213> Homo sapiens

<400> 3565
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 cgtgagcagg cacaggagac cttccgcgcc gccggccggg cgaccccgca ggaagtagga
 120
 aggacgagcg cgcacttcaa gtcccagaag ccccgcttcc ctggagcccg cgccgtgccg
 180
 cgctacgccc gccgggagcc gggcagagcg gccaatgt cgcagcccaa gaaaagaaag
 240
 cttgagtcgg ggggcggcgc cgaaggaggg gaggggaactg aagaggaaga tggcgcggag
 300

cgggaggcgg ccctggagcg accccggacg actaagcggg aacgggacca gctgtactac
 360
 gagtgctact cggacgtttc ggtccacgag gagatgatcg cggaccgcgt ccgcaccgat
 420
 gcctaccgct ggggtttccct tcggaactgg gcagcactgc gaggcaagac ggtactggac
 480
 gtgggcgcgg gcaccggcat tctgagcatc ttctgtgccc aggccggggc ccggcgcgtg
 540
 tacgcggtag aggccagcgc catctggcaa caggcccggg
 580

<210> 3566

<211> 193

<212> PRT

<213> Homo sapiens

<400> 3566

Thr	Arg	Arg	Gly	Trp	Glu	Lys	Gly	Cys	Gln	Asp	Thr	Arg	Arg	Ala	Ile
1			5						10					15	
Gln	Asn	Ser	Ser	Arg	Glu	Gln	Ala	Gln	Glu	Thr	Phe	Arg	Ala	Ala	Gly
		20					25					30			
Arg	Ala	Thr	Pro	Gln	Glu	Val	Gly	Arg	Thr	Ser	Ala	His	Phe	Lys	Ser
		35					40				45				
Gln	Lys	Pro	Pro	Phe	Pro	Gly	Ala	Arg	Ala	Val	Pro	Arg	Tyr	Ala	Arg
	50					55				60					
Arg	Glu	Pro	Gly	Arg	Ala	Ala	Lys	Met	Ser	Gln	Pro	Lys	Lys	Arg	Lys
65				70					75					80	
Leu	Glu	Ser	Gly	Gly	Gly	Ala	Glu	Gly	Gly	Glu	Gly	Thr	Glu	Glu	Glu
			85					90					95		
Asp	Gly	Ala	Glu	Arg	Glu	Ala	Ala	Leu	Glu	Arg	Pro	Arg	Thr	Thr	Lys
		100					105					110			
Arg	Glu	Arg	Asp	Gln	Leu	Tyr	Tyr	Glu	Cys	Tyr	Ser	Asp	Val	Ser	Val
	115					120					125				
His	Glu	Glu	Met	Ile	Ala	Asp	Arg	Val	Arg	Thr	Asp	Ala	Tyr	Arg	Trp
	130				135					140					
Val	Ser	Leu	Arg	Asn	Trp	Ala	Ala	Leu	Arg	Gly	Lys	Thr	Val	Leu	Asp
145				150					155					160	
Val	Gly	Ala	Gly	Thr	Gly	Ile	Leu	Ser	Ile	Phe	Cys	Ala	Gln	Ala	Gly
			165				170						175		
Ala	Arg	Arg	Val	Tyr	Ala	Val	Glu	Ala	Ser	Ala	Ile	Trp	Gln	Gln	Ala
		180					185					190			

Arg

<210> 3567

<211> 2811

<212> DNA

<213> Homo sapiens

<400> 3567

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 120

ataagcaggt ggaagagatc ctccgtctgg agaaagaaat cgaggacctg cagcgcatga
180
aggagcagca ggagctgtcg ctgaccgagg cttccctgca gaagctgcag gagcggcggg
240
accaggagct ccgaggctg gaggaggaga tttttgcacc tgaaaaaggc agccatagtt
300
ttccagaagc aactcagagg tcagattgct cggagagttt acagacaatt gctggcagag
360
aaaagggagc aagaagaaaa gaagaaacag gaagaggaag aaaagaagaa acgggaggaa
420
gaagaaagag aaagagagag agagcgaaga gaagccgagc tccgcgcca gcaggaagaa
480
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<211> 869

<212> PRT

<213> Homo sapiens

<400> 3568

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<211> 5070

<212> DNA

<213> Homo sapiens

<400> 3569

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<211> 893

<212> PRT

<213> Homo sapiens

<400> 3570

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Ser	Ile	Thr	Ser	Gln	Tyr

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<210> 3571

<211> 528

<212> DNA

<213> Homo sapiens

<400> 3571

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<210> 3573

<211> 1236

<212> DNA

<213> Homo sapiens

<400> 3573

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1200

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1236

<210> 3574

<211> 361

<212> PRT

<213> Homo sapiens

<400> 3574

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			20					25					30		
Ile	Asn	Pro	Ser	His	Thr	His	Ser	Pro	Ile	Phe	Ser	Ile	His	Ser	Gly
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Thr	Cys	Val	Phe	Asn	Lys	Pro	Gly	Gly	His	Thr	Ala	Ser	His	Thr	His
	50					55				60					
Thr	Leu	Thr	Ala	Thr	Asn	Pro	Arg	Ser	His	Ala	His	Ala	Asp	Ala	Pro
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Cys	Gly	Thr	Cys	Thr	His	Asn	His	Thr	Cys	Val	Gln	Ser	Gly	Arg	His
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Thr	His	Thr	Cys	Ile	Glu	Ala	Ser	Leu	Trp	Thr	Pro	Ser	Ala	Ser	His
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Pro	Phe	Asp	Val	Glu	Arg	Gly	Pro	Pro	Ser	Pro	Ala	Val	Gln	His	Phe
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Thr	Phe	Ala	Leu	Thr	Asp	Leu	Ala	Gly	Asn	Arg	Arg	Phe	Gly	Phe	Cys
			180					185					190		
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			260					265					270		
Arg	Gly	Asn	Ser	Lys	Pro	Leu	Ser	Cys	Phe	Val	Ala	Pro	Asp	Ser	Gly
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Ala	Val	Thr	Asp	Glu	Asn	Ile	Val	Gly	Leu	Phe	Ala	Ala	Leu	Leu	Ala
305					310					315					320
Glu	Arg	Arg	Val	Leu	Leu	Thr	Ala	Ser	Lys	Leu	Ser	Thr	Leu	Arg	Arg
				325					330					335	
Gly	Pro	Pro	Gly	Arg	Gly	Gly	Ser	Arg	Ala	Trp	Leu	Arg	Pro	Gly	Gly
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355

360

<210> 3575

<211> 769

<212> DNA

<213> Homo sapiens

<400> 3575

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 180
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 300
 gagaagtatg tggagtaatc ttgggggaat gaagagggga agaccagca gacaacgaca
 360
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 420
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 480
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 540
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 600
 gaatagtctc ctccatatca aggtttacat caggaaattt aatagcaaga gtgacaaaaa
 660
 atttaataaa ttaatggaag agtgggaagt aacagaattg tggctcttta taaaattatg
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<210> 3576

<211> 205

<212> PRT

<213> Homo sapiens

<400> 3576

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 20 25 30
 Ser Thr Thr Lys Gln Asp Lys Ile Ile Ser Phe Ile Phe Ala Leu Thr
 35 40 45
 Ile Pro Lys Met Met Phe Leu Pro Asn Glu Cys Leu His Phe Ile Phe
 50 55 60
 Gln Thr Cys Ser Leu Lys Pro Ile Ile Ala Pro Leu Arg Asn Ile Phe
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 Thr Ser Ser Ser Gly Met Ser Leu Ser Ala Gly Ser Ser Pro Leu His
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 Ser Pro Lys Ile Thr Pro His Thr Ser Pro Ala Pro Arg Arg Arg Ser


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180
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300
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360
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420
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480
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1020

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<210> 3578
 <211> 195
 <212> PRT
 <213> Homo sapiens

<400> 3578
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 Ile Ser Glu His Phe His Pro Thr Val Ile Gly Glu Ser Met Tyr Gly
 35 40 45
 Asp Phe Glu Glu Ala Phe Asp His Leu Gln Asn Arg Leu Ile Ala Thr
 50 55 60
 Lys Asn Pro Glu Glu Ile Arg Gly Gly Gly Leu Leu Lys Tyr Ser Asn
 65 70 75 80
 Leu Leu Val Arg Asp Phe Arg Pro Thr Asp Gln Glu Glu Ile Lys Thr
 85 90 95
 Leu Glu Arg Tyr Met Cys Ser Arg Phe Phe Ile Asp Phe Pro Asp Ile
 100 105 110
 Leu Glu Gln Gln Arg Lys Leu Glu Thr Tyr Leu Gln Asn His Phe Ala
 115 120 125
 Glu Glu Glu Arg Ser Lys Tyr Asp Tyr Leu Met Ile Leu Arg Arg Val
 130 135 140
 Val Asn Glu Ser Thr Val Cys Leu Met Gly His Glu Arg Arg Gln Thr
 145 150 155 160
 Leu Asn Leu Ile Ser Leu Leu Ala Leu Arg Val Leu Gly Gly Thr Lys
 165 170 175
 His His Pro Pro Val Pro Pro Arg Ser Pro Val Thr Thr Ser Gly Pro
 180 185 190
 Leu Ser Gln
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<210> 3579
 <211> 755
 <212> DNA
 <213> Homo sapiens

<400> 3579
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 120
 cagataactcc agccaccgcg aaggttccag gaaaggacaa tgcctgcga gaaaatcagg
 180

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 240
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 420
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<210> 3580

<211> 121

<212> PRT

<213> Homo sapiens

<400> 3580

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Ser	Leu	Trp	Ile	Leu	Pro	Ser	Phe	Phe	Gly	Val	Lys	Trp	Pro	Pro	Gln
			20					25					30		
Glu	Thr	Lys	Gln	His	Glu	Lys	Trp	Leu	Ser	Gln	Pro	Thr	Cys	Ser	Asp
		35				40					45				
Met	Pro	Arg	Asn	Phe	Ser	Ser	Gly	Pro	Gly	Ser	Gly	Gly	Leu	Leu	Ile
	50					55				60					
Phe	Ser	Gln	Asp	Ile	Val	Leu	Ser	Trp	Asn	Leu	Ala	Gly	Gly	Trp	Ser
65				70					75					80	
Ile	Cys	Ile	Trp	Ser	Ile	Ala	Arg	Leu	Ser	His	Leu	Ser	Ser	Asp	Gln
			85					90					95		
Lys	Cys	Ile	Ser	Lys	Ile	Ile	Thr	Ser	Thr	Lys	Thr	Ile	Ile	Asp	Cys
			100				105						110		
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<210> 3581

<211> 2132

<212> DNA

<213> Homo sapiens

<400> 3581

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<210> 3582

<211> 138

<212> PRT

<213> Homo sapiens

<400> 3582

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			20					25					30		
Ala	Ala	Pro	Gly	Val	Ala	Pro	Arg	Gly	Ala	Cys	Trp	Thr	Cys	Thr	Arg
		35					40					45			
Arg	Ala	Ser	Ser	Ala	Cys	Thr	Arg	Arg	Gly	Thr	Ala	Ala	Ala	Trp	Ser
	50					55				60					
Ser	Arg	Pro	Arg	Pro	Ser	Thr	Thr	Ala	Thr	Ser	Arg	Cys	Ser	Ser	Ala
65					70				75					80	
Arg	Trp	Arg	Arg	Arg	Thr	Arg	Gly	Cys	Thr	Pro	Ala	Thr	Cys	Thr	Ile
			85					90					95		
Thr	Thr	Ala	Thr	Ser	Thr	Arg	Ala	Trp	Pro	Ser	Ala	Trp	Arg	Ser	Pro
		100						105					110		
Thr	Ala	Pro	Arg	Pro	Pro	Pro	Pro	Thr	Gly	Thr	Ala	Arg	Arg	Arg	Cys
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Trp	Arg	Trp	Arg	Ala	Ala	His	Pro	Arg	Phe						
	130						135								

<210> 3583

<211> 1554

<212> DNA

<213> Homo sapiens

<400> 3583

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 240

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 720
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<210> 3584

<211> 356

<212> PRT

<213> Homo sapiens

<400> 3584

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Asp	Leu	Trp	Lys	Asp	Gly	Gln	Gln	Gln	Pro	Gln	Pro	Glu	Lys	Pro	Glu

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                35                40                45
Gly Asp Glu Ser Ser Ala Pro Asp Ser Gln Arg Ser Gln Thr Glu Pro
                50                55                60
Ala Arg Glu Arg Lys Arg Lys Lys Arg Arg Ile Met Lys Ala Pro Ala
65                70                75                80
Ala Glu Ala Val Ala Glu Gly Ala Ser Gly Arg His Gly Gln Gly Arg
                85                90                95
Ser Leu Glu Ala Glu Asp Lys Met Thr His Arg Ile Leu Arg Ala Ala
                100                105                110
Gln Glu Gly Asp Leu Pro Glu Leu Arg Arg Leu Leu Glu Pro His Glu
                115                120                125
Ala Gly Gly Ala Gly Gly Asn Ile Asn Ala Arg Asp Ala Phe Trp Trp
                130                135                140
Thr Pro Leu Met Cys Ala Ala Arg Ala Gly Gln Gly Ala Ala Val Ser
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Phe Gln Asp Ser Asn His Arg Thr Ser Thr Ala His Leu Leu Ser Leu
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<211> 2782

<212> DNA

<213> Homo sapiens

<400> 3585

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<211> 663

<212> PRT

<213> Homo sapiens

<400> 3586

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<211> 3148

<212> DNA

<213> Homo sapiens

<400> 3587

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<212> PRT

<213> Homo sapiens

<400> 3588

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<212> PRT

<213> Homo sapiens

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Pro	Gly	Pro	Cys	Phe	Val	Ser	Glu	Leu	Gly	Gly	Pro	Ile	Pro	Lys	His
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<210> 3591

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<212> DNA

<213> Homo sapiens

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<211> 223

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<213> Homo sapiens

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		20						25					30		
Lys	Gln	Val	Asn	Trp	Lys	Ala	Cys	Arg	Trp	Ser	Ser	Ser	Gly	Val	Ile
		35					40						45		
Pro	Asn	Glu	Lys	Ile	Arg	Asn	Ile	Gly	Ile	Ser	Ala	His	Ile	Asp	Ser
	50					55					60				
Gly	Lys	Thr	Thr	Leu	Thr	Glu	Arg	Val	Leu	Tyr	Tyr	Thr	Gly	Arg	Ile
65					70					75				80	
Ala	Lys	Met	His	Glu	Val	Lys	Gly	Lys	Asp	Gly	Val	Gly	Ala	Val	Met
			85						90					95	
Asp	Ser	Met	Glu	Leu	Glu	Arg	Gln	Arg	Gly	Ile	Thr	Ile	Gln	Ser	Ala
		100							105					110	
Ala	Thr	Tyr	Thr	Met	Trp	Lys	Asp	Val	Asn	Ile	Asn	Ile	Ile	Asp	Thr
	115						120					125			
Pro	Gly	His	Val	Asp	Phe	Thr	Ile	Glu	Val	Glu	Arg	Ala	Leu	Arg	Val
	130					135					140				
Leu	Asp	Gly	Ala	Val	Leu	Val	Leu	Cys	Ala	Val	Gly	Gly	Val	Gln	Cys
145					150					155				160	
Gln	Thr	Met	Thr	Val	Asn	Arg	Gln	Met	Lys	Arg	Tyr	Asn	Val	Pro	Phe
			165						170					175	
Leu	Thr	Phe	Ile	Asn	Lys	Leu	Asp	Arg	Met	Gly	Ser	Asn	Pro	Ala	Arg
		180						185					190		
Ala	Leu	Gln	Gln	Met	Arg	Ser	Lys	Leu	Asn	His	Asn	Ala	Ala	Phe	Met
	195						200					205			
Gln	Ile	Pro	Met	Gly	Leu	Glu	Gly	Asn	Phe	Lys	Gly	Ile	Val	Asp	
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<210> 3593
 <211> 1005
 <212> DNA
 <213> Homo sapiens

<400> 3593
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 180
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 240
 gagatagaga gaagcctgta ttcagaccac gagcttcgtg ctctggatga aaaccagcga
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 ctggcaaaga agaaagctga ccttcattgat gaagaagatg aacaggatat attgctggcg
 360
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 420
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 480
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 600
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 660
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 720
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 780
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 840
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 1005

<210> 3594
 <211> 282
 <212> PRT
 <213> Homo sapiens

<400> 3594
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 Gly Gly Trp Arg Arg Phe Glu Arg Leu Trp Ala Gly Ser Leu Ser Ser
 20 25 30
 Arg Ser Leu Ala Leu Ala Ala Ala Pro Ser Ser Asn Gly Ser Pro Trp
 35 40 45
 Arg Leu Leu Gly Ala Leu Cys Leu Gln Arg Pro Pro Val Val Ser Lys

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      50              55              60
Pro Leu Thr Pro Leu Gln Glu Glu Met Ala Ser Leu Leu Gln Gln Ile
65              70              75              80
Glu Ile Glu Arg Ser Leu Tyr Ser Asp His Glu Leu Arg Ala Leu Asp
      85              90              95
Glu Asn Gln Arg Leu Ala Lys Lys Lys Ala Asp Leu His Asp Glu Glu
      100             105             110
Asp Glu Gln Asp Ile Leu Leu Ala Gln Asp Leu Glu Asp Met Trp Glu
      115             120             125
Gln Lys Phe Leu Gln Phe Lys Leu Gly Ala Arg Ile Thr Glu Ala Asp
      130             135             140
Glu Lys Asn Asp Arg Thr Ser Leu Asn Arg Lys Leu Asp Arg Asn Leu
145             150             155             160
Val Leu Leu Val Arg Glu Lys Phe Gly Asp Gln Asp Val Trp Ile Leu
      165             170             175
Pro Gln Ala Glu Trp Gln Pro Gly Glu Thr Leu Arg Gly Thr Ala Glu
      180             185             190
Arg Thr Leu Ala Thr Leu Ser Glu Asn Asn Met Glu Ala Lys Phe Leu
      195             200             205
Gly Asn Ala Pro Cys Gly His Tyr Thr Phe Lys Phe Pro Gln Ala Met
      210             215             220
Arg Thr Glu Ser Asn Leu Gly Ala Lys Val Phe Phe Phe Lys Ala Leu
225             230             235             240
Leu Leu Thr Gly Asp Phe Ser Gln Ala Gly Asn Lys Gly His His Val
      245             250             255
Trp Val Thr Lys Asp Glu Leu Gly Asp Tyr Leu Lys Pro Lys Tyr Leu
      260             265             270
Ala Gln Val Arg Arg Phe Val Ser Asp Leu
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<210> 3595
 <211> 1903
 <212> DNA
 <213> Homo sapiens

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180
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360
gagaaggaca agttcctcac ccctgacttc acctccctgg atgttctcac cttcgtggc
420
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480
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540

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720
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780
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1320
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1740
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1800
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1903

<210> 3596

<211> 496

<212> PRT

<213> Homo sapiens

<400> 3596

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	20	25	30
Gln Met Leu	Ala Gln Tyr Ile	Glu Ser Phe Thr	Gln Gly Ser Ile Glu
	35	40	45
Ala His Lys	Arg Gly Ser Arg	Phe Trp Ile Gln	Asp Lys Gly Pro Ile
	50	55	60
Val Glu Ser	Tyr Ile Gly Phe	Ile Glu Ser Tyr	Arg Asp Pro Phe Gly
65	70	75	80
Ser Arg Gly	Glu Phe Glu Gly	Phe Val Ala Val	Val Asn Lys Ala Met
	85	90	95
Ser Ala Lys	Phe Glu Arg Leu	Val Ala Ser Ala	Glu Gln Leu Leu Lys
	100	105	110
Glu Leu Pro	Trp Pro Pro Thr	Phe Glu Lys Asp	Lys Phe Leu Thr Pro
	115	120	125
Asp Phe Thr	Ser Leu Asp Val	Leu Thr Phe Ala	Gly Ser Gly Ile Pro
	130	135	140
Ala Gly Ile	Asn Ile Pro Asn	Tyr Asp Asp Leu	Arg Gln Thr Glu Gly
145	150	155	160
Phe Lys Asn	Val Ser Leu Gly	Asn Val Leu Ala	Val Ala Tyr Ala Thr
	165	170	175
Gln Arg Glu	Lys Leu Thr Phe	Leu Glu Glu Asp	Asp Lys Asp Leu Tyr
	180	185	190
Ile Leu Trp	Lys Gly Pro Ser	Phe Asp Val Gln	Val Gly Leu His Glu
	195	200	205
Leu Leu Gly	His Gly Ser Gly	Lys Leu Phe Val	Gln Asp Glu Lys Gly
	210	215	220
Ala Phe Asn	Phe Asp Gln Glu	Thr Val Ile Asn	Pro Glu Thr Gly Glu
225	230	235	240
Gln Ile Gln	Ser Trp Tyr Arg	Ser Gly Glu Thr	Trp Asp Ser Lys Phe
	245	250	255
Ser Thr Ile	Ala Ser Ser Tyr	Glu Glu Cys Arg	Ala Glu Ser Val Gly
	260	265	270
Leu Tyr Leu	Cys Leu His Pro	Gln Val Leu Glu	Ile Phe Gly Phe Glu
	275	280	285
Gly Ala Asp	Ala Glu Asp Val	Ile Tyr Val Asn	Trp Leu Asn Met Val
	290	295	300
Arg Ala Gly	Leu Leu Ala Leu	Glu Phe Tyr Thr	Pro Glu Ala Phe Asn
305	310	315	320
Trp Arg Gln	Ala His Met Gln	Ala Arg Phe Val	Ile Leu Arg Val Leu
	325	330	335
Leu Glu Ala	Gly Glu Gly Leu	Val Thr Ile Thr	Pro Thr Thr Gly Ser
	340	345	350
Asp Gly Arg	Pro Asp Ala Arg	Val Arg Leu Asp	Arg Ser Lys Ile Arg
	355	360	365
Ser Val Gly	Lys Pro Ala Leu	Glu Arg Phe Leu	Arg Arg Leu Gln Val
	370	375	380
Leu Lys Ser	Thr Gly Asp Val	Ala Gly Gly Arg	Ala Leu Tyr Glu Gly
385	390	395	400
Tyr Ala Thr	Val Thr Asp Ala	Pro Pro Glu Cys	Phe Leu Thr Leu Arg
	405	410	415
Asp Thr Val	Leu Leu Arg Lys	Glu Ser Arg Lys	Leu Ile Val Gln Pro
	420	425	430
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<210> 3598

<211> 159
 <212> PRT
 <213> Homo sapiens

<400> 3598

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      20           25           30
Asp Tyr Asn Lys Asp Asp Met Ser Tyr Arg Arg Ile Ser Ala Val Glu
      35           40           45
Pro Lys Thr Ala Leu Pro Phe Asn Arg Phe Leu Pro Asn Lys Ser Arg
      50           55           60
Gln Pro Ser Tyr Val Pro Ala Pro Leu Arg Lys Lys Lys Pro Asp Lys
65           70           75           80
His Glu Asp Asn Arg Arg Ser Trp Ala Ser Pro Val Tyr Thr Glu Ala
      85           90           95
Asp Gly Thr Phe Ser Arg Ser Lys Ser Met Ser Asp Val Ser Ala Glu
      100          105          110
Asp Val Gln Asn Leu Arg Gln Leu Arg Tyr Glu Glu Met Gln Lys Ile
      115          120          125
Lys Ser Gln Leu Lys Glu Gln Asp Gln Lys Trp Gln Asp Asp Leu Ala
      130          135          140
Lys Trp Lys Asp Arg Arg Lys Ser Tyr Thr Ser Asp Leu Gln Lys
145          150          155

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<210> 3599
 <211> 691
 <212> DNA
 <213> Homo sapiens

<400> 3599

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660

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691

<210> 3600
<211> 98
<212> PRT
<213> Homo sapiens

<400> 3600
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Asn Lys Leu Gly Pro Cys Met Leu Leu Ala Leu Arg Gly Asn Gln Thr
20 25 30
Met Val Glu Val Arg Ser Trp Ser Gly Ser Leu Val Gly Trp Leu Ala
35 40 45
Pro Arg Pro Leu Ser Val Pro Ile Glu His Leu Leu Gly Ala Lys Asn
50 55 60
Cys Cys Arg His Gly Gly Gln Trp Val Arg Arg Ala Val Pro Ala Val
65 70 75 80
Leu Ser Leu Val Gly Ala Ser Ser Leu His His Ala Val Tyr Leu Phe
85 90 95
Leu Leu

<210> 3601
<211> 2963
<212> DNA
<213> Homo sapiens

<400> 3601
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180
aataaggcag cgatcattaa gaaaaacgtg tagccaatga aataaatgt tctgggcccc
240
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300
gctgctctcg caggcagggg ctctgctgct tacagcagtg cggccatctc ggcttctctc
360
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 2940
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<210> 3602

<211> 299

<212> PRT

<213> Homo sapiens

<400> 3602

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			20					25					30		
Glu	Ala	Arg	Glu	Leu	Met	Tyr	Ser	Gly	Ala	Leu	Leu	Phe	Phe	Ser	His
			35					40					45		
Gly	Gln	Gln	Asn	Ser	Ala	Ala	Asp	Leu	Ser	Met	Leu	Val	Leu	Glu	Ser
			50					55					60		
Leu	Glu	Lys	Ala	Glu	Val	Glu	Val	Ala	Asp	Glu	Leu	Leu	Glu	Asn	Leu
								70					75		80
Ala	Lys	Val	Phe	Ser	Leu	Met	Asp	Pro	Asn	Ser	Pro	Glu	Arg	Val	Thr
Phe	Val	Ser	Arg	Ala	Leu	Lys	Trp	Ser	Ser	Gly	Gly	Ser	Gly	Lys	Leu
Gly	His	Pro	Arg	Leu	His	Gln	Leu	Leu	Ala	Leu	Thr	Leu	Trp	Lys	Glu
Gln	Asn	Tyr	Cys	Glu	Ser	Arg	Tyr	His	Phe	Leu	His	Ser	Ala	Asp	Gly
Glu	Gly	Cys	Ala	Asn	Met	Leu	Val	Glu	Tyr	Ser	Thr	Ser	Arg	Gly	Phe
Arg	Ser	Glu	Val	Asp	Met	Phe	Val	Ala	Gln	Ala	Val	Leu	Gln	Phe	Leu
Cys	Leu	Lys	Asn	Lys	Ser	Ser	Ala	Ser	Val	Val	Phe	Thr	Thr	Tyr	Thr
Gln	Lys	His	Pro	Ser	Ile	Glu	Asp	Gly	Pro	Pro	Phe	Val	Glu	Pro	Leu

195	200	205
Leu Asn Phe Ile Trp Phe	Leu Leu Leu Ala Val Asp	Gly Gly Lys Leu
210	215	220
Thr Val Phe Thr Val Leu Cys Glu Gln Tyr Gln	Pro Ser Leu Arg Arg	
225	230	235
Asp Pro Met Tyr Asn Glu Tyr Leu Asp Arg Ile Gly Gln Leu Phe Phe		240
	245	250
Gly Val Pro Pro Lys Gln Thr Ser Ser Tyr Gly Gly Leu Leu Gly Asn		255
	260	265
Leu Leu Thr Ser Leu Met Gly Ser Ser Glu Gln Glu Asp Gly Glu Glu		270
	275	280
Ser Pro Ser Asp Gly Ser Pro Ile Glu Leu Asp		285
290	295	

<210> 3603

<211> 1082

<212> DNA

<213> Homo sapiens

<400> 3603

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360
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<210> 3604
 <211> 146
 <212> PRT
 <213> Homo sapiens

<400> 3604
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 Val Ala Ala Gln Glu Glu Pro Asp Lys Glu Gly Lys Glu Lys Pro His
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 Ala Gly Val Ser Pro Arg Gly Val Lys Arg Gln Arg Arg Ser Ser Ser
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 Gly Gly Ser Gln Glu Lys Arg Gly Arg Pro Ser Gln Glu Pro Pro Leu
 65 70 75 80
 Ala Pro Pro His Arg Arg Arg Arg Ser Arg Gln His Pro Gly Pro Leu
 85 90 95
 Pro Pro Thr Asn Ala Ala Pro Thr Val Pro Gly Pro Val Glu Pro Leu
 100 105 110
 Leu Leu Pro Pro Pro Pro Pro Ser Leu Ala Pro Ala Gly Pro Ala
 115 120 125
 Val Ala Ala Pro Leu Pro Ala Pro Ser Thr Arg Pro Ser Ser Pro Ser
 130 135 140
 Arg Leu
 145

<210> 3605
 <211> 2004
 <212> DNA
 <213> Homo sapiens

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 420
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 480

tatcattttc tgcactcagc ggacggggag ggctgtgcc aatgctggt ggagtattcc
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780
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1980
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2004

<210> 3606

<211> 324
 <212> PRT
 <213> Homo sapiens

<400> 3606

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Lys Gly Asp Tyr Tyr Glu Ala His Gln Met Tyr Arg Thr Leu Phe Phe
 35           40           45
Arg Tyr Met Ser Gln Ser Lys His Thr Glu Ala Arg Glu Leu Met Tyr
 50           55           60
Ser Gly Ala Leu Leu Phe Phe Ser His Gly Gln Gln Asn Ser Ala Ala
 65           70           75           80
Asp Leu Ser Met Leu Val Leu Glu Ser Leu Glu Lys Ala Glu Val Glu
 85           90           95
Val Ala Asp Glu Leu Leu Glu Asn Leu Ala Lys Val Phe Ser Leu Met
 100          105          110
Asp Pro Asn Ser Pro Glu Arg Val Thr Phe Val Ser Arg Ala Leu Lys
 115          120          125
Trp Ser Ser Gly Gly Ser Gly Lys Leu Gly His Pro Arg Leu His Gln
 130          135          140
Leu Leu Ala Leu Thr Leu Trp Lys Glu Gln Asn Tyr Cys Glu Ser Arg
 145          150          155          160
Tyr His Phe Leu His Ser Ala Asp Gly Glu Gly Cys Ala Asn Met Leu
 165          170          175
Val Glu Tyr Ser Thr Ser Arg Gly Phe Arg Ser Glu Val Asp Met Phe
 180          185          190
Val Ala Gln Ala Val Leu Gln Phe Leu Cys Leu Lys Asn Lys Ser Ser
 195          200          205
Ala Ser Val Val Phe Thr Thr Tyr Thr Gln Lys His Pro Ser Ile Glu
 210          215          220
Asp Gly Pro Pro Phe Val Glu Pro Leu Leu Asn Phe Ile Trp Phe Leu
 225          230          235          240
Leu Leu Ala Val Asp Gly Gly Lys Leu Thr Val Phe Thr Val Leu Cys
 245          250          255
Glu Gln Tyr Gln Pro Ser Leu Arg Arg Asp Pro Met Tyr Asn Glu Tyr
 260          265          270
Leu Asp Arg Ile Gly Gln Leu Phe Phe Gly Val Pro Pro Lys Gln Thr
 275          280          285
Ser Ser Tyr Gly Gly Leu Leu Gly Asn Leu Leu Thr Ser Leu Met Gly
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Ser Ser Glu Gln Glu Asp Gly Glu Glu Ser Pro Ser Asp Gly Ser Pro
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Ile Glu Leu Asp

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<210> 3607
 <211> 1726
 <212> DNA
 <213> Homo sapiens

<400> 3607

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240
atgatacatg cctatttatt tgtcactaat aacgacaaag accgagaagg gcatgggtcca
300
gaattttgta aacatatgca tcgcatcaac agcctgactg gagccaatat aacggtatac
360
catacttttc acgatgaggt ggatgagtat cggcgacact ggtggcgctg caatgggccg
420
tgccagcaca ggccaccgta ttacggctat gtcaaacgag ctactaacag ggaaccctct
480
gctcatgact attggtgggc tgagcaccag aaaacctgtg gaggcactta cataaaaaatc
540
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gtattggccg cagagaataa agataaaccc aacagagggtg aggccccagct agtaatccct
660
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1620

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 1726

<210> 3608
 <211> 436
 <212> PRT
 <213> Homo sapiens

<400> 3608
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 Glu Val Lys Trp Ser Val Arg Met Thr Leu Cys Ala Gly Ile Cys Ser
 35 40 45
 Tyr Glu Gly Lys Gly Gly Met Cys Ser Ile Arg Leu Ser Glu Pro Leu
 50 55 60
 Leu Lys Leu Arg Pro Arg Lys Asp Leu Val Glu Thr Leu Leu His Glu
 65 70 75 80
 Met Ile His Ala Tyr Leu Phe Val Thr Asn Asn Asp Lys Asp Arg Glu
 85 90 95
 Gly His Gly Pro Glu Phe Cys Lys His Met His Arg Ile Asn Ser Leu
 100 105 110
 Thr Gly Ala Asn Ile Thr Val Tyr His Thr Phe His Asp Glu Val Asp
 115 120 125
 Glu Tyr Arg Arg His Trp Trp Arg Cys Asn Gly Pro Cys Gln His Arg
 130 135 140
 Pro Pro Tyr Tyr Gly Tyr Val Lys Arg Ala Thr Asn Arg Glu Pro Ser
 145 150 155 160
 Ala His Asp Tyr Trp Trp Ala Glu His Gln Lys Thr Cys Gly Gly Thr
 165 170 175
 Tyr Ile Lys Ile Lys Glu Pro Glu Asn Tyr Ser Lys Lys Gly Lys Gly
 180 185 190
 Lys Ala Lys Leu Gly Lys Glu Pro Val Leu Ala Ala Glu Asn Lys Asp
 195 200 205
 Lys Pro Asn Arg Gly Glu Ala Gln Leu Val Ile Pro Phe Ser Gly Lys
 210 215 220
 Gly Tyr Val Leu Gly Glu Thr Ser Asn Leu Pro Ser Pro Gly Lys Leu
 225 230 235 240
 Ile Thr Ser His Ala Ile Asn Lys Thr Gln Asp Leu Leu Asn Gln Asn
 245 250 255
 His Ser Ala Asn Ala Val Arg Pro Asn Ser Lys Ile Lys Val Lys Phe
 260 265 270
 Glu Gln Asn Gly Ser Ser Lys Asn Ser His Leu Val Ser Pro Ala Val
 275 280 285
 Ser Asn Ser His Gln Asn Val Leu Ser Asn Tyr Phe Pro Arg Val Ser
 290 295 300
 Phe Ala Asn Gln Lys Ala Phe Arg Gly Val Asn Gly Ser Pro Arg Ile
 305 310 315 320
 Ser Val Thr Val Gly Asn Ile Pro Lys Asn Ser Val Ser Ser Ser Ser
 325 330 335
 Gln Arg Arg Val Ser Ser Ser Lys Ile Ser Leu Arg Asn Ser Ser Lys

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          340          345          350
Val Thr Glu Ser Ala Ser Val Met Pro Ser Gln Asp Val Ser Gly Ser
          355          360          365
Glu Asp Thr Phe Pro Asn Lys Arg Pro Arg Leu Glu Asp Lys Thr Val
          370          375          380
Phe Asp Asn Phe Phe Ile Lys Lys Glu Gln Ile Lys Ser Ser Gly Asn
385          390          395          400
Asp Pro Lys Tyr Ser Thr Thr Thr Ala Gln Asn Ser Ser Ser Ser Ser
          405          410          415
Ser Gln Ser Lys Met Val Asn Cys Pro Val Cys Gln Asn Glu Val Leu
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Gly Val Ser Asp
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<210> 3609

<211> 1286

<212> DNA

<213> Homo sapiens

<400> 3609

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900
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tcctctgggc cctctccttc gtctgggaag gcaccagcat gaggccaca caccagcct
1020

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 1080
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 1140
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 1260
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<210> 3610
 <211> 268
 <212> PRT
 <213> Homo sapiens

<400> 3610
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 Gly Gly Asn Glu Asp Gly Pro Gln Lys Leu Asp Leu Glu Ala Asp Ala
 20 25 30
 Glu Pro Gln Asp Leu Glu Ser Thr Asn Leu Leu Glu Ser Glu Ala Pro
 35 40 45
 Arg Asp Tyr Phe Leu Lys Phe Ala Tyr Ile Val Asp Leu Asp Ser Asp
 50 55 60
 Thr Ala Asp Lys Phe Leu Gln Leu Xaa Trp Asn Gln Arg Cys Gln Glu
 65 70 75 80
 Gly Ala Val Ser Tyr Gln Xaa Tyr Pro Leu Ser Pro Thr Arg Phe Thr
 85 90 95
 His Cys Glu Gln Val Leu Gly Glu Gly Ala Leu Asp Arg Gly Thr Tyr
 100 105 110
 Tyr Trp Glu Val Glu Ile Ile Glu Gly Trp Val Ser Met Gly Val Met
 115 120 125
 Ala Ala Asp Phe Ser Pro Gln Glu Pro Tyr Asp Arg Gly Arg Leu Gly
 130 135 140
 Arg Asn Ala His Ser Cys Cys Leu Gln Trp Asn Gly Arg Ser Phe Ser
 145 150 155 160
 Val Trp Phe His Gly Leu Glu Ala Pro Leu Pro His Pro Phe Ser Pro
 165 170 175
 Thr Val Gly Val Cys Leu Glu Tyr Ala Asp Arg Ala Leu Ala Phe Tyr
 180 185 190
 Ala Val Arg Asp Gly Lys Met Ser Leu Leu Arg Arg Leu Lys Ala Ser
 195 200 205
 Arg Pro Arg Arg Gly Gly Ile Pro Ala Ser Pro Ile Asp Pro Phe Gln
 210 215 220
 Ser Arg Leu Asp Ser His Phe Ala Gly Leu Phe Thr His Arg Leu Lys
 225 230 235 240
 Pro Ala Phe Phe Leu Glu Ser Val Asp Ala His Leu Gln Ile Gly Pro
 245 250 255
 Leu Lys Lys Ser Cys Ile Ser Val Leu Lys Arg Arg
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<210> 3611
 <211> 816

<212> DNA

<213> Homo sapiens

<400> 3611

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<210> 3612

<211> 272

<212> PRT

<213> Homo sapiens

<400> 3612

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 20 25 30
 Lys Val Lys Pro Arg Lys Ile Phe Gln Trp Arg Gln Leu Glu Asn Leu
 35 40 45
 Tyr Phe Arg Glu Lys Lys Phe Ser Val Glu Val His Asp Pro Arg Arg
 50 55 60
 Ala Ser Val Thr Arg Arg Thr Phe Gly His Ser Gly Ile Ala Val His
 65 70 75 80
 Thr Trp Tyr Ala Cys Pro Ala Leu Ile Lys Ser Ile Trp Ala Met Ala
 85 90 95
 Ile Ser Gln His Gln Phe Tyr Leu Asp Arg Lys Gln Ser Lys Ser Lys
 100 105 110
 Ile His Ala Ala Arg Ser Leu Ser Glu Ile Ala Ile Asp Leu Thr Glu

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<210> 3613
<211> 659
<212> DNA
<213> Homo sapiens
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<210> 3614
<211> 123
<212> PRT
<213> Homo sapiens
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<400> 3614

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Met Gln Ser Val Thr Arg Pro Gly Ile Pro Met Cys Ala Gln Leu Ala
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His Ser Ile Ile Val Pro Arg Lys Leu Leu Gln Phe Ile Lys Ser Ser
      20             25             30
Gly Leu Gly Ile Ser Leu Asn Ser Lys Arg Arg Lys Glu Glu Thr Phe
      35             40             45
Pro Thr Arg Cys Gly Cys Asp Ala Ser Gln Gly Pro Gln Gly His Cys
      50             55             60
Pro Arg Ala His Arg Pro Pro Leu Thr Ala Thr Gly Ala Trp Ile Arg
65             70             75             80
Ser Tyr Ile Val Gln Ser Phe Arg Pro Leu Pro Trp Ser Thr Arg Thr
      85             90             95
Arg Ala Arg Ile Ser Gly Arg Ala His Thr His Ser Tyr Thr Arg Thr
      100            105            110
Gln Thr Arg Ser Glu Lys Ser Pro Pro Pro Pro
      115            120

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<210> 3615

<211> 1388

<212> DNA

<213> Homo sapiens

<400> 3615

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120
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 1260
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 1388

<210> 3616
 <211> 290
 <212> PRT
 <213> Homo sapiens

<400> 3616
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 Glu Arg Ser Gly Ser Gln Thr Glu Ser Glu Glu Glu Ser Ser Glu Met
 35 40 45
 Asp Asp Glu Asp Tyr Glu Arg Arg Arg Ser Glu Cys Val Ser Glu Met
 50 55 60
 Leu Asp Leu Glu Lys Gln Phe Ser Glu Leu Lys Glu Lys Leu Phe Arg
 65 70 75 80
 Glu Arg Leu Ser Gln Leu Arg Leu Arg Leu Glu Glu Val Gly Ala Glu
 85 90 95
 Arg Ala Pro Glu Tyr Thr Glu Pro Leu Gly Gly Leu Gln Arg Ser Leu
 100 105 110
 Lys Ile Arg Ile Gln Val Ala Gly Ile Tyr Lys Gly Phe Cys Leu Asp
 115 120 125
 Val Ile Arg Asn Lys Tyr Glu Cys Glu Leu Gln Gly Ala Lys Gln His
 130 135 140
 Leu Glu Ser Glu Lys Leu Leu Leu Tyr Asp Thr Leu Gln Gly Glu Leu
 145 150 155 160
 Gln Glu Arg Ile Gln Arg Leu Glu Glu Asp Arg Gln Ser Leu Asp Leu
 165 170 175
 Ser Ser Glu Trp Trp Asp Asp Lys Leu His Ala Arg Gly Ser Ser Arg
 180 185 190
 Ser Trp Asp Ser Leu Pro Pro Ser Lys Arg Lys Lys Ala Pro Leu Val
 195 200 205
 Ser Gly Pro Tyr Ile Val Tyr Met Leu Gln Glu Ile Gly Ile Leu Glu
 210 215 220
 Asp Trp Thr Ala Ile Lys Lys Ala Arg Ala Ala Val Ser Pro Gln Lys

225		230		235		240									
Arg	Lys	Ser	Asp	Asp	Arg	Arg	Thr	His	Arg	Pro	Leu	Arg	Val	Cys	Pro
		245		250		255									
Ala	Arg	Leu	Leu	Trp	Cys	Cys	Trp	Ala	Leu	Pro	Leu	His	Leu	Ala	Leu
		260		265		270									
Ala	Trp	Thr	Pro	Pro	Leu	Pro	Ser	Ser	Arg	Pro	Ala	Gln	Leu	Trp	Pro
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<210> 3617
 <211> 804
 <212> DNA
 <213> Homo sapiens

<400> 3617
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<210> 3618
 <211> 148
 <212> PRT
 <213> Homo sapiens

<400> 3618
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Leu	Ala	Gly	His	His	Lys	Tyr	Leu	His	Thr	Thr	Ile	Phe	Gly	Leu	Thr
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Ser	Tyr	Cys	Pro	Asp	Cys	Ala	Leu	Leu	Leu	Val	Ser	Ala	Asn	Thr	Gly
	50					55					60				
Ile	Ala	Gly	Thr	Thr	Arg	Glu	His	Leu	Gly	Leu	Ala	Leu	Ala	Leu	Lys
65					70					75				80	
Val	Pro	Phe	Phe	Ile	Val	Val	Ser	Lys	Ile	Asp	Leu	Cys	Ala	Lys	Thr
			85						90					95	
Thr	Val	Glu	Arg	Thr	Val	Arg	Gln	Leu	Glu	Arg	Val	Leu	Lys	Gln	Pro
			100					105					110		
Gly	Cys	His	Lys	Val	Pro	Met	Leu	Val	Thr	Ser	Glu	Asp	Asp	Ala	Val
		115					120					125			
Thr	Ala	Ala	Gln	Gln	Phe	Ala	Gln	Ser	Pro	Asn	Val	Thr	Pro	Ile	Phe
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<210> 3619

<211> 948

<212> DNA

<213> Homo sapiens

<400> 3619

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<210> 3620
<211> 159
<212> PRT
<213> Homo sapiens

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35 40 45
Pro Gly Ala Ser Ser Gln Pro Cys Ser Thr Tyr Pro Pro Trp Arg Thr
50 55 60
Thr Thr Leu Ser Thr Ser Thr Ser Trp Ser Cys Leu Leu Leu Pro Cys
65 70 75 80
Ala Ser Cys Pro Ser Arg Cys Ser Cys Gln Thr Trp Pro Ser Ser Pro
85 90 95
Thr Ala Ser Thr Pro Thr Thr Ser Cys Thr Ser Phe Met Thr Thr Cys
100 105 110
Cys His Ser Ser Thr Pro Cys Gly Ser Phe Pro Ala Trp Pro Thr Arg
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Ser Thr Ser Cys Ser Ala Pro Ser Ser Leu Ser Cys Gly His Ser
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<210> 3621
<211> 2934
<212> DNA
<213> Homo sapiens

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<210> 3622

<211> 228

<212> PRT

<213> Homo sapiens

<400> 3622

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			20					25					30		
Glu	Ser	Gly	Phe	Asp	Pro	Asn	Ile	Arg	Asp	Ser	Arg	Gly	Arg	Thr	Gly
		35					40					45			
Leu	His	Leu	Ala	Ala	Ala	Arg	Gly	Asn	Val	Asp	Ile	Cys	Gln	Leu	Leu
		50				55					60				
His	Lys	Phe	Gly	Ala	Asp	Leu	Leu	Ala	Thr	Asp	Tyr	Gln	Gly	Asn	Thr
65				70					75					80	
Ala	Leu	His	Leu	Cys	Gly	His	Val	Asp	Thr	Ile	Gln	Phe	Leu	Val	Ser
			85					90					95		
Asn	Gly	Leu	Lys	Ile	Asp	Ile	Cys	Asn	His	Gln	Gly	Ala	Thr	Pro	Leu
		100					105					110			
Val	Leu	Ala	Lys	Arg	Arg	Gly	Val	Asn	Lys	Asp	Val	Ile	Arg	Leu	Leu
		115				120					125				
Glu	Ser	Leu	Glu	Glu	Gln	Glu	Val	Lys	Gly	Phe	Asn	Arg	Gly	Thr	His
		130			135					140					
Ser	Lys	Leu	Glu	Thr	Met	Gln	Thr	Ala	Glu	Ser	Glu	Ser	Ala	Met	Glu
145				150					155				160		
Ser	His	Ser	Leu	Leu	Asn	Pro	Asn	Leu	Gln	Gln	Gly	Glu	Gly	Val	Leu

165 170 175
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 180 185 190
 Trp Arg Val Leu Leu Leu Ile Phe Val Ile Ala Leu Leu Ser Leu Gly
 195 200 205
 Ile Ala Tyr Tyr Val Ser Gly Val Leu Pro Phe Val Glu Asn Gln Pro
 210 215 220
 Glu Leu Val His
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<210> 3623
 <211> 586
 <212> DNA
 <213> Homo sapiens

<400> 3623
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<210> 3624
 <211> 159
 <212> PRT
 <213> Homo sapiens

<400> 3624
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 35 40 45
 Glu Lys Lys Arg Met Asp Lys Ala Ile Gly Tyr Ser Phe Ala Ile Val
 50 55 60
 Gly Ile Asn Ile Thr Asp Leu Ala Tyr Asn Leu Leu Val Ser Gly Ala
 65 70 75 80
 Leu Lys Thr His Phe Tyr Asn Ile Ala Pro Glu Ala Pro Thr Leu Ser

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<210> 3625
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<212> DNA
<213> Homo sapiens
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2780

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<210> 3626

<211> 551

<212> PRT

<213> Homo sapiens

<400> 3626

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		20						25					30		
Trp	Gly	Pro	Ser	Ser	Ser	Leu	Met	Ser	Glu	Ile	Ala	Asp	Leu	Thr	Tyr
	35						40					45			
Asn	Val	Val	Ala	Phe	Ser	Glu	Ile	Met	Ser	Met	Ile	Trp	Lys	Arg	Leu
	50					55					60				
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65				70					75					80	
Met	Glu	Tyr	Leu	Ile	Lys	Thr	Gly	Ser	Glu	Arg	Val	Ser	Gln	Gln	Cys
			85					90					95		
Lys	Glu	Asn	Met	Tyr	Ala	Val	Gln	Thr	Leu	Lys	Asp	Phe	Gln	Tyr	Val
		100						105					110		
Asp	Arg	Asp	Gly	Lys	Asp	Gln	Gly	Val	Asn	Val	Arg	Glu	Lys	Ala	Lys
		115					120					125			
Gln	Leu	Val	Ala	Leu	Leu	Arg	Asp	Glu	Asp	Arg	Leu	Arg	Glu	Glu	Arg
	130					135					140				
Ala	His	Ala	Leu	Lys	Thr	Lys	Glu	Lys	Leu	Ala	Gln	Thr	Ala	Thr	Ala
145				150					155					160	
Ser	Ser	Ala	Ala	Val	Gly	Ser	Gly	Pro	Pro	Pro	Glu	Ala	Glu	Gln	Ala
			165					170					175		
Trp	Pro	Gln	Ser	Ser	Gly	Glu	Glu	Glu	Leu	Gln	Leu	Gln	Leu	Ala	Leu
		180					185					190			
Ala	Met	Ser	Lys	Glu	Glu	Ala	Asp	Gln	Glu	Glu	Arg	Ile	Arg	Arg	Gly
	195					200					205				
Asp	Asp	Leu	Arg	Leu	Gln	Met	Ala	Ile	Glu	Glu	Ser	Lys	Arg	Glu	Thr
	210				215						220				
Gly	Gly	Lys	Glu	Glu	Ser	Leu	Met	Asp	Leu	Ala	Asp	Val	Phe	Thr	
225				230					235				240		
Ala	Pro	Ala	Pro	Ala	Pro	Thr	Thr	Asp	Pro	Trp	Gly	Gly	Pro	Ala	Pro
			245					250					255		
Met	Ala	Ala	Ala	Val	Pro	Thr	Ala	Ala	Pro	Thr	Ser	Asp	Pro	Trp	Gly

260 265 270
 Gly Pro Pro Val Pro Pro Ala Ala Asp Pro Trp Gly Gly Pro Ala Pro
 275 280 285
 Thr Pro Ala Ser Gly Asp Pro Trp Arg Pro Ala Ala Pro Ala Gly Pro
 290 295 300
 Ser Val Asp Pro Trp Gly Gly Thr Pro Ala Pro Ala Ala Gly Glu Gly
 305 310 315 320
 Pro Thr Pro Asp Pro Trp Gly Ser Ser Asp Gly Gly Val Pro Val Ser
 325 330 335
 Gly Pro Ser Ala Ser Asp Pro Trp Thr Pro Ala Pro Ala Phe Ser Asp
 340 345 350
 Pro Trp Gly Gly Ser Pro Ala Lys Pro Ser Thr Asn Gly Thr Thr Thr
 355 360 365
 Ala Gly Gly Phe Asp Thr Glu Pro Asp Glu Phe Ser Asp Phe Asp Arg
 370 375 380
 Leu Arg Thr Ala Leu Pro Thr Ser Gly Ser Ser Ala Gly Glu Leu Glu
 385 390 395 400
 Leu Leu Ala Gly Glu Val Pro Ala Arg Ser Pro Gly Ala Phe Asp Met
 405 410 415
 Ser Gly Val Arg Gly Ser Leu Ala Glu Ala Val Gly Ser Pro Pro Pro
 420 425 430
 Ala Ala Thr Pro Thr Pro Thr Pro Thr Arg Lys Thr Pro Glu Ser
 435 440 445
 Phe Leu Gly Pro Asn Ala Ala Leu Val Asp Leu Asp Ser Leu Val Ser
 450 455 460
 Arg Pro Gly Pro Thr Pro Pro Gly Ala Lys Ala Ser Asn Pro Phe Leu
 465 470 475 480
 Pro Gly Gly Gly Pro Ala Thr Gly Pro Ser Val Thr Asn Pro Phe Gln
 485 490 495
 Pro Ala Pro Pro Ala Thr Leu Thr Leu Asn Gln Leu Arg Leu Ser Pro
 500 505 510
 Val Pro Pro Val Pro Gly Ala Pro Pro Thr Tyr Ile Ser Pro Leu Gly
 515 520 525
 Gly Gly Pro Gly Leu Pro Pro Met Met Pro Pro Gly Pro Pro Ala Pro
 530 535 540
 Asn Thr Asn Pro Phe Leu Leu
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<210> 3627

<211> 1760

<212> DNA

<213> Homo sapiens

<400> 3627

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 120
 aaaccaaaaca tcataaattt tgacaccagt ctgccgacat cacatacata cctaggtgct
 180
 gatatggaag aatttcatgg caggactttg cacgatgacg acagctgtca ggtgattcca
 240
 gttcttccac aagtgatgat gatcctgatt cccggacaga cattacctct tcagcttttt
 300

caccctcaag aagtcagtat ggtgcggaat ttaattcaga aagatagaac ctttgctgtt
360
cttgcataca gcaatgtaca ggaaagggaa gcacagtttg gaacaacagc agagatatat
420
gcctatcgag aagaacagga ttttggaatt gagatagtga aagtgaagc aattggaaga
480
caaaggttca aagtccttga gctaagaaca cagtcagatg gaatccagca agctaaagtg
540
caaattcttc ccgaatgtgt gttgccttca accatgtctg cagttcaatt agaatccctc
600
aataagtgcc agatatttcc ttcaaacct gtctcaagag aagaccaatg ttcataataa
660
tggtggcaga aataccagaa gagaaagttt cattgtgcaa atctaacttc atggcctcgc
720
tggtgtatt ccttatatga tgctgagacc ttaatggaca gaatcaagaa acagctacgt
780
gaatgggatg aaaatctaaa agatgattct cttccttcaa atccaataga ttttcttac
840
agagtagctg cttgtcttcc tattgatgat gtattgagaa ttcagctcct taaaattggc
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960
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1140
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1200
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1260
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1320
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1380
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1440
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1500
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1560
gcttggtgcc attatcctgt ggaatctgat atgtctggta gcatgtcatt gatgggacat
1620
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1760

<210> 3628

<211> 440

<212> PRT

<213> Homo sapiens

<400> 3628

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 20 25 30
 Asp Gln Asp Ser Lys Glu Ala Lys Lys Pro Asn Ile Ile Asn Phe Asp
 35 40 45
 Thr Ser Leu Pro Thr Ser His Thr Tyr Leu Gly Ala Asp Met Glu Glu
 50 55 60
 Phe His Gly Arg Thr Leu His Asp Asp Asp Ser Cys Gln Val Ile Pro
 65 70 75 80
 Val Leu Pro Gln Val Met Met Ile Leu Ile Pro Gly Gln Thr Leu Pro
 85 90 95
 Leu Gln Leu Phe His Pro Gln Glu Val Ser Met Val Arg Asn Leu Ile
 100 105 110
 Gln Lys Asp Arg Thr Phe Ala Val Leu Ala Tyr Ser Asn Val Gln Glu
 115 120 125
 Arg Glu Ala Gln Phe Gly Thr Thr Ala Glu Ile Tyr Ala Tyr Arg Glu
 130 135 140
 Glu Gln Asp Phe Gly Ile Glu Ile Val Lys Val Lys Ala Ile Gly Arg
 145 150 155 160
 Gln Arg Phe Lys Val Leu Glu Leu Arg Thr Gln Ser Asp Gly Ile Gln
 165 170 175
 Gln Ala Lys Val Gln Ile Leu Pro Glu Cys Val Leu Pro Ser Thr Met
 180 185 190
 Ser Ala Val Gln Leu Glu Ser Leu Asn Lys Cys Gln Ile Phe Pro Ser
 195 200 205
 Lys Pro Val Ser Arg Glu Asp Gln Cys Ser Tyr Lys Trp Trp Gln Lys
 210 215 220
 Tyr Gln Lys Arg Lys Phe His Cys Ala Asn Leu Thr Ser Trp Pro Arg
 225 230 235 240
 Trp Leu Tyr Ser Leu Tyr Asp Ala Glu Thr Leu Met Asp Arg Ile Lys
 245 250 255
 Lys Gln Leu Arg Glu Trp Asp Glu Asn Leu Lys Asp Asp Ser Leu Pro
 260 265 270
 Ser Asn Pro Ile Asp Phe Ser Tyr Arg Val Ala Ala Cys Leu Pro Ile
 275 280 285
 Asp Asp Val Leu Arg Ile Gln Leu Leu Lys Ile Gly Ser Ala Ile Gln
 290 295 300
 Arg Leu Arg Cys Glu Leu Asp Ile Met Asn Lys Cys Thr Ser Leu Cys
 305 310 315 320
 Cys Lys Gln Cys Gln Glu Thr Glu Ile Thr Thr Lys Asn Glu Ile Phe
 325 330 335
 Ser Leu Ser Leu Cys Gly Pro Met Ala Ala Tyr Val Asn Pro His Gly
 340 345 350
 Tyr Val His Glu Thr Leu Thr Val Tyr Lys Ala Cys Asn Leu Asn Leu
 355 360 365
 Ile Gly Arg Pro Ser Thr Glu His Ser Trp Phe Pro Gly Tyr Ala Trp
 370 375 380
 Thr Val Ala Gln Cys Lys Ile Cys Ala Ser His Ile Gly Trp Lys Phe
 385 390 395 400
 Thr Ala Thr Lys Lys Asp Met Ser Pro Gln Lys Phe Trp Gly Leu Thr

	405	410	415
Arg Ser Ala Leu Leu Pro Thr Ile Pro Asp Thr Glu Asp Glu Ile Ser			
	420	425	430
Pro Asp Lys Val Ile Leu Cys Leu			
	435	440	

<210> 3629

<211> 695

<212> DNA

<213> Homo sapiens

<400> 3629

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120
acggcgtatg ccatgctgcc cttgggcatg cgggacgccg ccgtcgcggg cctcgcctcc
180
tcactctcgc atctgctggt cctcgggctg tatcttgggc cacagccgga ctcacggcct
240
gcactgctgc cgcagttggc agcaaacgca gtgctgttcc tgtgcgggaa cgtggcagga
300
gtgtaccaca aggcgctgat ggagcgcgcc ctgcgggcca cgttccggga ggcactcagc
360
tccttgcaact cagcccggcg gctggacacc gagaagaagc accaggtcag ccgggcctag
420
gaaggtcaga gcagcgcctc gagggaggag ttgcttagat tacataacgg ggctcctcca
480
caagttgagt gactctgggc aggtttcttg acctgtttct tcttttgtat aaaatgtggg
540
tattgcccac ctagaaggt tgtgaggctc aaacaaacca aagcttataa aaagcacttt
600
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660
aaagtgatc agtgtaggat ggagtgctgg ggcgc
695

<210> 3630

<211> 139

<212> PRT

<213> Homo sapiens

<400> 3630

Thr Arg Pro Leu Ser Gly Leu Val Trp Val Ala Leu Leu Ala Leu Gly			
1	5	10	15
His Ala Phe Leu Phe Thr Gly Gly Val Val Ser Ala Trp Asp Gln Val			
	20	25	30
Ser Tyr Phe Leu Phe Val Ile Phe Thr Ala Tyr Ala Met Leu Pro Leu			
	35	40	45
Gly Met Arg Asp Ala Ala Val Ala Gly Leu Ala Ser Ser Leu Ser His			
	50	55	60
Leu Leu Val Leu Gly Leu Tyr Leu Gly Pro Gln Pro Asp Ser Arg Pro			
65	70	75	80
Ala Leu Leu Pro Gln Leu Ala Ala Asn Ala Val Leu Phe Leu Cys Gly			

		85					90				95				
Asn	Val	Ala	Gly	Val	Tyr	His	Lys	Ala	Leu	Met	Glu	Arg	Ala	Leu	Arg
		100						105					110		
Ala	Thr	Phe	Arg	Glu	Ala	Leu	Ser	Ser	Leu	His	Ser	Arg	Arg	Arg	Leu
		115					120					125			
Asp	Thr	Glu	Lys	Lys	His	Gln	Val	Ser	Arg	Ala					
		130					135								

<210> 3631

<211> 864

<212> DNA

<213> Homo sapiens

<400> 3631

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120
gctgcaaagg aatcagtcctt ggctggatca tgtctgcatt tcccagatgt gctatttccc
180
ggggattggg cctggtacat gcagtatctg gagaagcgca agaactctgt gtgccacttt
240
gtgacacccc tggacggctc tgtggacgta gacgagcacc gccggccgga ggccatcacc
300
acggaaggga agtactggaa gagccgcacg gagattgtga tccgggagta tcacaagtgg
360
agaacctact tcaagaaaag gctacagcag cacaaggatg aggacctctc cagcctggtc
420
caggacgatg acatgctgta ttggcacaag cacgggggatg gatggaagac ccccgctccc
480
atggaggagg atcccctgct ggacacagac atgctcatgt cggaattcag cgacaccctc
540
ttctccacac ttcttcaca ccagccggtg gcctggccca atccccggga aatagcacat
600
ctgggaaatg cagacatgat ccagccggga ctgattcctt tgcagcctaa cctggacttc
660
atggacacct ttgagccttt ccaggacctc ttctcttcta gccgctccat ttttggctcc
720
atgctacctg catctgcctc agcacctgta ccagatccca acaaccacc tgcacaggag
780
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840
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<210> 3632

<211> 222

<212> PRT

<213> Homo sapiens

<400> 3632

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1					5			10					15		
Pro	Leu	Asp	Gly	Ser	Val	Asp	Val	Asp	Glu	His	Arg	Arg	Pro	Glu	Ala

20 25 30
 Ile Thr Thr Glu Gly Lys Tyr Trp Lys Ser Arg Ile Glu Ile Val Ile
 35 40 45
 Arg Glu Tyr His Lys Trp Arg Thr Tyr Phe Lys Lys Arg Leu Gln Gln
 50 55 60
 His Lys Asp Glu Asp Leu Ser Ser Leu Val Gln Asp Asp Asp Met Leu
 65 70 75 80
 Tyr Trp His Lys His Gly Asp Gly Trp Lys Thr Pro Val Pro Met Glu
 85 90 95
 Glu Asp Pro Leu Leu Asp Thr Asp Met Leu Met Ser Glu Phe Ser Asp
 100 105 110
 Thr Leu Phe Ser Thr Leu Ser Ser His Gln Pro Val Ala Trp Pro Asn
 115 120 125
 Pro Arg Glu Ile Ala His Leu Gly Asn Ala Asp Met Ile Gln Pro Gly
 130 135 140
 Leu Ile Pro Leu Gln Pro Asn Leu Asp Phe Met Asp Thr Phe Glu Pro
 145 150 155 160
 Phe Gln Asp Leu Phe Ser Ser Ser Arg Ser Ile Phe Gly Ser Met Leu
 165 170 175
 Pro Ala Ser Ala Ser Ala Pro Val Pro Asp Pro Asn Asn Pro Pro Ala
 180 185 190
 Gln Glu Ser Ile Leu Pro Thr Thr Ala Leu Pro Thr Val Ser Leu Pro
 195 200 205
 Asp Ser Leu Ile Ala Pro Pro Thr Ala Pro Ser Leu Ala Arg
 210 215 220

<210> 3633

<211> 1570

<212> DNA

<213> Homo sapiens

<400> 3633

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 120
 aggagagcct gggcaagcat tcttaggttg atgctggggc ccagagtagc agtgagcatc
 180
 ctgtgtgaag atggcatttc tcaactgatta ttggaaaagc acaagagcca cgtgctggag
 240
 ccattgtcca gccttgccct ggaggagcag tgtctggcct tgtccctaga ttggtccact
 300
 gggaaaactg gaagggcccg ggaccagccc ttgaagatca tcagcagtga ctccacaggg
 360
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 420
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 480
 tattcagggg gcgacgatgg ccttctgagg ggctgggaca ccagggtacc cggcaaattt
 540
 ctcttcacca gcnaaaagac acaccatnng ggtgtgtgca gcatccagag cagccctcat
 600
 cgggagcaca tcctggccac gggaagctat gatgaacaca tcctactgtg ggacacacga
 660

aacatgaagc agccgttggc agatacgctt gtgcaggggtg gggatatggag aatcaagtgg
 720
 caccctttcc accaccacct gctcctggcc gcctgcatgc acagtggctt taagatcctc
 780
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 840
 cccgactcgc tgggtgatgg agccgactgg tcctggctgc tcttccgttc tctgcagcgg
 900
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 960
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 1020
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 1080
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 1140
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 1260
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<210> 3634

<211> 277

<212> PRT

<213> Homo sapiens

<400> 3634

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Ala	His	Gln	Phe	Glu	Ala	Trp	Ile	Ala	Ala	Phe	Asn	Tyr	Trp	His	Pro
		20						25					30		
Glu	Ile	Val	Tyr	Ser	Gly	Gly	Asp	Asp	Gly	Leu	Leu	Arg	Gly	Trp	Asp
	35					40						45			
Thr	Arg	Val	Pro	Gly	Lys	Phe	Leu	Phe	Thr	Ser	Xaa	Lys	Thr	His	His
	50				55						60				
Xaa	Gly	Val	Cys	Ser	Ile	Gln	Ser	Ser	Pro	His	Arg	Glu	His	Ile	Leu
65					70					75				80	
Ala	Thr	Gly	Ser	Tyr	Asp	Glu	His	Ile	Leu	Leu	Trp	Asp	Thr	Arg	Asn
			85						90					95	
Met	Lys	Gln	Pro	Leu	Ala	Asp	Thr	Pro	Val	Gln	Gly	Gly	Val	Trp	Arg
			100					105					110		
Ile	Lys	Trp	His	Pro	Phe	His	His	His	Leu	Leu	Leu	Ala	Ala	Cys	Met

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      115      120      125
His Ser Gly Phe Lys Ile Leu Asn Cys Gln Lys Ala Met Glu Glu Arg
      130      135      140
Gln Glu Ala Thr Val Leu Thr Ser His Thr Leu Pro Asp Ser Leu Val
145      150      155      160
Tyr Gly Ala Asp Trp Ser Trp Leu Leu Phe Arg Ser Leu Gln Arg Ala
      165      170      175
Pro Ser Trp Ser Phe Pro Ser Asn Leu Gly Thr Lys Thr Ala Asp Leu
      180      185      190
Lys Gly Ala Ser Glu Leu Pro Thr Pro Cys His Glu Cys Arg Glu Asp
      195      200      205
Asn Asp Gly Glu Gly His Ala Arg Pro Gln Ser Gly Met Lys Pro Leu
      210      215      220
Thr Glu Gly Met Arg Lys Asn Gly Thr Trp Leu Gln Ala Thr Ala Ala
225      230      235      240
Thr Thr Arg Asp Cys Gly Val Asn Pro Glu Glu Ala Asp Ser Ala Phe
      245      250      255
Ser Leu Leu Ala Thr Cys Ser Phe Tyr Asp His Ala Leu His Leu Trp
      260      265      270
Glu Trp Glu Gly Asn
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<210> 3635

<211> 835

<212> DNA

<213> Homo sapiens

<400> 3635

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120
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180
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240
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300
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360
cctgctcaga ccctcaatga cacgctggat gacatcatgg cagcagtcag tggaagagca
420
tctgcaatgt caaactctcc taccacagct attgctgcat ccatttccca acctcagact
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540
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600
cacgaggaac tgggtacaaac actgctagag agaggagcta gtatagagca ccgagacaag
660
aaagggttta ctccactcat cttggctgcc acagctggtc atgttggtgt tgtggaaata
720
ttgctggaca atggtgcaga cattgaagcc cagtctgaaa gaaccaagga cacaccactc
780

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tccttggtt gttctggggg aagacaggag gtggtggagc tattgttagc tcgag
835

<210> 3636

<211> 278

<212> PRT

<213> Homo sapiens

<400> 3636

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20 25 30
Ala Arg Leu Gln Gln Val Asp Pro Val Leu Leu Lys Asp Glu Pro Gln
35 40 45
Gln Thr Ala Ala Gln Met Gly Cys Ala Pro Ile Gln Pro Leu Ala Met
50 55 60
Pro Gln Ala Leu Pro Leu Ala Ala Gly Pro Leu Pro Pro Gly Ser Ile
65 70 75 80
Ala Asn Leu Thr Glu Leu Gln Gly Val Ile Val Gly Gln Pro Val Leu
85 90 95
Gly Gln Ala Gln Leu Ala Gly Leu Gly Gln Gly Ile Leu Thr Glu Thr
100 105 110
Gln Gln Gly Leu Met Val Ala Ser Pro Ala Gln Thr Leu Asn Asp Thr
115 120 125
Leu Asp Asp Ile Met Ala Ala Val Ser Gly Arg Ala Ser Ala Met Ser
130 135 140
Asn Thr Pro Thr His Ser Ile Ala Ala Ser Ile Ser Gln Pro Gln Thr
145 150 155 160
Pro Thr Pro Ser Pro Ile Ile Ser Pro Ser Ala Met Leu Pro Ile Tyr
165 170 175
Pro Ala Ile Asp Ile Asp Ala Gln Thr Glu Ser Asn His Asp Thr Ala
180 185 190
Leu Thr Leu Ala Cys Ala Gly Gly His Glu Glu Leu Val Gln Thr Leu
195 200 205
Leu Glu Arg Gly Ala Ser Ile Glu His Arg Asp Lys Lys Gly Phe Thr
210 215 220
Pro Leu Ile Leu Ala Ala Thr Ala Gly His Val Gly Val Val Glu Ile
225 230 235 240
Leu Leu Asp Asn Gly Ala Asp Ile Glu Ala Gln Ser Glu Arg Thr Lys
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Asp Thr Pro Leu Ser Leu Ala Cys Ser Gly Gly Arg Gln Glu Val Val
260 265 270
Glu Leu Leu Leu Ala Arg
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<210> 3637

<211> 2128

<212> DNA

<213> Homo sapiens

<400> 3637

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120
cctgccaacc cctgctcttc caggtcgggc cccgggggttc tgcggtgtt agggacagag
180
gcaaagaagg gcaggacggt ccggtttccc gtggatgttc ccgcccgaga aagacagcaa
240
gttggtgtg cgcccgggac ggggagggga aggtagccgc cgcccgccag ccatggacca
300
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1680

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<210> 3638

<211> 200

<212> PRT

<213> Homo sapiens

<400> 3638

Met	Ala	Ser	Ser	Leu	Thr	Cys	Thr	Gly	Val	Ile	Trp	Ala	Leu	Leu	Ser
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			20					25					30		
Leu	Trp	Gly	Ser	Gln	Leu	Gly	Lys	Pro	Val	Ser	Phe	Gly	Thr	Phe	Arg
		35					40					45			
Arg	Cys	Ser	Tyr	Pro	Val	His	Asp	Glu	Ser	Arg	Gln	Met	Met	Val	Met
		50				55					60				
Val	Glu	Glu	Cys	Gly	Arg	Tyr	Ala	Ser	Phe	Gln	Gly	Ile	Pro	Ser	Ala
65					70					75				80	
Glu	Trp	Arg	Ile	Cys	Thr	Ile	Val	Thr	Gly	Leu	Gly	Cys	Gly	Leu	Leu
			85						90					95	
Leu	Leu	Val	Ala	Leu	Thr	Ala	Leu	Met	Gly	Cys	Cys	Val	Ser	Asp	Leu
			100					105					110		
Ile	Ser	Arg	Thr	Val	Gly	Arg	Val	Ala	Gly	Gly	Ile	Gln	Phe	Leu	Gly
		115					120					125			
Gly	Leu	Leu	Ile	Gly	Ala	Gly	Cys	Ala	Leu	Tyr	Pro	Leu	Gly	Trp	Asp
		130				135					140				
Ser	Glu	Glu	Val	Arg	Gln	Thr	Cys	Gly	Tyr	Thr	Ser	Gly	Gln	Phe	Asp
145					150					155				160	
Leu	Gly	Lys	Cys	Glu	Ile	Gly	Trp	Ala	Tyr	Tyr	Cys	Thr	Gly	Ala	Gly
			165						170					175	
Ala	Thr	Ala	Ala	Met	Leu	Leu	Cys	Thr	Trp	Leu	Ala	Cys	Phe	Ser	Gly
			180					185					190		
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		195					200								

<210> 3639

<211> 726

<212> DNA

<213> Homo sapiens

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 120
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 180
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 240
 aagcacatta atgtaggcag attatcaatg ttatgcattt cactgattgc atatctcttt
 300
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 360
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 420
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 480
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 540
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 600
 tgtgccttct ccctgctctt tctaggtcct gattctcacc tctgcctgtg taataaccct
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 720
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 726

<210> 3640
 <211> 102
 <212> PRT
 <213> Homo sapiens

<400> 3640
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 20 25 30
 Ser Leu Leu Asn Pro Leu Lys Gly Glu Ile Phe Leu Leu Pro Ala Arg
 35 40 45
 Val Tyr Gly Asp Asp Thr Leu Arg Pro Cys Trp Cys Trp Lys Asn His
 50 55 60
 Leu Trp Gln Cys His Phe Leu Arg Lys Thr Tyr Gln Ser Phe Ala Met
 65 70 75 80
 Phe Thr Ile Asp Lys Lys Arg Asp Met Gln Ser Val Lys Cys Ile Thr
 85 90 95
 Leu Ile Ile Cys Leu His
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<210> 3641
 <211> 455
 <212> DNA
 <213> Homo sapiens

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 120
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 180
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 240
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 300
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<210> 3642

<211> 148

<212> PRT

<213> Homo sapiens

<400> 3642

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Pro	Arg	Gly	Arg	Ala	Gly	Gly	Ala	Ala	Pro	Gly	Gly	Glu	Glu	Met	Ser
			20					25					30		
Gln	Ser	Pro	Glu	Glu	Ser	Arg	Ser	Ser	His	Ala	Ser	Arg	Asp	Leu	Ala
			35				40					45			
Pro	Leu	Glu	Arg	Arg	Ser	Gly	Arg	Gly	Ala	Arg	Asp	Ala	Arg	Ala	Leu
			50			55					60				
Thr	Ser	Trp	Ala	Pro	Val	Arg	Gly	Glu	Val	Arg	Lys	Lys	Thr	Pro	Ser
					70					75				80	
Glu	Val	Thr	Val	Pro	Thr	Arg	Val	Asp	Ser	Pro	Arg	Pro	Asp	His	Ala
					85					90				95	
Arg	Arg	Trp	Pro	Lys	Gly	Arg	Gly	Trp	Gly	Arg	Gly	Cys	Ser	Ala	Pro
				100				105					110		
Ser	Ser	Arg	Ala	Ala	Ser	Leu	Gln	Val	Phe	Ala	Leu	Ala	Arg	Arg	Ser
							120					125			
Pro	Arg	Glu	Gln	Phe	Gly	Thr	Val	Arg	Ile	Gly	Phe	Arg	Glu	Pro	Ala
							135					140			
Phe	Lys	Thr	Arg												
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<210> 3643

<211> 2243

<212> DNA

<213> Homo sapiens

<400> 3643

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120
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240
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360
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1680

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<210> 3644

<211> 560

<212> PRT

<213> Homo sapiens

<400> 3644

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Gln	Val	Ala	Ser	Lys	Ala	Glu	Glu	Asn	Leu	Leu	Met	Val	Leu	Gly	Thr
			20					25					30		
Asp	Met	Ser	Asp	Arg	Arg	Ala	Ala	Val	Ile	Phe	Ala	Asp	Thr	Leu	Thr
		35				40					45				
Leu	Leu	Phe	Glu	Gly	Ile	Ala	Arg	Ile	Val	Glu	Thr	His	Gln	Pro	Ile
	50				55					60					
Val	Glu	Thr	Tyr	Tyr	Gly	Pro	Gly	Arg	Leu	Tyr	Thr	Leu	Ile	Lys	Tyr
65				70					75					80	
Leu	Gln	Val	Glu	Cys	Asp	Arg	Gln	Val	Glu	Lys	Val	Val	Asp	Lys	Phe
			85					90						95	
Ile	Lys	Gln	Arg	Asp	Tyr	His	Gln	Gln	Phe	Arg	His	Val	Gln	Asn	Asn
			100					105					110		
Leu	Met	Arg	Asn	Ser	Thr	Thr	Glu	Lys	Ile	Glu	Pro	Arg	Glu	Leu	Asp
	115						120					125			
Pro	Ile	Leu	Thr	Glu	Val	Thr	Leu	Met	Asn	Ala	Arg	Ser	Glu	Leu	Tyr
	130					135					140				
Leu	Arg	Phe	Leu	Lys	Lys	Arg	Ile	Ser	Ser	Asp	Phe	Glu	Val	Gly	Asp
145				150					155					160	
Ser	Met	Ala	Ser	Glu	Glu	Val	Lys	Gln	Glu	His	Gln	Lys	Cys	Leu	Asp
			165					170						175	
Lys	Leu	Leu	Asn	Asn	Cys	Leu	Leu	Ser	Cys	Thr	Met	Gln	Glu	Leu	Ile
			180					185					190		
Gly	Leu	Tyr	Val	Thr	Met	Glu	Glu	Tyr	Phe	Met	Arg	Glu	Thr	Val	Asn
	195					200						205			
Lys	Ala	Val	Ala	Leu	Asp	Thr	Tyr	Glu	Lys	Gly	Gln	Leu	Thr	Ser	Ser

210	215	220
Met Val Asp Asp Val Phe Tyr Ile Val Lys Lys Cys Ile Gly Arg Ala		
225	230	235
Leu Ser Ser Ser Ser Ile Asp Cys Leu Cys Ala Met Ile Asn Leu Ala		240
	245	250
Thr Thr Glu Leu Glu Ser Asp Phe Arg Asp Val Leu Cys Asn Lys Leu		255
	260	265
Arg Met Gly Phe Pro Ala Thr Thr Phe Gln Asp Ile Gln Arg Gly Val		270
	275	280
Thr Ser Ala Val Asn Ile Met His Ser Ser Leu Gln Gln Gly Lys Phe		285
	290	295
Asp Thr Lys Gly Ile Glu Ser Thr Asp Glu Ala Lys Met Ser Phe Leu		300
305	310	315
Val Thr Leu Asn Asn Val Glu Val Cys Ser Glu Asn Ile Ser Thr Leu		320
	325	330
Lys Lys Thr Leu Glu Ser Asp Cys Thr Lys Leu Phe Ser Gln Gly Ile		335
	340	345
Gly Gly Glu Gln Ala Gln Ala Lys Phe Asp Ser Cys Leu Ser Asp Leu		350
	355	360
Ala Ala Val Ser Asn Lys Phe Arg Asp Leu Leu Gln Glu Gly Leu Thr		365
	370	375
Glu Leu Asn Ser Thr Ala Ile Lys Pro Gln Val Gln Pro Trp Ile Asn		380
385	390	395
Ser Phe Phe Ser Val Ser His Asn Ile Glu Glu Glu Glu Phe Asn Asp		400
	405	410
Tyr Glu Ala Asn Asp Pro Trp Val Gln Gln Phe Ile Leu Asn Leu Glu		415
	420	425
Gln Gln Met Ala Glu Phe Lys Ala Ser Leu Ser Pro Val Ile Tyr Asp		430
	435	440
Ser Leu Thr Gly Leu Met Thr Ser Leu Val Ala Val Glu Leu Glu Lys		445
	450	455
Val Val Leu Lys Ser Thr Phe Asn Arg Leu Gly Gly Leu Gln Phe Asp		460
465	470	475
Lys Glu Leu Arg Ser Leu Ile Ala Tyr Leu Thr Thr Val Thr Thr Trp		480
	485	490
Thr Ile Arg Asp Lys Phe Ala Arg Leu Ser Gln Met Ala Thr Ile Leu		495
	500	505
Asn Leu Glu Arg Val Thr Glu Ile Leu Asp Tyr Trp Gly Pro Asn Ser		510
	515	520
Gly Pro Leu Thr Trp Arg Leu Thr Pro Ala Glu Val Arg Gln Val Leu		525
	530	535
Ala Leu Arg Ile Asp Phe Arg Ser Glu Asp Ile Lys Arg Leu Arg Leu		540
545	550	555
		560

<210> 3645

<211> 823

<212> DNA

<213> Homo sapiens

<400> 3645

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120

tcgggttgat ttcctcatct tctatttgat gggctaactg ctctatggaa ggaagatctt
 180
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 300
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 420
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 480
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 660
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 720
 gccattcat ttgagtagta tctattggag aatttgggtga gggagccagc agctctgatg
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 823

<210> 3646

<211> 243

<212> PRT

<213> Homo sapiens

<400> 3646

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Leu	Ala	Ala	Ala	Met	Leu	His	Leu	Phe	Asp	Pro	Thr	Leu	Glu	Pro	Val
			20					25					30		
Thr	Glu	Pro	Pro	Ala	Asn	Leu	Asp	Arg	Leu	Ile	Pro	Met	Tyr	Lys	Gly
		35				40						45			
Ala	Lys	Ile	Gln	Gly	Gly	Ile	Leu	Pro	Gly	Ser	Tyr	His	Tyr	Leu	His
	50				55					60					
Ile	Ala	Lys	Pro	Ala	Ile	Pro	Thr	Pro	Leu	Glu	Val	Gln	Met	Ala	Gln
65					70				75					80	
Pro	Asn	Tyr	Gly	Leu	Glu	Leu	Val	Thr	Gly	Ser	Ala	Lys	Asn	Gly	Thr
			85					90					95		
Tyr	Phe	Arg	Ile	His	Ile	Asn	Lys	Tyr	Lys	Met	Val	Glu	Thr	Ile	Thr
		100					105						110		
Cys	Leu	Ser	Arg	Glu	Pro	Phe	Pro	Ala	Ser	Asn	Tyr	Ile	Arg	Leu	Phe
		115					120					125			
Gly	Gln	His	Glu	Gln	Leu	Leu	Asn	Asn	Leu	Cys	Ala	Arg	Tyr	Asp	Glu
	130				135					140					
Asn	Leu	Ile	Thr	Asp	Leu	Tyr	Ser	Tyr	Phe	Thr	Glu	Pro	Trp	Cys	Leu
145					150				155					160	
Ala	Leu	Phe	His	Asp	Arg	Phe	Ile	Asp	Leu	Arg	Lys	Glu	Leu	Arg	Gln
			165					170					175		
Ile	Leu	Ala	Ser	Lys	Glu	Glu	Glu	Asp	Leu	Pro	Ser	Ile	Glu	Gln	Leu


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                180                185                190
Ala His Gln Ile Glu Asp Glu Glu Ile Asn Pro Thr Glu Lys Pro Arg
                195                200                205
Gln Tyr Leu Lys Arg Val Phe Glu Glu Ser Ile Tyr Lys Thr Leu Val
                210                215                220
Glu Arg Ser Thr Leu Asp Tyr Leu His Tyr Asn Arg Tyr His Leu Pro
225                230                235                240
Met Tyr Ala

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<210> 3647
 <211> 584
 <212> DNA
 <213> Homo sapiens

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<400> 3647
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240
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420
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480
atgtcatcgt ccccgagagc cgagccact tcttcagca gctgggctac gtgctggcca
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584

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<210> 3648
 <211> 63
 <212> PRT
 <213> Homo sapiens

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<400> 3648
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Val Ser Ser Arg Trp Arg Ser Pro Thr Arg Ala Pro Thr Pro Ala Thr
35        40        45
Cys Thr Thr Ile Thr Val Ala Cys Thr Asn Ala Ala Ser Ser Thr
50        55        60

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<210> 3649
 <211> 648

<212> DNA

<213> Homo sapiens

<400> 3649

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gaagttctgt taactgatgg gaatgaaaag gccatcagaa atgtgcaaga catcatcaca
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<210> 3650

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3650

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20           25           30
Ile Ser Ala Asp Val Lys Glu Val Leu Leu Thr Asp Gly Asn Glu Lys
35           40           45
Ala Ile Arg Asn Val Gln Asp Ile Ile Thr Arg Asn Gln Lys Ala Gly
50           55           60
Val Phe Lys Thr Gln Lys Ile Ser Ser Cys Val Leu Arg Trp Asp Asn
65           70           75           80
Glu Thr Asp Val Ser Gln Leu Glu Gly His Phe Asp Ile Val Met Cys
85           90           95
Ala Asp Cys Leu Phe Leu Asp Gln Tyr Arg Ala Ser Leu Val Asp Ala
100          105          110
Ile Lys Arg Leu Leu Gln Pro Arg Gly Lys Ala Met Val Phe Ala Pro
115          120          125
Arg Arg Gly Asn Thr Leu Asn Gln Phe Cys Asn Leu Ala Glu Lys Ala
130          135          140
Gly Phe Cys Ile Gln Arg His Glu Asn Tyr Asp Glu His Ile Ser Asn
145          150          155          160
Phe His Ser Lys Leu Lys Lys Glu Asn Pro Asp Ile Tyr Glu Glu Asn

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<210> 3651

<211> 2469

<212> DNA

<213> Homo sapiens

<400> 3651

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<210> 3652

<211> 384

<212> PRT

<213> Homo sapiens

<400> 3652

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 Glu Gly Ala Thr Val Val Ile Leu Asn Met Pro Lys Gly Thr Glu Phe
 20 25 30
 Gly Ile Asp Tyr Asn Ser Trp Glu Val Gly Pro Lys Phe Arg Gly Val
 35 40 45
 Lys Met Ile Pro Pro Gly Ile His Phe Leu His Tyr Ser Ser Val Asp

50					55					60					
Lys	Ala	Asn	Pro	Lys	Glu	Val	Gly	Pro	Arg	Met	Gly	Phe	Phe	Leu	Ser
65					70					75					80
Leu	His	Gln	Arg	Gly	Leu	Thr	Val	Leu	Arg	Trp	Ser	Thr	Leu	Arg	Glu
				85					90					95	
Glu	Val	Asp	Leu	Ser	Pro	Ala	Pro	Glu	Ser	Glu	Val	Glu	Ala	Met	Arg
			100					105					110		
Ala	Asn	Leu	Gln	Glu	Leu	Asp	Gln	Phe	Leu	Gly	Pro	Tyr	Pro	Tyr	Ala
	115						120					125			
Thr	Leu	Lys	Lys	Trp	Ile	Ser	Leu	Thr	Asn	Phe	Ile	Ser	Glu	Ala	Thr
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Val	Glu	Lys	Leu	Gln	Pro	Glu	Asn	Arg	Gln	Ile	Cys	Ala	Phe	Ser	Asp
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			165					170					175		
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		180					185					190			
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Ser	Glu	Leu	Pro	Thr	Gln	Met	Phe	Pro	Glu	Gly	Ala	Thr	Pro	Ala	Glu
	210				215						220				
Ile	Thr	Lys	His	Ser	Met	Asp	Leu	Ser	Tyr	Ala	Leu	Glu	Thr	Val	Leu
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Ile	Lys	Gln	Phe	Pro	Ser	Ser	Pro	Gln	Asp	Val	Leu	Gly	Glu	Leu	Gln
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Phe	Ala	Phe	Val	Cys	Phe	Leu	Leu	Gly	Asn	Val	Tyr	Glu	Ala	Phe	Glu
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His	Trp	Lys	Arg	Leu	Leu	His	Leu	Leu	Cys	Arg	Ser	Glu	Ala	Ala	Met
	275						280					285			
Met	Lys	His	His	Thr	Leu	Tyr	Ile	Asn	Leu	Met	Ser	Ile	Leu	Tyr	His
	290				295					300					
Gln	Leu	Gly	Glu	Ile	Pro	Ala	Asp	Phe	Phe	Val	Asp	Ile	Val	Ser	Gln
305				310					315					320	
Asp	Asn	Phe	Leu	Thr	Ser	Thr	Leu	Gln	Val	Phe	Phe	Ser	Ser	Ala	Cys
		325						330					335		
Ser	Ile	Ala	Val	Asp	Ala	Thr	Leu	Arg	Lys	Lys	Ala	Glu	Lys	Phe	Gln
	340						345					350			
Ala	His	Leu	Thr	Lys	Lys	Phe	Arg	Trp	Asp	Phe	Ala	Ala	Glu	Pro	Glu
	355					360					365				
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<210> 3653

<211> 283

<212> DNA

<213> Homo sapiens

<400> 3653

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120

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<210> 3654

<211> 88

<212> PRT

<213> Homo sapiens

<400> 3654

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Ile	Pro	Ile	Arg	Ala	Ser	Phe	Ala	Ala	Glu	Met	Glu	Arg	Cys	His	
			20					25				30			
Gln	Ala	Val	Phe	Ser	Thr	Gly	Asp	Ala	Pro	Ser	Ala	Gln	Gln	Asp	Ala
			35				40					45			
Ser	Ser	Glu	Leu	Arg	Leu	His	Ile	Phe	Ala	Asp	Trp	Glu	Glu	Gly	Arg
			50			55				60					
Arg	Arg	Gly	Arg	Ile	Val	Ser	Gly	Ala	Ala	Phe	Trp	Gly	Cys	Leu	Pro
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Val	Gly	Ile	Phe	Ser	Thr	Pro	Arg								
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<210> 3655

<211> 3477

<212> DNA

<213> Homo sapiens

<400> 3655

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 720

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<210> 3656

<211> 429

<212> PRT

<213> Homo sapiens

<400> 3656

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Cys	Met	Ala	Ser	Leu	Phe	Pro	Ala	Trp	Glu	Pro	Pro	Leu	Ile	Thr	Leu
			20					25				30			
Lys	Ala	Gly	Thr	Gly	Ser	Met	Arg	Ser	Gly	Phe	Pro	Ala	Lys	Ser	Ala
		35					40				45				
Met	Trp	Arg	Tyr	Arg	Gly	Thr	Pro	Phe	Ser	Lys	Ala	Val	Glu	His	Ile
	50				55					60					
Asn	Lys	Thr	Ile	Ala	Pro	Ala	Leu	Val	Ser	Lys	Lys	Leu	Asn	Val	Thr


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65          70          75          80
Glu Gln Glu Lys Ile Asp Lys Leu Met Ile Glu Met Asp Gly Thr Glu
85          90          95
Asn Lys Ser Lys Phe Gly Ala Asn Ala Ile Leu Gly Val Ser Leu Ala
100        105        110
Val Cys Lys Ala Gly Ala Val Glu Lys Gly Val Pro Leu Tyr Arg His
115        120        125
Ile Ala Asp Leu Ala Gly Asn Ser Glu Val Ile Leu Pro Val Pro Ala
130        135        140
Phe Asn Val Ile Asn Gly Gly Ser His Ala Gly Asn Lys Leu Ala Met
145        150        155        160
Gln Glu Phe Met Ile Leu Pro Val Gly Ala Ala Asn Phe Arg Glu Ala
165        170        175
Met Arg Ile Gly Ala Glu Val Tyr His Asn Leu Lys Asn Val Ile Lys
180        185        190
Glu Lys Tyr Gly Lys Asp Ala Thr Asn Val Gly Asp Glu Gly Gly Phe
195        200        205
Ala Pro Asn Ile Leu Glu Asn Lys Glu Gly Leu Glu Leu Leu Lys Thr
210        215        220
Ala Ile Gly Lys Ala Gly Tyr Thr Asp Lys Val Val Ile Gly Met Asp
225        230        235        240
Val Ala Ala Ser Glu Phe Phe Arg Ser Gly Lys Tyr Asp Leu Asp Phe
245        250        255
Lys Ser Pro Asp Asp Pro Ser Arg Tyr Ile Ser Pro Asp Gln Leu Ala
260        265        270
Asp Leu Tyr Lys Ser Phe Ile Lys Asp Tyr Pro Val Val Ser Ile Glu
275        280        285
Asp Pro Phe Asp Gln Asp Asp Trp Gly Ala Trp Gln Lys Phe Thr Ala
290        295        300
Ser Ala Gly Ile Gln Val Val Gly Asp Asp Leu Thr Val Thr Asn Pro
305        310        315        320
Lys Arg Ile Ala Gln Ala Val Asn Glu Lys Ser Cys Asn Cys Leu Leu
325        330        335
Leu Lys Val Asn Gln Ile Gly Ser Val Thr Glu Ser Leu Gln Ala Cys
340        345        350
Lys Leu Ala Gln Ala Asn Gly Trp Gly Val Met Val Ser His Arg Ser
355        360        365
Gly Glu Thr Glu Asp Thr Phe Ile Ala Asp Leu Val Val Gly Leu Cys
370        375        380
Thr Gly Gln Ile Lys Thr Gly Ala Pro Cys Arg Ser Glu Arg Leu Ala
385        390        395        400
Lys Tyr Asn Gln Leu Leu Arg Ile Glu Glu Glu Leu Gly Ser Lys Ala
405        410        415
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<210> 3657

<211> 337

<212> DNA

<213> Homo sapiens

<400> 3657

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<210> 3658

<211> 99

<212> PRT

<213> Homo sapiens

<400> 3658

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Leu	Arg	Val	His	Phe	Arg	Leu	Lys	Ala	Tyr	Thr	Cys	Arg	Cys	Val	Thr
			20					25					30		
Cys	Ser	Phe	Ser	Ala	Gln	Gly	Val	His	Val	Gln	Val	Cys	Tyr	Val	Phe
		35					40					45			
Ile	Phe	Gly	Ser	Arg	Leu	Thr	Arg	Ala	Gly	Val	Pro	His	Val	His	Phe
		50				55				60					
Arg	Leu	Lys	Ala	Tyr	Met	Cys	Arg	Cys	Val	Thr	Cys	Ser	Leu	Ser	Ala
65					70					75				80	
Gln	Arg	Val	His	Val	Gln	Val	Cys	His	Met	Phe	Ile	Phe	Gly	Ser	Arg
			85						90					95	

Arg Thr Arg

<210> 3659

<211> 1025

<212> DNA

<213> Homo sapiens

<400> 3659

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 480

gaccactta aggatgaatt aaaccttgct gattctgaag tggataacca aaaacgaggg
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 600
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<211> 341

<212> PRT

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<400> 3660

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Val	Asn	Gly	Asp	Cys	Gln	Trp	Ile	Thr	Ala	Leu	His	Tyr	Ala	Phe	Gln
		130				135						140			
Asp	Glu	Asn	His	Leu	Tyr	Leu	Val	Met	Asp	Tyr	Tyr	Val	Gly	Gly	Asp
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Leu	Leu	Thr	Leu	Leu	Ser	Lys	Phe	Glu	Asp	Lys	Leu	Pro	Glu	Asp	Met
			165					170					175		
Ala	Arg	Phe	Tyr	Ile	Gly	Glu	Met	Val	Leu	Ala	Ile	Asp	Ser	Ile	His
		180					185					190			
Gln	Leu	His	Tyr	Val	His	Arg	Asp	Ile	Lys	Pro	Asp	Asn	Val	Leu	Leu
		195				200						205			
Asp	Val	Asn	Gly	His	Ile	Arg	Leu	Ala	Asp	Phe	Gly	Ser	Cys	Leu	Lys
	210					215					220				
Met	Asn	Asp	Asp	Gly	Thr	Val	Gln	Ser	Ser	Val	Ala	Val	Gly	Thr	Pro

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225                230                235                240
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Lys Tyr Gly Pro Glu Cys Asp Trp Trp Ser Leu Gly Val Cys Met Tyr
                260                265                270
Glu Met Leu Tyr Gly Glu Thr Pro Phe Tyr Ala Glu Ser Leu Val Glu
                275                280                285
Thr Tyr Gly Lys Ile Met Asn His Glu Glu Arg Phe Gln Phe Pro Ser
                290                295                300
His Val Thr Asp Val Ser Glu Glu Ala Lys Asp Leu Ile Gln Arg Leu
305                310                315                320
Ile Cys Ser Arg Glu Arg Arg Leu Gly Gln Asn Gly Ile Glu Asp Phe
                325                330                335
Lys Lys His Ala Phe Phe Glu Gly Leu Asn Trp Glu Asn Ile Arg Asn
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Leu Glu Ala Pro Tyr Ile Pro Asp Val Ser Ser Pro Ser Asp Thr Ser
                355                360                365
Asn Phe Asp Val Asp Asp Asp Val Leu Arg Asn Thr Glu Ile Leu Pro
370                375                380
Pro Gly Ser His Thr Gly Phe Ser Gly Leu His Leu Pro Phe Ile Gly
385                390                395                400
Phe Thr Phe Thr Thr Glu Ser Cys Phe Ser Asp Arg Gly Ser Leu Lys
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Ser Ile Met Gln Ser Asn Thr Leu Thr Lys Asp Glu Asp Val Gln Arg
                420                425                430
Asp Leu Glu His Ser Leu Gln Met Glu Ala Tyr Glu Arg Arg Ile Arg
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Arg Leu Glu Gln Glu Lys Leu Glu Leu Ser Arg Lys Leu Gln Glu Ser
450                455                460
Thr Gln Thr Val Gln Ser Leu His Gly Ser Ser Arg Ala Leu Ser Asn
465                470                475                480
Ser Asn Arg Asp Lys Glu Ile Lys Lys Leu Asn Glu Glu Ile Glu Arg
                485                490                495
Leu Lys Asn Lys Ile Ala Asp Ser Asn Arg Leu Glu Arg Gln Leu Glu
500                505                510
Asp Thr Val Ala Leu Arg Gln Glu Arg Glu Asp Ser Thr Gln Arg Leu
515                520                525
Arg Gly Leu Glu Lys Gln His Arg Val Val Arg Gln Glu Lys Glu Glu
530                535                540
Leu His Lys Gln Leu Val Glu Ala Ser Glu Arg Leu Lys Ser Gln Ala
545                550                555                560
Lys Glu Leu Lys Asp Ala His Gln Gln Arg Lys Leu Ala Leu Gln Glu
                565                570                575
Phe Ser Glu Leu Asn Glu Arg Met Ala Glu Leu Arg Ala Gln Lys Gln
580                585                590
Lys Val Ser Arg Gln Leu Arg Asp Lys Glu Glu Glu Met Glu Val Ala
595                600                605
Thr Gln Lys Val Asp Ala Met Arg Gln Glu Met Arg Arg Ala Glu Lys
610                615                620
Leu Arg Lys Glu Leu Glu Ala Gln Leu Asp Asp Ala Val Ala Glu Ala
625                630                635                640
Ser Lys Glu Arg Lys Leu Arg Glu His Ser Glu Asn Phe Cys Lys Gln
                645                650                655
Met Glu Ser Glu Leu Glu Ala Leu Lys Val Lys Gln Gly Gly Arg Gly

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2821

1090	1095	1100
Val Asp Val Gln Arg Gly Ile Gly Thr Ala Tyr Lys Gly His Val Lys		
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Val Pro Lys Pro Thr Gly Val Lys Lys Gly Trp Gln Arg Ala Tyr Ala		
	1125	1130
Val Val Cys Asp Cys Lys Leu Phe Leu Tyr Asp Leu Pro Glu Gly Lys		1135
	1140	1145
Ser Thr Gln Pro Gly Val Ile Ala Ser Gln Val Leu Asp Leu Arg Asp		1150
	1155	1160
Asp Glu Phe Ser Val Ser Ser Val Leu Ala Ser Asp Val Ile His Ala		1165
	1170	1175
Thr Arg Arg Asp Ile Pro Cys Ile Phe Arg Val Thr Ala Ser Leu Leu		1180
1185	1190	1195
Gly Ala Pro Ser Lys Thr Ser Ser Leu Leu Ile Leu Thr Glu Asn Glu		1200
	1205	1210
Asn Glu Lys Arg Lys Trp Val Gly Ile Leu Glu Gly Leu Gln Ser Ile		1215
	1220	1225
Leu His Lys Asn Arg Leu Arg Asn Gln Val Val His Val Pro Leu Glu		1230
	1235	1240
Ala Tyr Asp Ser Ser Leu Pro Leu Ile Lys Ala Ile Leu Thr Ala Ala		1245
	1250	1255
Ile Val Asp Ala Asp Arg Ile Ala Val Gly Leu Glu Glu Gly Leu Tyr		1260
1265	1270	1275
Val Ile Glu Val Thr Arg Asp Val Ile Val Arg Ala Ala Asp Cys Lys		1280
	1285	1290
Lys Val His Gln Ile Glu Leu Ala Pro Arg Glu Lys Ile Val Ile Leu		1295
	1300	1305
Leu Cys Gly Arg Asn His His Val His Leu Tyr Pro Trp Ser Ser Leu		1310
	1315	1320
Asp Gly Ala Glu Gly Ser Phe Asp Ile Lys Leu Pro Glu Thr Lys Gly		1325
	1330	1335
Cys Gln Leu Met Ala Thr Ala Thr Leu Lys Arg Asn Ser Gly Thr Cys		1340
1345	1350	1355
Leu Phe Val Ala Val Lys Arg Leu Ile Leu Cys Tyr Glu Ile Gln Arg		1360
	1365	1370
Thr Lys Pro Phe His Arg Lys Phe Asn Glu Ile Val Ala Pro Gly Ser		1375
	1380	1385
Val Gln Cys Leu Ala Val Leu Arg Asp Arg Leu Cys Val Gly Tyr Pro		1390
	1395	1400
Ser Gly Phe Cys Leu Leu Ser Ile Gln Gly Asp Gly Gln Pro Leu Asn		1405
	1410	1415
Leu Val Asn Pro Asn Asp Pro Ser Leu Ala Phe Leu Ser Gln Gln Ser		1420
1425	1430	1435
Phe Asp Ala Leu Cys Ala Val Glu Leu Glu Ser Glu Glu Tyr Leu Leu		1440
	1445	1450
Cys Phe Ser His Met Gly Leu Tyr Val Asp Pro Gln Gly Arg Arg Ala		1455
	1460	1465
Arg Ala Gln Glu Leu Met Trp Pro Ala Ala Pro Val Ala Cys Ser Cys		1470
	1475	1480
Ser Pro Thr His Val Thr Val Tyr Ser Glu Tyr Gly Val Asp Val Phe		1485
	1490	1495
Asp Val Arg Thr Met Glu Trp Val Gln Thr Ile Gly Leu Arg Arg Ile		1500
1505	1510	1515
Arg Pro Leu Asn Ser Glu Gly Thr Leu Asn Leu Leu Asn Cys Glu Pro		1520

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 Pro Arg Leu Ile Tyr Phe Lys Ser Lys Phe Ser Gly Ala Val Leu Asn
 1540 1545 1550
 Val Pro Asp Thr Ser Asp Asn Ser Lys Lys Gln Met Leu Arg Thr Arg
 1555 1560 1565
 Ser Lys Arg Arg Phe Val Phe Lys Val Pro Glu Glu Glu Arg Leu Gln
 1570 1575 1580
 Gln Arg Arg Glu Met Leu Arg Asp Pro Glu Leu Arg Ser Lys Met Ile
 1585 1590 1595 1600
 Ser Asn Pro Thr Asn Phe Asn His Val Ala His Met Gly Pro Gly Asp
 1605 1610 1615
 Gly Met Gln Val Leu Met Asp Leu Pro Leu Ser Ala Val Pro Pro Ser
 1620 1625 1630
 Gln Glu Glu Arg Pro Gly Pro Ala Pro Thr Asn Leu Ala Arg Gln Pro
 1635 1640 1645
 Pro Ser Arg Asn Lys Pro Tyr Ile Ser Trp Pro Ser Ser Gly Gly Ser
 1650 1655 1660
 Glu Pro Ser Val Thr Val Pro Leu Arg Ser Met Ser Asp Pro Asp Gln
 1665 1670 1675 1680
 Asp Phe Asp Lys Glu Pro Asp Ser Asp Ser Thr Lys His Ser Thr Pro
 1685 1690 1695
 Ser Asn Ser Ser Asn Pro Ser Gly Pro Pro Ser Pro Asn Ser Pro His
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<210> 3667

<211> 505

<212> DNA

<213> Homo sapiens

<400> 3667

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 tgattgtatt tactctttct tccctactca tagtatgcgt tccattttga ggaatcacag
 180
 atatcgaaga gatgccagaa cactagaaga tgaagaagag atgtggttta acacagatga
 240
 agatgacatg gaagatggag aagctgtagt gtctccatct gacaaaacta aaaatgatga
 300
 tgatattatg gatccaataa gtaaattcat ggaaaggaag aaattaaaag aaagtgagga
 360
 aaaggaagtg cttctgaaaa caaacctttc tggacggcag agcccaagtt tcaagctttc
 420
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<210> 3668

<211> 117

<212> PRT

<213> Homo sapiens

<400> 3668

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      20           25           30
Glu Asp Gly Glu Ala Val Val Ser Pro Ser Asp Lys Thr Lys Asn Asp
      35           40           45
Asp Asp Ile Met Asp Pro Ile Ser Lys Phe Met Glu Arg Lys Lys Leu
      50           55           60
Lys Glu Ser Glu Glu Lys Glu Val Leu Leu Lys Thr Asn Leu Ser Gly
      65           70           75           80
Arg Gln Ser Pro Ser Phe Lys Leu Ser Leu Ser Ser Gly Thr Lys Thr
      85           90           95
Asn Leu Thr Ser Gln Ser Ser Thr Thr Asn Leu Pro Gly Ser Pro Gly
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Ser Pro Gly Ser Pro
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<210> 3669

<211> 1226

<212> DNA

<213> Homo sapiens

<400> 3669

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120
ggattaatct ttacattaa tcattcactt tatgaaaacc tggatgaaga attaaatgaa
180
gaattagcag caaaagtggg tcagatgttt tatgtggctg agccaaagca agtgcccat
240
attctctgta gtccttctat gaagaatatt aatcctttaa ctgccatgag ctatctaagg
300
aagatggata cttctgggtt ttcattccatc ttagtgacac tgagcaaggc agcagtggca
360
ctgaaaatgg gagatcttga cgtgtacaga aatgaaatga aaagccatcc agagatgaag
420
ttggtgtgtg gcttcatttt ggaaccacgc ctgttgattc aacacaggaa gggacagatt
480
gttccaactg agcttgcgac tcaattgaag gagactcagc caggattgct tgtggcttca
540
gtcctgggat tgcagaagaa cagcaaaatt gggattgaag aagcagattc tttctttaag
600
gtgctttgtg gtaaggatga agataccatc cctcagctct tgatagactt ttgggaagct
660
cagctagtgg catgtctccc agatgtggta cttcaggaac tctttttcaa actcacatca
720
cagtacatct ggagattgtc taagaggcag cctcctgaca ccacaccatt gcgaacatcg
780
gaggatctga taaatgcctg tagtcattat ggcttaattt atccatgggt tcacgtcgta
840

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atatcatctg attctttagc tgataaaaat tatacagaag atctttcaaa attacagtct
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 960
 gaagacacta ttgccggcct cagtgtccat gttctgtgtc gtacacgctt gaaagagtat
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 1080
 catgaactga aagaagagaa ccggactctg tgggtggaaa aactgttgcc tgaactttgt
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<210> 3670

<211> 385

<212> PRT

<213> Homo sapiens

<400> 3670

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Val	Glu	Asp	Gly	Leu	Gln	Lys	Tyr	Glu	Arg	Gly	Leu	Ile	Phe	Tyr	Ile
			20					25					30		
Asn	His	Ser	Leu	Tyr	Glu	Asn	Leu	Asp	Glu	Glu	Leu	Asn	Glu	Glu	Leu
		35					40					45			
Ala	Ala	Lys	Val	Val	Gln	Met	Phe	Tyr	Val	Ala	Glu	Pro	Lys	Gln	Val
	50					55					60				
Pro	His	Ile	Leu	Cys	Ser	Pro	Ser	Met	Lys	Asn	Ile	Asn	Pro	Leu	Thr
65					70					75				80	
Ala	Met	Ser	Tyr	Leu	Arg	Lys	Met	Asp	Thr	Ser	Gly	Phe	Ser	Ser	Ile
				85					90					95	
Leu	Val	Thr	Leu	Ser	Lys	Ala	Ala	Val	Ala	Leu	Lys	Met	Gly	Asp	Leu
			100					105					110		
Asp	Val	Tyr	Arg	Asn	Glu	Met	Lys	Ser	His	Pro	Glu	Met	Lys	Leu	Val
		115				120					125				
Cys	Gly	Phe	Ile	Leu	Glu	Pro	Arg	Leu	Leu	Ile	Gln	His	Arg	Lys	Gly
	130					135					140				
Gln	Ile	Val	Pro	Thr	Glu	Leu	Ala	Thr	His	Leu	Lys	Glu	Thr	Gln	Pro
145					150					155				160	
Gly	Leu	Leu	Val	Ala	Ser	Val	Leu	Gly	Leu	Gln	Lys	Asn	Ser	Lys	Ile
				165				170						175	
Gly	Ile	Glu	Glu	Ala	Asp	Ser	Phe	Phe	Lys	Val	Leu	Cys	Gly	Lys	Asp
			180				185						190		
Glu	Asp	Thr	Ile	Pro	Gln	Leu	Leu	Ile	Asp	Phe	Trp	Glu	Ala	Gln	Leu
	195					200						205			
Val	Ala	Cys	Leu	Pro	Asp	Val	Val	Leu	Gln	Glu	Leu	Phe	Phe	Lys	Leu
	210					215					220				
Thr	Ser	Gln	Tyr	Ile	Trp	Arg	Leu	Ser	Lys	Arg	Gln	Pro	Pro	Asp	Thr
225					230				235					240	
Thr	Pro	Leu	Arg	Thr	Ser	Glu	Asp	Leu	Ile	Asn	Ala	Cys	Ser	His	Tyr
				245				250						255	
Gly	Leu	Ile	Tyr	Pro	Trp	Val	His	Val	Val	Ile	Ser	Ser	Asp	Ser	Leu

	260		265		270										
Ala	Asp	Lys	Asn	Tyr	Thr	Glu	Asp	Leu	Ser	Lys	Leu	Gln	Ser	Leu	Ile
	275		280		285										
Cys	Gly	Pro	Ser	Phe	Asp	Ile	Ala	Ser	Ile	Ile	Pro	Phe	Leu	Glu	Pro
	290		295		300										
Leu	Ser	Glu	Asp	Thr	Ile	Ala	Gly	Leu	Ser	Val	His	Val	Leu	Cys	Arg
305			310		315									320	
Thr	Arg	Leu	Lys	Glu	Tyr	Glu	Gln	Cys	Ile	Asp	Ile	Leu	Leu	Glu	Arg
	325		330		335										
Cys	Pro	Glu	Ala	Val	Ile	Pro	Tyr	Ala	Asn	His	Glu	Leu	Lys	Glu	Glu
	340		345		350										
Asn	Arg	Thr	Leu	Trp	Trp	Lys	Lys	Leu	Leu	Pro	Glu	Leu	Cys	Gln	Arg
	355		360		365										
Ile	Lys	Cys	Gly	Gly	Glu	Lys	Tyr	Gln	Leu	Tyr	Leu	Ser	Ser	Leu	Lys
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Ala															
385															

<210> 3671

<211> 828

<212> DNA

<213> Homo sapiens

<400> 3671

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agggcatctg gggtaagtaa aaacaaacac atagagcctg cctggagaag ctcatggtct
180
gatggaaaga taagcaagaa gagttaattt ctaatcaata tgataaaaag gtcagagagc
240
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300
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360
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480
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600
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660
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720
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828

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<210> 3672

<211> 124
 <212> PRT
 <213> Homo sapiens

<400> 3672
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 20 25 30
 Gly Gly Arg Met Val Thr Tyr Glu His Leu Arg Glu Val Val Phe Gly
 35 40 45
 Lys Ser Glu Asp Glu His Tyr Pro Leu Trp Lys Ser Val Ile Gly Gly
 50 55 60
 Met Met Ala Gly Val Ile Gly Gln Phe Leu Ala Asn Pro Thr Asp Leu
 65 70 75 80
 Val Lys Val Gln Met Gln Met Glu Gly Lys Arg Lys Leu Glu Gly Lys
 85 90 95
 Pro Leu Arg Phe Arg Gly Val His His Ala Phe Ala Lys Ile Leu Ala
 100 105 110
 Glu Gly Gly Ile Arg Gly Leu Trp Ala Gly Trp Val
 115 120

<210> 3673
 <211> 1052
 <212> DNA
 <213> Homo sapiens

<400> 3673
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 120
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 180
 aaaacacatg gtggatcttc aggaagcaga ggatattatt ctagtgtctt cgcaagtcc
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 300
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 360
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 420
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 480
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 600
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 660
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 720
 gagccatttt acaccatttt tagttgggtct gtacttagaa ttttcctgag aaagggtttt
 780

tttttattgt agcaatgaac ataatttaca ttttgtatat ggtcttaca tgtagaataa
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 960
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 1020
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 1052

<210> 3674

<211> 263

<212> PRT

<213> Homo sapiens

<400> 3674

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			20					25					30		
Ala	Cys	Ile	Lys	Ser	Phe	Ser	Asp	Glu	Gln	Trp	Tyr	Ser	Phe	Asn	Asp
		35					40					45			
Gln	His	Val	Ser	Arg	Ile	Thr	Gln	Glu	Asp	Ile	Lys	Lys	Thr	His	Gly
	50					55					60				
Gly	Ser	Ser	Gly	Ser	Arg	Gly	Tyr	Tyr	Ser	Ser	Ala	Phe	Ala	Ser	Ser
65					70					75				80	
Thr	Asn	Ala	Tyr	Met	Leu	Ile	Tyr	Arg	Leu	Lys	Asp	Pro	Ala	Arg	Asn
				85					90					95	
Ala	Lys	Phe	Leu	Glu	Val	Asp	Glu	Tyr	Pro	Glu	His	Ile	Lys	Asn	Leu
			100					105					110		
Val	Gln	Lys	Glu	Arg	Glu	Leu	Glu	Gln	Glu	Lys	Arg	Gln	Arg	Glu	
		115					120				125				
Ile	Glu	Arg	Asn	Thr	Cys	Lys	Ile	Lys	Leu	Phe	Cys	Leu	His	Pro	Thr
	130					135					140				
Lys	Gln	Val	Met	Met	Glu	Asn	Lys	Leu	Glu	Val	His	Lys	Asp	Lys	Thr
145					150					155				160	
Leu	Lys	Glu	Ala	Val	Glu	Met	Ala	Tyr	Lys	Met	Met	Asp	Leu	Glu	Glu
			165						170				175		
Val	Ile	Pro	Leu	Asp	Cys	Cys	Arg	Leu	Val	Lys	Tyr	Asp	Glu	Phe	His
			180					185					190		
Asp	Tyr	Leu	Glu	Arg	Ser	Tyr	Glu	Gly	Glu	Glu	Asp	Thr	Pro	Met	Gly
	195						200				205				
Leu	Leu	Leu	Gly	Gly	Val	Lys	Ser	Thr	Tyr	Met	Phe	Asp	Leu	Leu	Leu
	210					215					220				
Glu	Thr	Arg	Lys	Pro	Asp	Gln	Val	Phe	Gln	Ser	Tyr	Lys	Pro	Gly	Gly
225				230						235				240	
Glu	Pro	Phe	Tyr	Thr	Ile	Phe	Ser	Trp	Ser	Val	Leu	Arg	Ile	Phe	Leu
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<210> 3675

<211> 837

<212> DNA

<213> Homo sapiens

<400> 3675

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180
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300
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360
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420
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480
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<210> 3676

<211> 154

<212> PRT

<213> Homo sapiens

<400> 3676

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20           25           30
Gln Glu Gly Gly Gly Ile Ser Arg Val Gly Val Cys Lys Val Met His
35           40           45
Pro Glu Gly Asn Gly Arg Ser Gly Phe Leu Ile His Gly Glu Arg Gln
50           55           60
Lys Asp Lys Leu Val Val Leu Glu Cys Tyr Val Arg Lys Asp Leu Val
65           70           75           80
Tyr Thr Lys Ala Asn Pro Thr Phe His His Trp Lys Val Asp Asn Arg
85           90           95
Lys Phe Gly Leu Thr Phe Gln Ser Pro Ala Asp Ala Arg Ala Phe Asp
100          105          110
Arg Gly Val Arg Lys Ala Ile Glu Asp Leu Ile Glu Glu Val Glu Asn

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Asn Gln Arg Pro Arg Val Tyr Ser Cys His
      145              150

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<210> 3677
 <211> 418
 <212> DNA
 <213> Homo sapiens

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<400> 3677
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tgccgaaaga gcatggagga agatgaaagg cagacaggtc gagaacatgc agtggcgatc
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tcttctcct catcatcctc atcctcgtcc tcctcttctt gccctgggaa ctcgaggagac
300
tgggatccta gctcgttcct gtcggcacat aagctctcgg gcctctggaa ttccccacat
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418

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<210> 3678
 <211> 139
 <212> PRT
 <213> Homo sapiens

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<400> 3678
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      20              25              30
Met Pro Leu Trp Val Cys Gln Ser Cys Arg Lys Ser Met Glu Glu Asp
      35              40              45
Glu Arg Gln Thr Gly Arg Glu His Ala Val Ala Ile Ser Leu Ser His
      50              55              60
Thr Ser Cys Lys Ser Gln Ser Cys Gly Asp Asp Ser His Ser Ser Ser
      65              70              75              80
Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Ser Cys Pro Gly
      85              90              95
Asn Ser Gly Asp Trp Asp Pro Ser Ser Phe Leu Ser Ala His Lys Leu
      100              105              110
Ser Gly Leu Trp Asn Ser Pro His Ser Ser Gly Ala Met Pro Gly Ser
      115              120              125
Ser Leu Gly Ser Pro Pro Thr Ile Pro Gly Ala
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<210> 3679
 <211> 567

<212> DNA

<213> Homo sapiens

<400> 3679

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 120
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 180
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 240
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 300
 ctggagggtc ctggagtgc tgagagccgc ccctcagtgc tacggggcga ccacctgttt
 360
 gcccttttgt cctcgagac acaccaggag gaccccatca catataaggg ctttgtgcac
 420
 aaggtggaat tggaccgtgt caagctgagc tttccatga gcctcctgag ccgctttgtg
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<210> 3680

<211> 189

<212> PRT

<213> Homo sapiens

<400> 3680

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Tyr	Pro	Pro	Pro	Arg	Leu	Arg	Gln	Leu	Leu	Pro	Met	Leu	Leu	Gln	Gly
			20					25					30		
Thr	Ser	Ile	Phe	Thr	Ala	Pro	Lys	Glu	Ile	Ala	Glu	Ile	Lys	Ala	Gln
		35					40					45			
Leu	Glu	Thr	Ala	Leu	Lys	Trp	Arg	Asn	Tyr	Glu	Val	Lys	Leu	Arg	Leu
	50					55					60				
Leu	Leu	His	Leu	Glu	Glu	Leu	Gln	Met	Glu	His	Asp	Ile	Arg	His	Tyr
65				70					75					80	
Asp	Leu	Glu	Ser	Val	Pro	Met	Thr	Trp	Asp	Pro	Val	Asp	Gln	Asn	Pro
			85					90					95		
Arg	Leu	Leu	Thr	Leu	Glu	Val	Pro	Gly	Val	Thr	Glu	Ser	Arg	Pro	Ser
			100					105					110		
Val	Leu	Arg	Gly	Asp	His	Leu	Phe	Ala	Leu	Leu	Ser	Ser	Glu	Thr	His
	115						120					125			
Gln	Glu	Asp	Pro	Ile	Thr	Tyr	Lys	Gly	Phe	Val	His	Lys	Val	Glu	Leu
	130					135					140				
Asp	Arg	Val	Lys	Leu	Ser	Phe	Ser	Met	Ser	Leu	Leu	Ser	Arg	Phe	Val
145				150						155				160	
Asp	Gly	Leu	Thr	Phe	Lys	Val	Asn	Phe	Thr	Phe	Asn	Arg	Gln	Pro	Leu
			165					170					175		
Arg	Val	Gln	His	Arg	Ala	Trp	Glu	Leu	Thr	Gly	Arg	Trp			

180

185

<210> 3681
 <211> 788
 <212> DNA
 <213> Homo sapiens

<400> 3681
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 120
 gagaccggga ggcagagctt cagcagctgc gggacagcct ggggctgagc atggagcagc
 180
 gggcgaggag tcgcctgcga ggccgctggc caggcctgag cctctgccac catggccatt
 240
 gtgcagactc tgccagtgcc actggagcct gctcctgaag ctgccactgc ccacaagct
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 540
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<210> 3682
 <211> 185
 <212> PRT
 <213> Homo sapiens

<400> 3682
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 20 25 30
 Ile Ser Gly Arg Pro Cys Pro Gly Gly Pro Ala Pro Pro Arg His His
 35 40 45
 Gly Pro Pro Gly Pro Thr Phe Phe Arg Gln Gln Asp Gly Leu Leu Arg
 50 55 60
 Gly Gly Tyr Glu Ala Gln Glu Pro Leu Cys Pro Ala Val Pro Pro Arg
 65 70 75 80
 Lys Ala Val Pro Val Thr Ser Phe Thr Tyr Ile Asn Glu Asp Phe Arg


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<400> 3683
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60
t g c t g t t t a c   a t g c c g g t g a   g g t c c c c g g c   c g c t c c g a a c   c c c t c c g a g c   c c c g g c t c c c
120
c g a g g g t g a a   g c c c g c c g g c   c c g c g a a c t g   g a c t g g t g g a   t c t c t c a g a c   c t g g g g c c c c
180
g g a c t c c g a t   c t c c g c c g t c   t c c g c c a c c a   t c a g g g c g g g   a t c c g g c t c t   g g t g t t t t g a
240
g g a g g g g g t g   t g g t g t a g g g   a a a g g a a t c c   c g t c c c t c t c   c a c c t t t t t t   c g c c t t c g g g
300
g c t t c a g a c t   c a g g g a a c t c   g c t c a t g g c t   t t c t t g a t g a   a g a a g a a g a a   a t t c a a a t t c
360
c a a a c t a c t t   t c a c c c t g g a   g g a g c t g a c t   g c g g t t c c c t   t c g t g a a c g g   g g t c c t c t t c
420
t g c a a g g t c c   g g c t g c t g g a   t g g a g g g g a t   t t t g t c a g c t   t g t c g t c a a g   g g a g g a g g t a
480
c a g g a g a a c t   g t g t g c g g t g   g c g a a a g a g g   t t c a c c t t c g   t g t g t a a g a t   g a g t g c t a a c
540
c c g g c c a c c g   g c c t g c t g g a   c c c c t g t g t c   t t c c g t g t g t   c t g t g c g c a a   g g a g c t g a a a
600
g g c g g g a a g g   c t t a t t c c a a   g c t g g g c t t c   g c t g a c t t g a   a c c t g g c c g a   g t t t g c g g g c
660
t c g g g c t c c a   c g g t g c g c t g   c t g c c t g c t c   g a g g g a t a t g   a c a c g a a g a a   c a c t c g c c a g
720
g a c a a c t c c a   t c c t t a a g g t   c a c c a t t g g t   a t g t t c c t g c   t c t c t g g a g a   t c c c t g c t t c
780
a a g a c g c c a c   c a t c g a c t g c   c a a g t c c a t c   t c c a t c c c a g   g c c a g g a t t c   c t c c c t g c a g
840
c t g a c g t g t a   a g g g t g g t g g   g a c c a g c a g t   g g g g g c a g c a   g c a c c a a c t c   c c t g a c t g g g
900
t c c c g g c c c c   c c a a g g c t c g   g c c c a c t a t t   c t c a g c t c a g   g g c t g c c a g a   g g a a c c c g a c
960
c a g a a c c t g t   c c a g c c c t g a   g g a g g t g t t c   c a c t c t g g c c   a c t c c c g c a a   c t c c a g c t a t
1020

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gccagccagc agtccaagat ctccggctac agcacagagc actcgcactc ctccagcctc
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<211> 384

<212> PRT

<213> Homo sapiens

<400> 3684

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Thr	Leu	Glu	Glu	Leu	Thr	Ala	Val	Pro	Phe	Val	Asn	Gly	Val	Leu	Phe
			20					25					30		
Cys	Lys	Val	Arg	Leu	Leu	Asp	Gly	Gly	Asp	Phe	Val	Ser	Leu	Ser	Ser
			35				40					45			
Arg	Glu	Glu	Val	Gln	Glu	Asn	Cys	Val	Arg	Trp	Arg	Lys	Arg	Phe	Thr
	50					55					60				
Phe	Val	Cys	Lys	Met	Ser	Ala	Asn	Pro	Ala	Thr	Gly	Leu	Leu	Asp	Pro
65					70					75				80	
Cys	Val	Phe	Arg	Val	Ser	Val	Arg	Lys	Glu	Leu	Lys	Gly	Gly	Lys	Ala
			85						90					95	
Tyr	Ser	Lys	Leu	Gly	Phe	Ala	Asp	Leu	Asn	Leu	Ala	Glu	Phe	Ala	Gly
			100					105					110		
Ser	Gly	Ser	Thr	Val	Arg	Cys	Cys	Leu	Leu	Glu	Gly	Tyr	Asp	Thr	Lys
		115				120						125			
Asn	Thr	Arg	Gln	Asp	Asn	Ser	Ile	Leu	Lys	Val	Thr	Ile	Gly	Met	Phe
			130			135					140				
Leu	Leu	Ser	Gly	Asp	Pro	Cys	Phe	Lys	Thr	Pro	Pro	Ser	Thr	Ala	Lys
145					150					155				160	
Ser	Ile	Ser	Ile	Pro	Gly	Gln	Asp	Ser	Ser	Leu	Gln	Leu	Thr	Cys	Lys
			165					170						175	
Gly	Gly	Gly	Thr	Ser	Ser	Gly	Gly	Ser	Ser	Thr	Asn	Ser	Leu	Thr	Gly
			180					185					190		
Ser	Arg	Pro	Pro	Lys	Ala	Arg	Pro	Thr	Ile	Leu	Ser	Ser	Gly	Leu	Pro
		195				200						205			
Glu	Glu	Pro	Asp	Gln	Asn	Leu	Ser	Ser	Pro	Glu	Glu	Val	Phe	His	Ser
		210				215					220				
Gly	His	Ser	Arg	Asn	Ser	Ser	Tyr	Ala	Ser	Gln	Gln	Ser	Lys	Ile	Ser
225					230					235				240	
Gly	Tyr	Ser	Thr	Glu	His	Ser	His	Ser	Ser	Ser	Leu	Ser	Asp	Leu	Thr
			245					250						255	
His	Arg	Arg	Asn	Thr	Ser	Thr	Ser	Ser	Ser	Ala	Ser	Gly	Gly	Leu	Gly
			260					265					270		
Met	Thr	Val	Glu	Gly	Pro	Glu	Gly	Ser	Glu	Arg	Glu	His	Arg	Pro	Pro
		275				280						285			
Glu	Lys	Pro	Pro	Arg	Pro	Pro	Arg	Pro	Leu	His	Leu	Ser	Asp	Arg	Ser
		290				295					300				
Phe	Arg	Arg	Lys	Lys	Asp	Ser	Val	Glu	Ser	His	Pro	Thr	Trp	Val	Asp
305					310					315				320	
Asp	Thr	Arg	Ile	Asp	Ala	Asp	Ala	Ile	Val	Glu	Lys	Ile	Val	Gln	Ser

2837

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aagcaggggt tggtcagggg aggacagcgg ccg
1293

<210> 3686
<211> 111
<212> PRT
<213> Homo sapiens

<400> 3686
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Ala Pro Ser Pro Leu Ser Ser Gly Ala His Cys Arg Leu Leu Phe
20 25 30
Pro Val Cys Cys Glu Thr Asp His Arg Pro Ala Gln Arg Ser Pro Arg
35 40 45
Arg Val Pro Cys Leu Cys Pro Pro Arg Arg Arg His Pro Pro Arg Ser
50 55 60
Phe Thr Ser Cys Thr Phe Ser Gly Ser Arg Ser His Ile His Pro Thr
65 70 75 80
Trp Arg Ser Pro His Asp Val Pro Gly Ser Val Leu Ala Pro Ala Ala
85 90 95
Ala Leu Gly Asn Arg Ile Gly Lys Arg Ser Pro Arg Val Asp Ala
100 105 110

<210> 3687
<211> 566
<212> DNA
<213> Homo sapiens

<400> 3687
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120
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180
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240
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360
cccatggtgc ccacatcccg ggtgcccggt actctggcac cagtggctac ctcccttagt
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<210> 3688

<211> 57
 <212> PRT
 <213> Homo sapiens

<400> 3688
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 Gly Phe Ala Met Val Ala Met Val Glu Val Gln Leu Glu Ser Asp His
 20 25 30
 Glu Tyr Pro Pro Gly Leu Leu Val Ala Val His Leu Phe Ala Leu Met
 35 40 45
 Xaa Leu His Val Ser Ala Ala Pro His
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<210> 3689
 <211> 1562
 <212> DNA
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<400> 3689
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<210> 3690
<211> 504
<212> PRT
<213> Homo sapiens

<400> 3690
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Arg Ser Gly Arg Ala Thr Asn His Asp Ser Cys Asp Ser Cys Lys Glu
50 55 60
Gly Gly Asp Leu Leu Cys Cys Asp His Cys Pro Ala Ala Phe His Leu
65 70 75 80
Gln Cys Cys Asn Pro Pro Leu Ser Glu Glu Met Leu Pro Pro Gly Glu
85 90 95
Trp Met Cys His Arg Cys Thr Val Arg Arg Lys Lys Arg Glu Gln Lys
100 105 110
Lys Glu Leu Gly His Val Asn Gly Leu Val Asp Lys Ser Gly Lys Arg
115 120 125
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130 135 140
Lys Thr Glu Leu Lys Ala Ile Ala His Ala Arg Ile Leu Glu Arg Arg
145 150 155 160
Ala Ser Arg Pro Gly Thr Pro Thr Ser Ser Ala Ser Thr Glu Thr Pro
165 170 175
Thr Ser Glu Gln Asn Asp Val Asp Glu Asp Ile Ile Asp Val Asp Glu
180 185 190
Glu Pro Val Ala Ala Glu Pro Asp Tyr Val Gln Pro Gln Leu Arg Arg
195 200 205
Pro Phe Glu Leu Leu Ile Ala Ala Met Glu Arg Asn Pro Thr Gln

210 215 220
 Phe Gln Leu Pro Asn Glu Leu Thr Cys Thr Thr Ala Leu Pro Gly Ser
 225 230 235 240
 Ser Lys Arg Arg Arg Lys Glu Glu Thr Thr Gly Lys Asn Val Lys Lys
 245 250 255
 Thr Gln His Glu Leu Asp His Asn Gly Leu Val Pro Leu Pro Val Lys
 260 265 270
 Val Cys Phe Thr Cys Asn Arg Ser Cys Arg Val Ala Pro Leu Ile Gln
 275 280 285
 Cys Asp Tyr Cys Pro Leu Leu Phe His Met Asp Cys Leu Glu Pro Pro
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 305 310 315 320
 His Val Val Leu Asn Gln Lys Asn Met Thr Leu Ser Asn Arg Cys Gln
 325 330 335
 Val Phe Asp Arg Phe Gln Asp Thr Val Ser Gln His Val Val Lys Val
 340 345 350
 Asp Phe Leu Asn Arg Ile His Lys Lys His Pro Pro Asn Arg Arg Val
 355 360 365
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 370 375 380
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 385 390 395 400
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 405 410 415
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 420 425 430
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 435 440 445
 Ala Lys Gln Met Pro Ser His Trp Asp Ser Glu Gln Thr Glu Lys Ala
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<210> 3691

<211> 418

<212> DNA

<213> Homo sapiens

<400> 3691

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<210> 3692

<211> 94

<212> PRT

<213> Homo sapiens

<400> 3692

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			20					25					30		
Ala	Arg	Gln	Ser	Trp	Gly	Gln	Cys	Gln	Pro	Phe	Tyr	Val	Leu	Arg	Gln
		35					40					45			
Arg	Ile	Ala	Arg	Ile	Arg	Cys	Gln	Leu	Lys	Ala	Val	Cys	Gln	Pro	Arg
	50					55					60				
Cys	Lys	His	Gly	Glu	Cys	Ile	Gly	Pro	Asn	Lys	Cys	Lys	Cys	His	Pro
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<210> 3693

<211> 2641

<212> DNA

<213> Homo sapiens

<400> 3693

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<210> 3694

<211> 390

<212> PRT

<213> Homo sapiens

<400> 3694

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			20					25				30		Gly
Cys	Cys	Ala	Pro	Leu	Gly	Val	Arg	Ala	Ser	Gly	Arg	Ala	Val	Pro
		35					40				45			Arg
Ala	Val	Phe	Ala	Gly	Met	Lys	Arg	Pro	Cys	Glu	Glu	Thr	Thr	Ser
	50					55				60				Glu
Ser	Asp	Met	Asp	Glu	Thr	Ile	Asp	Val	Gly	Ser	Glu	Asn	Asn	Tyr
65				70					75					80
Gly	Gln	Ser	Thr	Ser	Ser	Val	Ile	Arg	Leu	Asn	Ser	Pro	Thr	Thr
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			100					105					110	Arg
Arg	Arg	Asp	Arg	Ile	Asn	Asn	Ser	Leu	Ser	Glu	Leu	Arg	Arg	Leu
		115					120				125			Val
Pro	Thr	Ala	Phe	Glu	Lys	Gln	Gly	Ser	Ala	Lys	Leu	Glu	Lys	Ala
	130					135					140			Glu
Ile	Leu	Gln	Met	Thr	Val	Asp	His	Leu	Lys	Met	Leu	Gln	Ala	Thr
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		180					185					190		Ser
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His	Leu	Ser	Thr	Cys	Ala	Thr	Gln	Arg	Glu	Ala	Ala	Ala	Met	Thr
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225				230					235				240	Arg
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			245					250					255	Pro
Cys	Leu	Arg	Val	Asn	Pro	Leu	Ser	Pro	Leu	His	Asn	Phe	Arg	Ser
		260					265					270		Ala
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Ala Thr Ala Ile Ser Pro Pro Leu Ser Val Ser Ala Thr Ser Ser Pro		
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<210> 3695

<211> 1615

<212> DNA

<213> Homo sapiens

<400> 3695

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<210> 3696

<211> 146

<212> PRT

<213> Homo sapiens

<400> 3696

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			20					25					30		
Tyr	Phe	Ala	Glu	Tyr	Trp	Tyr	Gln	Ala	Gln	Cys	Cys	Gln	Tyr	Asp	Tyr
		35					40					45			
Cys	Asn	Ser	Trp	Ser	Ser	Pro	Gln	Leu	Gln	Ser	Ser	Leu	Pro	Glu	Pro
	50					55					60				
His	Asp	Arg	Pro	Leu	Ala	Leu	Pro	Leu	Ser	Asp	Ser	Gln	Ile	Gln	Trp
65				70					75					80	
Phe	Tyr	Gln	Ala	Leu	Asn	Leu	Ser	Leu	Pro	Leu	Pro	Asn	Phe	His	Ala
			85					90					95		
Gly	Thr	Glu	Pro	Asp	Gly	Leu	Asp	Pro	Met	Val	Thr	Leu	Ser	Leu	Asn
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Leu	Gly	Leu	Ser	Phe	Ala	Glu	Leu	Arg	Arg	Met	Tyr	Leu	Phe	Leu	Asn
		115					120					125			
Ser	Ser	Gly	Leu	Leu	Val	Leu	Pro	Gln	Ala	Gly	Leu	Leu	Thr	Pro	His
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<210> 3697

<211> 550

<212> DNA

<213> Homo sapiens

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 35 40 45
 Lys His Gly Glu Cys Ile Gly Pro Asn Lys Cys Lys Cys His Pro Gly
 50 55 60
 Tyr Ala Gly Lys Thr Cys Asn Gln Asp Leu Asn Glu Cys Gly Leu Lys
 65 70 75 80
 Pro Arg Pro Cys Lys His Arg Cys Met Asn Thr Tyr Gly Ser Tyr Lys
 85 90 95
 Cys Tyr Cys Leu Asn Gly Tyr Met Leu Met Pro Asp Gly Ser Cys Ser
 100 105 110
 Ser Ala Leu Thr Cys Ser Met Ala Asn Cys Gln Tyr Gly Cys Asp Val
 115 120 125
 Val Lys Gly Gln Ile Arg Cys Gln Cys Pro Ser Pro Gly Leu Gln Leu
 130 135 140
 Ala Pro Asp Gly Arg Thr Cys Val Asp Val Asp Glu Cys Ala Thr Gly
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 Arg Ala Ser Cys Pro Lys Phe Arg Gln Cys Val Asn Thr Phe Gly Ser
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 Tyr Ile Cys Lys Cys His Lys
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<210> 3699
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 <212> DNA
 <213> Homo sapiens

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 50 55 60
 Asp Ser Ser Gly Leu Arg Leu Trp Lys Arg Arg Trp Phe Val Leu Ser
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 Gly His Cys Leu Phe Tyr Tyr Lys Asp Ser Arg Glu Glu Ser Val Leu
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<400> 3701

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<210> 3702

<211> 236

<212> PRT

<213> Homo sapiens

<400> 3702

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<210> 3703

<211> 3294

<212> DNA

<213> Homo sapiens

<400> 3703

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<211> 619

<212> PRT

<213> Homo sapiens

<400> 3704

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<212> DNA

<213> Homo sapiens

<400> 3705

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<210> 3706
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 <212> PRT
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<400> 3706
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<210> 3707
 <211> 585
 <212> DNA
 <213> Homo sapiens

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<210> 3708

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<212> PRT

<213> Homo sapiens

<400> 3708

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<210> 3709

<211> 3768

<212> DNA

<213> Homo sapiens

<400> 3709

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<212> PRT

<213> Homo sapiens

<400> 3710

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		20					25					30			
Cys	Asp	Val	Ile	Leu	Val	Ala	Gly	Asp	Arg	Arg	Ile	Pro	Ala	His	Arg
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Leu	Val	Leu	Ser	Ser	Val	Ser	Asp	Tyr	Phe	Ala	Ala	Met	Phe	Thr	Asn
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<210> 3711

<211> 1366

<212> DNA

<213> Homo sapiens

<400> 3711

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<211> 368

<212> PRT

<213> Homo sapiens

<400> 3712

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Leu	Gly	Arg	Gly	Phe	Asn	Thr	Gly	Val	Ile	Leu	Leu	Arg	Leu	Asp	Arg	35	40	45	
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Asn	Ala	Val	Ile	Lys	Glu	His	Pro	Gly	Leu	Val	Gln	Arg	Leu	Pro	Cys	85	90	95	
Val	Trp	Asn	Val	Gln	Leu	Ser	Asp	His	Thr	Leu	Ala	Glu	Arg	Cys	Tyr	100	105	110	
Ser	Glu	Ala	Ser	Asp	Leu	Lys	Val	Ile	His	Trp	Asn	Ser	Pro	Lys	Lys	115	120	125	
Leu	Arg	Val	Lys	Asn	Lys	His	Val	Glu	Phe	Phe	Arg	Asn	Phe	Tyr	Leu	130	135	140	
Thr	Phe	Leu	Glu	Tyr	Asp	Gly	Asn	Leu	Leu	Arg	Arg	Glu	Leu	Phe	Val	145	150	155	160
Cys	Pro	Ser	Gln	Pro	Pro	Gly	Ala	Glu	Gln	Leu	Gln	Gln	Ala	Leu		165	170	175	
Ala	Gln	Leu	Asp	Glu	Glu	Asp	Pro	Cys	Phe	Glu	Phe	Arg	Gln	Gln	Gln	180	185	190	
Leu	Thr	Val	His	Arg	Val	His	Val	Thr	Phe	Leu	Pro	His	Glu	Pro	Pro	195	200	205	
Pro	Pro	Arg	Pro	His	Asp	Val	Thr	Leu	Val	Ala	Gln	Leu	Ser	Met	Asp	210	215	220	
Arg	Leu	Gln	Met	Leu	Glu	Ala	Leu	Cys	Arg	His	Trp	Pro	Gly	Pro	Met				

225		230		235		240									
Ser	Leu	Ala	Leu	Tyr	Leu	Thr	Asp	Ala	Glu	Ala	Gln	Gln	Phe	Leu	His
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Phe	Val	Glu	Ala	Ser	Pro	Val	Leu	Ala	Ala	Arg	Gln	Asp	Val	Ala	Tyr
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Pro	Ala	Phe	Glu	Thr	Leu	Arg	Tyr	Arg	Phe	Ser	Phe	Pro	His	Ser	Lys
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<211> 1719

<212> DNA

<213> Homo sapiens

<400> 3713

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<211> 488

<212> PRT

<213> Homo sapiens

<400> 3714

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			20				25					30		
Val	Asn	Glu	Gln	His	Ser	Gly	Ser	Asp	Thr	Gly	Ser	Val	Glu	Arg
			35				40					45		
Ser	Glu	Asn	Glu	Thr	Ser	Asp	Arg	Glu	Asp	Gly	Pro	Pro	Lys	Gly
			50				55				60			
His	Val	Thr	Asp	Ser	Glu	Asn	Asp	Glu	Pro	Leu	Asn	Leu	Asn	Ala
						70				75				80
Asp	Ser	Glu	Ser	Glu	Glu	Leu	His	Arg	Gln	Lys	Asp	Ser	Asp	Ser
						85				90				95
Ser	Glu	Glu	Arg	Ala	Glu	Pro	Pro	Ala	Ser	Asp	Ser	Glu	Asn	Glu
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Val	Asn	Gln	His	Gly	Ser	Asp	Ser	Glu	Ser	Glu	Glu	Thr	Arg	Lys
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Pro	Gly	Ser	Asp	Ser	Glu	Asn	Glu	Glu	Leu	Leu	Asn	Gly	His	Ala
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Asp	Ser	Glu	Asn	Glu	Asp	Val	Gly	Lys	His	Pro	Ala	Ser	Asp	Ser
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Ser Asp Ser Glu Ser Glu Glu Leu Pro Lys Pro Gln Val Ser Asp Ser
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Glu Ser Glu Glu Pro Pro Arg His Gln Ala Ser Asp Ser Glu Asn Glu
225          230          235          240
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Arg His Gln Ala Ser Asp Ser Glu Asn Glu Glu Leu Pro Lys Pro Arg
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Ile Ser Asp Ser Glu Ser Glu Asp Pro Pro Arg Asn Gln Ala Ser Asp
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          435          440          445
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<211> 288

<212> DNA

<213> Homo sapiens

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 Lys Ala His Lys Arg Tyr Leu Leu Met Ser Ile Asp Gln Arg Lys Lys
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<211> 374

<212> PRT

<213> Homo sapiens

<400> 3718

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			20					25					30		
Cys	Leu	Glu	Arg	Glu	Glu	Tyr	Leu	Leu	Phe	Asp	Ser	Asp	Lys	Leu	Ser
			35				40					45			
His	Leu	Ile	Leu	Asp	Ser	Ser	Ser	Lys	Ile	Cys	Asp	Leu	Asn	Ala	Asn
			50				55				60				
Thr	Glu	Ser	Glu	Val	Pro	Gly	Gly	Gln	Ser	Val	Gly	Val	Gln	Gly	Glu
65					70				75					80	
Ala	Ala	Cys	Val	Ser	Ile	Pro	His	Leu	Asp	Leu	Lys	Asn	Val	Ser	Asp
			85					90					95		
Gly	Asp	Lys	Trp	Glu	Glu	Pro	Phe	Pro	Ala	Phe	Lys	Ser	Trp	Gln	Glu
			100					105					110		
Asp	Ser	Glu	Ser	Gly	Glu	Ala	Gln	Leu	Ser	Pro	Gln	Ala	Gly	Arg	Met
			115				120					125			
Asn	His	His	Pro	Leu	Glu	Glu	Asp	Cys	Pro	Pro	Val	Leu	Ser	His	Arg

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 Leu Val Lys Lys Leu Gln Lys Lys Ile Arg Gln Phe Glu Glu Gln Phe
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 Glu Arg Glu Arg Asn Ser Lys Pro Ser Tyr Ser Asp Ile Ala Ala Asn
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 Pro Lys Val Leu Lys Trp Met Thr Glu Leu Thr Lys Leu Arg Lys Gln
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 Ile Lys Asp Ala Lys His Lys Asn Ser Asp Gly Glu Phe Val Pro Gln
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 Thr Arg Pro Arg Ser Asn Thr Leu Pro Lys Ser Phe Gly Ser Ser Leu
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 Asp His Glu Asp Glu Glu Asn Glu Asp Glu Pro Lys Val Ile Gln Lys
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<210> 3719

<211> 422

<212> DNA

<213> Homo sapiens

<400> 3719

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<211> 1216

<212> PRT

<213> Homo sapiens

<400> 3722

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Gln	Lys	Ile	Ser	Lys	Gln	Gln	Leu	Gln	Thr	Val	Lys	Asp	Arg	Phe	Gln
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Ala	Arg	Met	Val	Gln	Ser	Gly	Gly	Cys	Ser	Ala	Asn	Asp	Ser	Arg	Glu
			100					105					110		
Val	Phe	Lys	Lys	His	Ile	Glu	Lys	Arg	Val	Arg	Ser	Leu	Pro	Glu	Ile
			115				120					125			
Asp	Gly	Leu	Ser	Lys	Glu	Thr	Val	Leu	Ser	Ser	Trp	Met	Ala	Lys	Phe
			130				135					140			
Asp	Ala	Ile	Tyr	Arg	Gly	Glu	Glu	Asp	Pro	Arg	Lys	Gln	Gln	Ala	Arg
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Met	Thr	Ala	Ser	Ala	Ala	Ser	Glu	Leu	Ile	Leu	Ser	Lys	Glu	Gln	Leu

2871

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Leu	Leu	Glu	Arg	Ala	Glu	Asn	Gly	Ala	Met	Ile	Asp	Pro	Thr	Leu	Leu
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His	Tyr	Ser	Phe	Ala	Phe	Cys	Ala	Ser	His	Val	His	Gly	Asn	Arg	Pro
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Asp	Gly	Ile	Gly	Thr	Val	Thr	Val	Glu	Glu	Lys	Glu	Arg	Phe	Glu	Glu
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Arg	Tyr	Cys	Phe	Pro	Phe	Gly	Arg	Pro	Glu	Gly	Ala	Leu	Lys	Ala	Thr
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Lys	Leu	Glu	Asp	Thr	Ile	Arg	Leu	Ala	Glu	Leu	Val	Ile	Glu	Val	Leu
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Gln	Gln	Asn	Glu	Glu	His	His	Ala	Glu	Pro	His	Val	Asp	Lys	Gly	Glu
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Cys	Thr	Met	Phe	Asn	Val	Met	Val	Asp	Ala	Lys	Ala	Gln	Ser	Thr	Lys
995					1000					1005					
Leu	Cys	Ser	Met	Glu	Met	Gly	Gln	Glu	Phe	Ala	Lys	Met	Trp	His	Gln
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 1075 1080 1085
 Gly Met Asp Val Ala Asp Ala Tyr Val Thr Phe Val Arg His Ser Gln
 1090 1095 1100
 Asp Val Leu Arg Asp Lys Val Asn Glu Glu Met Tyr Ile Glu Arg Leu
 1105 1110 1115 1120
 Phe Asp Gln Trp Tyr Asn Ser Ser Met Asn Val Ile Cys Thr Trp Leu
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 1170 1175 1180
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<211> 830

<212> DNA

<213> Homo sapiens

<400> 3723

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<400> 3724
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 Asp Phe Gly Leu Ala Arg Arg Tyr Asn Pro Asn Glu Lys Leu Lys Val
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 Asn Phe Gly Thr Pro Glu Phe Leu Ser Pro Glu Val Val Asn Tyr Asp
 50 55 60
 Gln Ile Ser Asp Lys Thr Asp Met Trp Ser Met Gly Val Ile Thr Tyr
 65 70 75 80
 Met Leu Leu Ser Gly Leu Ser Pro Phe Leu Gly Asp Asp Asp Thr Glu
 85 90 95
 Thr Leu Asn Asn Val Leu Ser Gly Asn Trp Tyr Phe Asp Glu Glu Thr
 100 105 110
 Phe Glu Ala Val Ser Asp Glu Ala Lys Asp Phe Val Ser Asn Leu Ile
 115 120 125
 Val Lys Asp Gln Arg Ala Arg Met Asn Ala Ala Gln Cys Leu Ala His
 130 135 140
 Pro Trp Leu Asn Asn Leu Ala Glu Lys Ala Lys Arg Cys Asn Arg Arg
 145 150 155 160
 Leu Lys Ser Gln Ile Leu Leu Lys Lys Tyr Leu Met Lys Arg Arg Trp
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 <213> Homo sapiens

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<210> 3726

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<212> PRT

<213> Homo sapiens

<400> 3726

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		20						25					30		
Gly	Arg	Glu	Leu	Asp	Phe	Arg	Ser	Asp	His	Leu	His	Phe	Cys	Phe	Gln
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Ala	Phe	Lys	Ile	Val	Pro	Tyr	Asn	Thr	Glu	Thr	Leu	Asp	Lys	Leu	Leu
	50					55					60				
Thr	Glu	Ser	Leu	Lys	Asn	Asn	Ile	Pro	Ala	Ser	Gly	Leu	His	Leu	Phe
65				70					75					80	
Gly	Ile	Asn	Gln	Leu	Glu	Glu	Glu	Asp	Met	Met	Thr	Asn	Gln	Arg	Asp
		85						90					95		
Glu	Glu	Leu	Pro	Thr	Leu	Leu	His	Phe	Ala	Ala	Lys	Tyr	Gly	Leu	Lys
		100					105						110		
Asn	Leu	Thr	Ala	Leu	Leu	Leu	Thr	Cys	Pro	Gly	Ala	Leu	Gln	Ala	Tyr

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      115      120      125
Ser Val Ala Asn Lys His Gly His Tyr Pro Asn Thr Ile Ala Glu Lys
      130      135      140
His Gly Phe Arg Asp Leu Arg Gln Phe Ile Asp Glu Tyr Val Glu Thr
      145      150      155      160
Val Asp Met Leu Lys Ser His Ile Lys Glu Glu Leu Met His Gly Glu
      165      170      175
Glu Ala Asp Ala Val Tyr Glu Ser Met Ala His Leu Ser Thr Asp Leu
      180      185      190
Leu Met Lys Cys Ser Leu Asn Pro Gly Cys Asp Glu Asp Leu Tyr Glu
      195      200      205
Ser Met Ala Ala Phe Val Pro Ala Ala Thr Glu Asp Leu Tyr Val Glu
      210      215      220
Met Leu Gln Ala Ser Thr Ser Asn Pro Ile Pro Gly Asp Gly Phe Ser
      225      230      235      240
Arg Ala Thr Lys Asp Ser Met Ile Arg Lys Phe Leu Glu Gly Asn Ser
      245      250      255
Met Gly Met Thr Asn Leu Glu Arg Asp Gln Cys His Leu Gly Gln Glu
      260      265      270
Glu Asp Val Tyr His Thr Val Asp Asp Asp Glu Ala Phe Ser Val Asp
      275      280      285
Leu Ala Ser Arg Pro Pro Val Pro Val Pro Arg Pro Glu Thr Thr Ala
      290      295      300
Pro Gly Ala His Gln Leu Pro Asp Asn Glu Pro Tyr Ile Phe Lys Gly
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Lys Tyr Gly Arg Glu
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<210> 3727

<211> 630

<212> DNA

<213> Homo sapiens

<400> 3727

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120
ctcgaccccg ctgagaaaca agaaacaggc tgctctcctt tgggtctgga gtccttgcga
180
gtttcagata gccggcttga ggcattccagc agccagtcct ttggtcttgg accacaccga
240
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360
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420
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480
atggacgcag tatttctctg caattcagac ccagaaactc cagtgtgaa cctcctgccc
540
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<210> 3728
<211> 210
<212> PRT
<213> Homo sapiens

<400> 3728
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20 25 30
Val Thr Pro Thr Pro Ala Gly Thr Leu Asp Pro Ala Glu Lys Gln Glu
35 40 45
Thr Gly Cys Pro Pro Leu Gly Leu Glu Ser Leu Arg Val Ser Asp Ser
50 55 60
Arg Leu Glu Ala Ser Ser Ser Gln Ser Phe Gly Leu Gly Pro His Arg
65 70 75 80
Gly Arg Leu Asn Ile Gln Ser Gly Leu Glu Asp Gly Asp Leu Tyr Asp
85 90 95
Gly Ala Trp Cys Ala Glu Glu Gln Asp Ala Asp Pro Trp Phe Gln Val
100 105 110
Asp Ala Gly His Pro Thr Arg Phe Ser Gly Val Ile Thr Gln Gly Arg
115 120 125
Asn Ser Val Trp Arg Tyr Asp Trp Val Thr Ser Tyr Lys Val Gln Phe
130 135 140
Ser Asn Asp Ser Arg Thr Trp Trp Gly Ser Arg Asn His Ser Ser Gly
145 150 155 160
Met Asp Ala Val Phe Pro Ala Asn Ser Asp Pro Glu Thr Pro Val Leu
165 170 175
Asn Leu Leu Pro Glu Pro Gln Val Ala Arg Phe Ile Arg Leu Leu Pro
180 185 190
Gln Thr Trp Leu Gln Gly Gly Ala Pro Cys Leu Arg Ala Glu Ile Leu
195 200 205
Ala Cys
210

<210> 3729
<211> 1552
<212> DNA
<213> Homo sapiens

<400> 3729
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180
tggttagagt cctcagaagc atgtgtcttc cccagctctg cagccacata ctatccgttt
240
gttcaggaac caccagtgc agagcagaaa atatatactg aagacatggc ctttggagct
300

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 360
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 420
 aaccaacca gttgttacgg aggttttcaa acagtgaagc atcgaaatga gaacacatgc
 480
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 540
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 600
 tcagctagag gttcacatca tttgtccatt tacgctgaga atagtttgaa atcagatggt
 660
 taccataagc gaacagacag gaaatccaga atcattgcaa aaaatgtatc tacctccaaa
 720
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 780
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 840
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 960
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 1080
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 1200
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 1260
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 1320
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<210> 3730

<211> 422

<212> PRT

<213> Homo sapiens

<400> 3730

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 20 25 30
 Gln Asn Val Tyr Ser Val Pro Gly Ser Gln Tyr Leu Tyr Asn Gln Pro

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      35      40      45
Ser Cys Tyr Arg Gly Phe Gln Thr Val Lys His Arg Asn Glu Asn Thr
  50      55      60
Cys Pro Leu Pro Gln Glu Met Lys Ala Leu Phe Lys Lys Lys Thr Tyr
  65      70      75      80
Asp Glu Lys Lys Thr Tyr Asp Gln Gln Lys Phe Asp Ser Glu Arg Ala
      85      90      95
Asp Gly Thr Ile Ser Ser Glu Ile Lys Ser Ala Arg Gly Ser His His
      100      105      110
Leu Ser Ile Tyr Ala Glu Asn Ser Leu Lys Ser Asp Gly Tyr His Lys
      115      120      125
Arg Thr Asp Arg Lys Ser Arg Ile Ile Ala Lys Asn Val Ser Thr Ser
      130      135      140
Lys Pro Glu Phe Glu Phe Thr Thr Leu Asp Phe Pro Glu Leu Gln Gly
  145      150      155      160
Ala Glu Asn Asn Met Ser Glu Ile Gln Lys Gln Pro Lys Trp Gly Pro
      165      170      175
Val His Ser Val Ser Thr Asp Ile Ser Leu Leu Arg Glu Val Val Lys
      180      185      190
Pro Ala Ala Val Leu Ser Lys Gly Glu Ile Val Val Lys Asn Asn Pro
      195      200      205
Asn Glu Ser Val Thr Ala Asn Ala Ala Thr Asn Ser Pro Ser Cys Thr
      210      215      220
Arg Glu Leu Ser Trp Thr Pro Met Gly Tyr Val Val Arg Gln Thr Leu
  225      230      235      240
Ser Thr Glu Leu Ser Ala Ala Pro Lys Asn Val Thr Ser Met Ile Asn
      245      250      255
Leu Lys Thr Ile Ala Ser Ser Ala Asp Pro Lys Asn Val Ser Ile Pro
      260      265      270
Ser Ser Glu Ala Leu Ser Ser Asp Pro Ser Tyr Asn Lys Glu Lys His
      275      280      285
Ile Ile His Pro Thr Gln Lys Ser Lys Ala Ser Gln Gly Ser Asp Leu
      290      295      300
Glu Gln Asn Glu Ala Ser Arg Lys Asn Lys Lys Lys Lys Glu Lys Ser
  305      310      315      320
Thr Ser Lys Tyr Glu Val Leu Thr Val Gln Glu Pro Pro Arg Ile Glu
      325      330      335
Asp Ala Glu Glu Phe Pro Asn Leu Ala Val Ala Ser Glu Arg Arg Asp
      340      345      350
Arg Ile Glu Thr Pro Lys Phe Gln Ser Lys Gln Gln Pro Gln Asp Asn
      355      360      365
Phe Lys Asn Asn Val Lys Lys Ser Gln Leu Pro Val Gln Leu Asp Leu
      370      375      380
Gly Gly Met Leu Thr Ala Leu Glu Lys Lys Gln His Ser Gln His Ala
  385      390      395      400
Lys Gln Ser Ser Lys Pro Val Val Val Ser Val Gly Ala Val Pro Val
      405      410      415
Leu Ser Lys Glu Cys Ala
      420

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<210> 3731

<211> 1704

<212> DNA

<213> Homo sapiens

<400> 3731
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120
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180
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240
caagcaaata actgcttcag tacaggcttg tctcggcggg tcctgttgac caacgtgggtg
300
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360
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420
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480
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540
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660
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720
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1200
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1320
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1440
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1560

attcaagggc ccggcggtcaa aggaaattgg ttttgacttt ttgtaattcta ggagcgacag
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 1680
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 1704

<210> 3732
 <211> 281
 <212> PRT
 <213> Homo sapiens

<400> 3732
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 Glu Gly Ile Thr Asp Ala Ser Ser Cys Ala Val Leu Leu Pro Ala Ser
 35 40 45
 Leu Phe Val Asn Ser His Pro Gly Ile Asp Arg Pro Gly Met Leu Cys
 50 55 60
 Ser Phe Arg Ile Pro Gly Ala Trp Ser Cys Ala Trp Ser Leu Asn Ile
 65 70 75 80
 Gln Ala Asn Asn Cys Phe Ser Thr Gly Leu Ser Arg Arg Val Leu Leu
 85 90 95
 Thr Asn Val Val Thr Gly His Arg Gln Ser Phe Gly Thr Asn Ser Asp
 100 105 110
 Val Leu Ala Gln Gln Phe Ala Leu Met Ala Pro Leu Leu Phe Asn Gly
 115 120 125
 Cys Arg Ser Gly Glu Ile Phe Ala Ile Asp Leu Arg Cys Gly Asn Gln
 130 135 140
 Gly Lys Gly Trp Lys Ala Thr Arg Leu Phe His Asp Ser Ala Val Thr
 145 150 155 160
 Ser Val Arg Ile Leu Gln Asp Glu Gln Tyr Leu Met Ala Ser Asp Met
 165 170 175
 Ala Gly Lys Ile Lys Leu Trp Asp Leu Arg Thr Thr Lys Cys Val Arg
 180 185 190
 Gln Tyr Glu Gly His Val Asn Glu Tyr Ala Tyr Leu Pro Leu His Val
 195 200 205
 His Glu Glu Glu Gly Ile Leu Val Ala Val Gly Gln Asp Cys Tyr Thr
 210 215 220
 Arg Ile Trp Ser Leu His Asp Ala Arg Leu Leu Arg Thr Ile Pro Ser
 225 230 235 240
 Pro Tyr Pro Ala Ser Lys Ala Asp Ile Pro Ser Val Ala Phe Ser Ser
 245 250 255
 Arg Leu Gly Gly Ser Arg Gly Ala Pro Gly Leu Leu Met Ala Val Gly
 260 265 270
 Gln Asp Leu Tyr Cys Tyr Ser Tyr Ser
 275 280

<210> 3733
 <211> 515
 <212> DNA
 <213> Homo sapiens

<400> 3733

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 120
 tcctcagtgc gggagaggga gacgccgggg gcangtccat gcctcccgcg gcgtgggtgg
 180
 tgcgtcccag gtgacgtcag aagcagcccg ccctgcctg gatggtgcgc cctgagtgac
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 300
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 360
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 420
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 515

<210> 3734

<211> 171

<212> PRT

<213> Homo sapiens

<400> 3734

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Val	Ser	Gly	Ser	Arg	Tyr	Arg	Arg	Gly	Arg	Arg	Arg	Gly	Arg	Leu	Lys
			20					25					30		
Gly	Lys	Asp	Pro	Gly	Ser	Ala	Pro	Ser	Ser	Val	Arg	Glu	Arg	Glu	Thr
		35					40				45				
Pro	Gly	Ala	Xaa	Pro	Cys	Leu	Pro	Arg	Arg	Gly	Trp	Cys	Val	Pro	Gly
	50					55					60				
Asp	Val	Arg	Ser	Ser	Pro	Pro	Leu	Pro	Gly	Trp	Cys	Ala	Leu	Ser	Asp
65					70				75					80	
Val	Arg	Ser	Arg	Gly	Arg	Ser	Cys	Pro	Ser	Ala	Pro	Lys	Ala	Ala	Gly
			85					90					95		
Gly	Leu	Arg	Ala	Trp	Gly	Arg	Gly	Ser	Gly	Ala	Ala	Arg	Ala	Pro	Ala
			100				105						110		
Pro	Ala	Pro	Ser	Pro	Ser	Ser	Gly	Xaa	Ser	Pro	Ser	Ser	Arg	Thr	Pro
		115					120					125			
Arg	Asp	Trp	Ser	Ala	Ser	Arg	Cys	Trp	Thr	Trp	Ser	Gly	Ala	Ala	Thr
	130					135					140				
Ala	Pro	Thr	Pro	Phe	Ser	Pro	Ala	Gln	Gln	Pro	Pro	Ser	Ser	His	Asp
145					150					155					160
Gly	Leu	Ser	Leu	Asp	Pro	Ser	Gln	Leu	Glu	Pro					
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<210> 3735

<211> 2512

<212> DNA

<213> Homo sapiens

<400> 3735
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120
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180
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240
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300
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360
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480
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600
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660
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720
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780
tgctctatgg gtctttggta tgcattgtcca aggacaactt cgagacattt ctttttgcca
840
ccgtatctaa cagggagcag gaagatctct gccgaggaat tgtccagctc tgcttcaatg
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1260
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1440
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1560

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 2280
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<210> 3736

<211> 155

<212> PRT

<213> Homo sapiens

<400> 3736

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Ser	Gly	Arg	Pro	Ser	Ala	Thr	Gln	Lys	Lys	Lys	Met	Lys	Lys	Arg	Val
			20					25					30		
Lys	Asp	Glu	Leu	Arg	Lys	Leu	Asn	Thr	Met	Pro	Ala	Ala	Glu	Ala	Asn
			35				40					45			
Glu	Ile	Glu	Asp	Val	Trp	His	Leu	Asp	Leu	Ser	Ser	Arg	Trp	Gln	Leu
			50			55				60					
Tyr	Arg	Leu	Trp	Leu	Gln	Leu	Tyr	Gln	Ala	Asp	Thr	Pro	Pro	Gly	Lys
65				70					75					80	
Ile	Leu	Ser	Tyr	Glu	Arg	Gln	Tyr	Arg	Thr	Ser	Ala	Glu	Arg	Met	Ala
			85					90						95	
Glu	Leu	Arg	Leu	Gln	Glu	Asp	Leu	His	Ile	Leu	Lys	Asp	Ala	Gln	Val
			100					105						110	
Val	Gly	Met	Thr	Thr	Thr	Gly	Ala	Ala	Lys	Tyr	Arg	Gln	Ile	Leu	Gln

	115		120		125										
Lys	Val	Glu	Pro	Arg	Ile	Val	Ile	Val	Glu	Glu	Ala	Ala	Glu	Val	Leu
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Glu	Ala	His	Thr	Ile	Ala	Thr	Leu	Ser	Lys	Ala					
145					150					155					

<210> 3737

<211> 1046

<212> DNA

<213> Homo sapiens

<400> 3737

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120
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180
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420
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540
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gccaacaatc tatcagcgtg gccactgag gcctggccc cctgcgtgc cctgcagtac
720
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780
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900
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1046

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<210> 3738

<211> 348

<212> PRT

<213> Homo sapiens

<400> 3738

Xaa Ala Val Ala Ala Gly Trp Gln Val Ala Ala Pro Cys Pro Gly Ala
 1 5 10 15
 Cys Val Cys Tyr Asn Glu Pro Lys Val Thr Thr Ser Cys Pro Gln Gln
 20 25 30
 Gly Leu Gln Ala Val Pro Val Gly Ile Pro Ala Ala Ser Gln Arg Ile
 35 40 45
 Phe Leu His Gly Asn Arg Ile Ser His Val Pro Ala Ala Ser Phe Arg
 50 55 60
 Ala Cys Arg Asn Leu Thr Ile Leu Trp Leu His Ser Asn Val Leu Ala
 65 70 75 80
 Arg Ile Asp Ala Ala Ala Phe Thr Gly Leu Ala Leu Leu Gly Ala Leu
 85 90 95
 Asp Leu Ser Asp Asn Ala Gln Leu Arg Ser Val Asp Pro Ala Thr Phe
 100 105 110
 His Gly Leu Gly Arg Leu His Thr Leu His Leu Asp Arg Cys Gly Leu
 115 120 125
 Gln Glu Leu Gly Pro Gly Leu Phe Arg Gly Leu Ala Ala Leu Gln Tyr
 130 135 140
 Leu Tyr Leu Gln Asp Asn Ala Leu Gln Ala Leu Pro Asp Asp Thr Phe
 145 150 155 160
 Arg Asp Leu Gly Asn Leu Thr His Leu Phe Leu His Gly Asn Arg Ile
 165 170 175
 Ser Ser Val Pro Glu Arg Ala Phe Arg Gly Leu His Ser Leu Asp Arg
 180 185 190
 Leu Leu Leu His Gln Asn Arg Val Ala His Val His Pro His Ala Phe
 195 200 205
 Arg Asp Leu Gly Arg Leu Met Thr Leu Tyr Leu Phe Ala Asn Asn Leu
 210 215 220
 Ser Ala Leu Pro Thr Glu Ala Leu Ala Pro Leu Arg Ala Leu Gln Tyr
 225 230 235 240
 Leu Arg Leu Asn Asp Asn Pro Trp Val Cys Asp Cys Arg Ala Arg Pro
 245 250 255
 Leu Trp Ala Trp Leu Gln Lys Phe Arg Gly Ser Ser Ser Glu Val Pro
 260 265 270
 Cys Ser Leu Pro Gln Arg Leu Ala Gly Arg Asp Leu Lys Arg Leu Ala
 275 280 285
 Ala Asn Asp Leu Gln Gly Cys Ala Val Ala Thr Gly Pro Tyr His Pro
 290 295 300
 Ile Trp Thr Gly Arg Ala Thr Asp Glu Glu Pro Leu Gly Leu Pro Lys
 305 310 315 320
 Cys Cys Gln Pro Asp Ala Ala Asp Lys Ala Ser Val Leu Glu Pro Gly
 325 330 335
 Arg Pro Ala Ser Ala Gly Asn Ala Leu Lys Gly Arg
 340 345

<210> 3739

<211> 1252

<212> DNA

<213> Homo sapiens

<400> 3739

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agtgaggagg gcctggagat gctcattcaa tgagcgggag gcacctctcc cttcccgtaa
180
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240
tatttcttct gtcggttggc caggaagccg gccagttgag ttagaaaaca tctctctttg
300
aggtttctga actgctgttt gttctctgcc aactgggggc gcaatttctc gttgatttct
360
agaatgttca tctctgcctt ctgctggac aaagggccgg ctgataccac catgctgacg
420
tttgtggcag aagaggtgga gtcagggact tactgttgtg aaaaatgtga tcaactccca
480
cagcacttta ggatccttca ccacaaaaac aaggttcgag gtgcctcaac tcagagctga
540
aagcactgcc agtagctcag actctgataa gagtgaggta gattgtggcc agcgtgccag
600
gtaaccgtct tgateccatag gctcacattt gatcccaact ggcggctgct tcttggcatt
660
aactttggat tccaaccag taaatcttag caagatctga gtttctccag gtatgatatt
720
attttgtttg accatcetta tcttcaaggg ctgttggatc tggcagctct tgatgtcagc
780
ccacaccatg tgaggctgct cttggtgcac cgaatgggga agtttctaca tcagggcctc
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960
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1020
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1080
gcgcgcgcgc gcctcgcccc agctcctggc gccgcagatc gcccgctccc cgttcccaaa
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agccccgcgc tcgctcagaa gctcgggcag cctcgcgacc ctcacctacc cctcccaata
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1252

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<210> 3740

<211> 139

<212> PRT

<213> Homo sapiens

<400> 3740

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Met Gly Lys Phe Leu His Gln Gly Leu Gly Glu Ser Thr Gly Ser Pro
  1             5             10             15
Gly Gln Trp Glu Ser Ala Ala Pro Pro Val Trp Arg Pro Arg Ala His
             20             25             30
Ser Thr Glu Ala Pro Gly His Pro Gln Glu Asp Gly Lys Gly Gln Leu
             35             40             45
Ala Gly Glu Ser Pro Gly His Arg Glu Pro Ser Pro Gly Ser Lys Gln

```

```

      50              55              60
Asp Leu Pro Ser Asp Cys Leu Arg Asn Ala Gly Trp Thr Ser Arg Asn
65              70              75              80
Phe Pro Phe Thr Gly Gln Pro Ala Ala Ala Pro Pro Arg Leu Gly Pro
      85              90              95
Ala Pro Gly Ala Ala Asp Arg Pro Ser Arg Val Pro Lys Ser Pro Ala
      100             105             110
Leu Ala Gln Lys Leu Gly Gln Pro Arg Asp Pro His Leu Pro Leu Pro
      115             120             125
Ile Ser Pro Leu Ser Gln Pro Pro Pro Ser Pro
      130             135

```

<210> 3741
 <211> 562
 <212> DNA
 <213> Homo sapiens

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<400> 3741
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gtcgtgtcca ctgtggggat ccacgtcctg actaaccttg tgttccctaga aatccctcac
120
cggcagatcg gtgcctcctg aatccccacc aaaattccca ctgggaatgt gttcctgaaa
180
gagctgcccc ggcttgagaa agcctctttt cagaccaaac ttcgtattca aagctcaaaa
240
agaactgcac acaattagga cagtcataca agatgctgcc cctaactctg ccacaatctg
300
cgagaagggg ggcgggggctt ccgagggcaa agtgcccctg ggaagggatc cgcaggggaa
360
agctttgaaa ggaccacagc cccagccac gaggggagca agcacgagcc ggggagagag
420
ctctgcgctc gcacacggga ttcatctccg ccgcctctgc ccgtttccag caacacggag
480
ccaggcggaa acagtttctc cagccattc gcctccccga ctcttctctt cacggcacgg
540
ctgggctgct ttcatcacgc gt
562

```

<210> 3742
 <211> 138
 <212> PRT
 <213> Homo sapiens

```

<400> 3742
Met Gly Trp Arg Asn Cys Phe Arg Leu Ala Pro Cys Cys Trp Lys Arg
1              5              10              15
Ala Glu Ala Ala Glu Met Asn Pro Val Cys Glu Arg Arg Ala Leu Ser
      20              25              30
Pro Ala Arg Ala Cys Ser Pro Arg Gly Trp Gly Leu Trp Ser Phe Gln
      35              40              45
Ser Cys Ser Leu Arg Ile Pro Ser Gln Gly His Phe Ala Leu Gly Ser
      50              55              60
Pro Ala Ser Leu Leu Ala Asp Cys Gly Arg Ile Arg Gly Ser Ile Leu

```



```

65              70              75              80
Tyr Asp Cys Pro Asn Cys Val Gln Phe Phe Leu Ser Phe Glu Tyr Glu
              85              90              95
Val Trp Ser Glu Lys Arg Leu Ser Gln Ala Trp Ala Ala Leu Ser Gly
              100              105              110
Thr His Ser Gln Trp Glu Phe Trp Val Gly Phe Arg Arg His Arg Ser
              115              120              125
Ala Gly Glu Gly Phe Leu Gly Thr Gln Gly
              130              135

```

<210> 3743

<211> 468

<212> DNA

<213> Homo sapiens

<400> 3743

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nntcatgagc cttcttacaa gctccatttt ggcaaggcgc tgacaatggc ggaggctgaa
60
ggcaatgcaa gctgcacagt cagtctaggg ggtgccaaata tggcagagac ccacaaagcc
120
atgatcctgc aactcaatcc cagtgagaac tgcacctgga caatagaaag accagaaaaa
180
aaaagcatca gaattatctt ttectatgtc cagcttgatc cagatggaag ctgtgaaagt
240
gaaaacatta aagtctttga cggaacctcc agcaatgggc ctctgctagg gcaagtctgc
300
agtaaaaaacg actatgttcc tgtatttgaa tcatcatcca gtacattgac gtttcaaata
360
gttactgact cagcaagaat tcaaagaact gtctttgtgt tctagtagtt cttatttcct
420
aacatcttta ttccaaagtg tggcgggttac ctggatccct ggaaggat
468

```

<210> 3744

<211> 134

<212> PRT

<213> Homo sapiens

<400> 3744

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Xaa His Glu Pro Ser Tyr Lys Leu His Phe Gly Lys Ala Leu Thr Met
1              5              10              15
Ala Glu Ala Glu Gly Asn Ala Ser Cys Thr Val Ser Leu Gly Gly Ala
              20              25              30
Asn Met Ala Glu Thr His Lys Ala Met Ile Leu Gln Leu Asn Pro Ser
              35              40              45
Glu Asn Cys Thr Trp Thr Ile Glu Arg Pro Glu Asn Lys Ser Ile Arg
50              55              60
Ile Ile Phe Ser Tyr Val Gln Leu Asp Pro Asp Gly Ser Cys Glu Ser
65              70              75              80
Glu Asn Ile Lys Val Phe Asp Gly Thr Ser Ser Asn Gly Pro Leu Leu
              85              90              95
Gly Gln Val Cys Ser Lys Asn Asp Tyr Val Pro Val Phe Glu Ser Ser
100              105              110
Ser Ser Thr Leu Thr Phe Gln Ile Val Thr Asp Ser Ala Arg Ile Gln

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115
Arg Thr Val Phe Val Phe
130

120

125

<210> 3745
<211> 345
<212> DNA
<213> Homo sapiens

<400> 3745
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60
gacgctgtgg gagaggaaaa cagccacatg tgggctggct gcttgaggga gacacatgag
120
ccgtgaacac gtctcccccg gccgctccct ggttccatgc gtgctcgtct tgggcaccac
180
gagaacacag ccatgcagcc cccgatcctg cagccacagc cacggcatcg cctggtcgga
240
tgcagcatct gctccggacg cctctcgtg tcggtgccag gctgccagg ccaagccccg
300
attctcaggg gcggcaggag gtgggaggca cgtttgggag gatcc
345

<210> 3746
<211> 102
<212> PRT
<213> Homo sapiens

<400> 3746
Met Ala Gly Trp Cys Val Tyr Gly Thr Leu Trp Glu Arg Lys Thr Ala
1 5 10 15
Thr Cys Gly Leu Ala Ala Trp Arg Arg His Met Ser Arg Glu His Val
20 25 30
Ser Pro Gly Arg Ser Leu Val Pro Cys Val Leu Val Leu Gly Thr Thr
35 40 45
Arg Thr Gln Pro Cys Ser Pro Arg Ser Cys Ser His Ser His Gly Ile
50 55 60
Ala Trp Ser Asp Ala Ala Ser Ala Pro Asp Ala Ser Arg Cys Arg Cys
65 70 75 80
Gln Ala Cys Gln Ala Lys Pro Arg Phe Ser Gly Ala Ala Gly Gly Gly
85 90 95
Arg His Val Trp Ala Asp
100

<210> 3747
<211> 800
<212> DNA
<213> Homo sapiens

<400> 3747
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cgcccgac cctgggatgc tcttcggccg catcccgtg cgctacgcca tactggtgag
120

aagggggcgc gcccgggccac tttctgcctg agccccgcac cctctctggt ggtctcctct
 180
 ggggcgcccc tgccaatccc cgcttcccc tcccgagat gcagatgcgc ttcgatggac
 240
 gcctgggctt ccccggcgga ttcgtggaca cgcaggacag aagcctagag gacgggctga
 300
 accgcgagct gcgcgaggag ctggggcgaag cggctgccgc tttccgcgtg gagcgactg
 360
 actaccgcag ctcccacgtc ggggtcaggg ccacgcgttg tggcccactt ctatgccaa
 420
 cgtctgacgc tcgaggagct gttggctgtg gaggccggcg caacacgcgc caaggaccac
 480
 gggctggagg tgggaccagc ctgggactct gtccctttcc caatttcctc ttctcccaaa
 540
 gctttctctc ccccaagaaa gcatccctgg agaaaagtct ttgccctct gaccttgccc
 600
 tctcccagc tttcttggtg gagttgggat cgtgatcatc tatactctga attagtactg
 660
 ccaacctggg ctttctgtaa aggtctttcc caccctttac caggagagat ctttctaga
 720
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 780
 tctaggtgtg gcaacctagg
 800

<210> 3748
 <211> 138
 <212> PRT
 <213> Homo sapiens

<400> 3748
 Met Gln Met Arg Phe Asp Gly Arg Leu Gly Phe Pro Gly Gly Phe Val
 1 5 10 15
 Asp Thr Gln Asp Arg Ser Leu Glu Asp Gly Leu Asn Arg Glu Leu Arg
 20 25 30
 Glu Glu Leu Gly Glu Ala Ala Ala Phe Arg Val Glu Arg Thr Asp
 35 40 45
 Tyr Arg Ser Ser His Val Gly Val Arg Ala Thr Arg Cys Gly Pro Leu
 50 55 60
 Leu Cys Gln Ala Ser Asp Ala Arg Gly Ala Val Gly Cys Gly Gly Arg
 65 70 75 80
 Arg Asn Thr Arg Gln Gly Pro Arg Ala Gly Gly Gly Thr Ser Leu Gly
 85 90 95
 Leu Cys Pro Phe Pro Asn Phe Leu Phe Ser Gln Ser Phe Leu Ser Pro
 100 105 110
 Lys Lys Ala Ser Leu Glu Lys Ser Leu Cys Pro Ser Asp Leu Ala Leu
 115 120 125
 Ser Pro Ala Phe Leu Val Glu Leu Gly Ser
 130 135

<210> 3749
 <211> 648
 <212> DNA
 <213> Homo sapiens

<400> 3749

cgcgccccct gggaggatcc tgccaagtgg gtgatggaca catatccatg ggcagccagc
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ccacaacagc acgagtggcc tccccctgctg cagttacggc ctgaggatgt cggcttcgac
120
ggctactcca tgcctcggga gggatcgaca agcaagcaga tgccccccag tgatgctgaa
180
ggtgacccgc tgatgaacat gctgatgagg ctgcaggagg cagccaacta ctccagcccc
240
cagagctatg acagcgactc caacagcaac agccatcacg atgacatctt ggactcctct
300
ttggagtcca ctctgtgaca ggggcccgga gccagcgcc ctctcttct cctcacgca
360
ttccacctgc atccccaca tcacctgaa gatgacttcc tgagccagcc cccagccaca
420
gccttagagc tgcgggaaca ccgagacccc ccgtccttca gcctcgacct ggggtgcaggc
480
atcccgggccc agctgcctgc ggaccgcttc cttccacagc gagaactgca ctaccttctg
540
ttgtacttta attattgttt tgccttggtg ctgtgacctc cctaagacac tgaagatact
600
tctcgggaaa ggatcatcgc cgttgaaatg aaaaaaaaaa aaaaaaaaaa
648

<210> 3750

<211> 105

<212> PRT

<213> Homo sapiens

<400> 3750

Arg	Ala	Pro	Trp	Glu	Asp	Pro	Ala	Lys	Trp	Val	Met	Asp	Thr	Tyr	Pro
1				5					10					15	
Trp	Ala	Ala	Ser	Pro	Gln	Gln	His	Glu	Trp	Pro	Pro	Leu	Leu	Gln	Leu
		20					25						30		
Arg	Pro	Glu	Asp	Val	Gly	Phe	Asp	Gly	Tyr	Ser	Met	Pro	Arg	Glu	Gly
		35				40					45				
Ser	Thr	Ser	Lys	Gln	Met	Pro	Pro	Ser	Asp	Ala	Glu	Gly	Asp	Pro	Leu
		50			55					60					
Met	Asn	Met	Leu	Met	Arg	Leu	Gln	Glu	Ala	Ala	Asn	Tyr	Ser	Ser	Pro
65					70				75					80	
Gln	Ser	Tyr	Asp	Ser	Asp	Ser	Asn	Ser	Asn	Ser	His	His	Asp	Asp	Ile
			85					90					95		
Leu	Asp	Ser	Ser	Leu	Glu	Ser	Thr	Leu							
			100					105							

<210> 3751

<211> 554

<212> DNA

<213> Homo sapiens

<400> 3751

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cctggccccg ctgctgctcg cggctcggtc gccccgagcg gggccaaggg cgtttctac
 120
 acgcagggcc agagtccgga gccgcggacc cgcgaggtat ttctactacg tggaccacca
 180
 gggccagctt ttcttgatg attccaaaat gaagaatttc atcacctgct tcaaagaccc
 240
 gcagttctcg gtcaccttct tctcccgct gagaccaac cgcagcgggc gctacgaggc
 300
 cgctttcccc ttctctcgc cctgcggcag agagcgcaac ttctgcgct gcgaggaccg
 360
 gccggtggtc ttcacgcacc tgctgaccgc ggaccacggg cctccgcgc tctctactg
 420
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 480
 caacggggcg ctgtaccacc cggcgccgga gcgtgcgggc ggcgggggc tgggtgcgc
 540
 ttcgccccg gcc
 554

<210> 3752

<211> 66

<212> PRT

<213> Homo sapiens

<400> 3752

Ala	Arg	Leu	Ser	Ala	Leu	Ala	Arg	Ala	Leu	Ala	Gly	Pro	Pro	Pro	Arg
1			5						10				15		
Pro	His	His	Gly	Pro	Gly	Pro	Ala	Ala	Ala	Arg	Gly	Ser	Val	Ala	Pro
			20					25					30		
Ser	Gly	Ala	Lys	Gly	Val	Ser	Tyr	Thr	Gln	Gly	Gln	Ser	Pro	Glu	Pro
			35				40					45			
Arg	Thr	Arg	Glu	Val	Phe	Leu	Leu	Arg	Gly	Pro	Pro	Gly	Pro	Ala	Phe
			50				55					60			
Pro	Gly														
65															

<210> 3753

<211> 1426

<212> DNA

<213> Homo sapiens

<400> 3753

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 gaaccactc tctaaccaca cccccgagag gcggagagaa tgtgggagca cttcagagag
 120
 gcctaggctc cggagatcgg gccatctggg ctctgaaagc aaattagttt tccaactcat
 180
 gtctggctcc ggcgttacc agacgcctgg aaggctcttc ctgcagtctg atcaccattt
 240
 ttctgctgc actgaccaat cagctccctc tggccttcaa cctcggaat gatggattag
 300
 gggagtctag aaatggacga agccctagaa acgcagctga agacgagcag aggacgcttc
 360

tcggctacag aatccctccc caccttgagg ctcttatctc aggtggacat ggactgcagg
 420
 gtccacatgc gaccatcgg cctgacgtgg gtgctgcaac tgaccttggc atggatcctg
 480
 ctagaagcct gtggaggag cgcgccactc caagccaggc cccagcaaca ccatgggctg
 540
 gcagctgacg tgggcaaagg caagctgcac ctggcaggac cttgttgtcc ctacagagatg
 600
 gacacaacag agacatcggg ccctggaaac catccagaac gctgtggagt gccgagccct
 660
 gaatgcgaat ccttcctgga acacctcaa cgtgcccttc gcagtcgctt ccgcctgcgg
 720
 ctattggggg tacgccaggc acagccgctc tgcgaggagc tctgccaggc ctggttcgcc
 780
 aactgcgaag atgatatac ctgcggcccg acttggtctc cactctcaga aaaaaggggc
 840
 tgtgagccca gctgccttac ctatggacag accttcgcag acgggacgga cttttgtcgc
 900
 tcggtcttgg gccacgccct accggtggct gctcctggag ccggtcactg cttcaacatc
 960
 tccatctccg cggtagctcg tcccagacca ggacgacggg gccgggaagc tccctcccg
 1020
 cgttcccgcg gccctcgcac ctccatcctg gacgtgcgg gcagcgggag tggcagtgga
 1080
 agcggcagcg gcccttagcg gacgcgtggc cctgagttag gggagcgacc cttccccag
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 1260
 agaaatgacc caactctctc acttttccct ctccccttg aataaagtcg ccagctaaaa
 1320
 aaaaagtcca tgtccacctg agataagagc tgttggttgg attgggggt ccacatgcga
 1380
 cccatcggcc tgacgtgggt gctgcaactg acctcggcat ggatcc
 1426

<210> 3754

<211> 261

<212> PRT

<213> Homo sapiens

<400> 3754

Met Asp Glu Ala Leu Glu Thr Gln Leu Lys Thr Ser Arg Gly Arg Phe
 1 5 10 15
 Ser Ala Thr Glu Ser Leu Pro Thr Leu Glu Leu Leu Ser Gln Val Asp
 20 25 30
 Met Asp Cys Arg Val His Met Arg Pro Ile Gly Leu Thr Trp Val Leu
 35 40 45
 Gln Leu Thr Leu Ala Trp Ile Leu Leu Glu Ala Cys Gly Gly Ser Arg
 50 55 60
 Pro Leu Gln Ala Arg Ser Gln Gln His His Gly Leu Ala Ala Asp Leu
 65 70 75 80
 Gly Lys Gly Lys Leu His Leu Ala Gly Pro Cys Cys Pro Ser Glu Met

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<210> 3755
<211> 3149
<212> DNA
<213> Homo sapiens
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<400> 3755
atgaatctct gttccaaatg ctttgctgat tttcaaaaga aacagccaga cgatgattcc
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gctccaagta caagtaacag ccaatcagat ttgttttccg aagagaccac cagtgcacaac
120
aacaatacct cgataaccac gccaaactctt agtcccagcc agcagccgct tccgacagaa
180
ctgaatgtaa cttcaccgag taaagaggag tgtgggccat gcacagacac agctcatgtc
240
tcattaatca caccaacaaa aagatcctgt ggtacagatt cacagtctga gaatgaggct
300
tcaccagtaa aacggccacg actacttgag aatacggaac ggtccgagga aaccagtcca
360
tctaaacaga agagtcgacg tcggtgcttc cagtgccaaa ccaaactgga gctggtgcag
420
caggaattgg gatcgtgtcg ctgcggttat gtgttctgta tgttacatcg cctccccgag
480
cagcacgact gcacattcga ccacatgggc cgtggccggg aggaagccat catgaaaatg
540
gtgaagctgg accggaagt ggggcgctcc tgccagcgca tcggggaggg gtgctcctga
600
aggccaggca tggccaccac gtgacgctgt tcttagttca ctaatgtag cttatttag
660
gacaaaagtca gccagacacc ttgtactggg cacgcgtcag actgcagcca gtccgtttcc
720

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tttcttttagc cagccatcct ggtactgtag tttaggggtt gatgggtggtt gaaattgatt
780
tctggctggt tactaagggtg cctgctagcc attgtataaa attaaaacat gaagaatatt
840
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<210> 3756

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3756

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			20					25					30		
Ser	Glu	Glu	Thr	Thr	Ser	Asp	Asn	Asn	Asn	Thr	Ser	Ile	Thr	Thr	Pro
			35				40					45			
Thr	Leu	Ser	Pro	Ser	Gln	Gln	Pro	Leu	Pro	Thr	Glu	Leu	Asn	Val	Thr
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65				70					75					80	
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			85					90						95	
Glu	Asn	Glu	Ala	Ser	Pro	Val	Lys	Arg	Pro	Arg	Leu	Leu	Glu	Asn	Thr
			100				105						110		
Glu	Arg	Ser	Glu	Glu	Thr	Ser	Arg	Ser	Lys	Gln	Lys	Ser	Arg	Arg	Arg
			115			120						125			
Cys	Phe	Gln	Cys	Gln	Thr	Lys	Leu	Glu	Leu	Val	Gln	Gln	Glu	Leu	Gly
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Gln	His	Asp	Cys	Thr	Phe	Asp	His	Met	Gly	Arg	Gly	Arg	Glu	Glu	Ala
					165					170				175	
Ile	Met	Lys	Met	Val	Lys	Leu	Asp	Arg	Lys	Val	Gly	Arg	Ser	Cys	Gln
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<210> 3757
 <211> 1046
 <212> DNA
 <213> Homo sapiens

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<210> 3758
 <211> 199
 <212> PRT

<213> Homo sapiens

<400> 3758

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Gly Lys Ser Gly Leu Leu Thr Ser His Thr Thr Asp Ser Leu Gln Leu
          35           40           45
Trp Phe Val Arg Leu Ala Leu Leu Val Lys Leu Gly Leu Phe Gln Asn
          50           55           60
Ala Glu Met Glu Phe Glu Pro Phe Gly Asn Leu Asp Gln Pro Asp Leu
65           70           75           80
Tyr Ser Glu Tyr Tyr Pro His Val Tyr Pro Gly Arg Arg Gly Ser Met
          85           90           95
Val Pro Phe Ser Met Arg Ile Leu His Ala Glu Leu Gln Gln Tyr Leu
          100          105          110
Gly Asn Pro Gln Glu Ser Leu Asp Arg Leu His Lys Val Lys Thr Val
          115          120          125
Cys Ser Lys Val Gly Gly Ala Val Ile Leu Pro Cys His Gly Glu Asn
          130          135          140
Met Pro Ser Thr Pro Ser Pro Gln Asp Met Pro Val Leu Phe Pro Ala
145          150          155          160
Arg Pro Ala Pro Cys Thr Ile Ala Ala Ser Ala Phe Arg Arg Leu Gly
          165          170          175
Asp Pro Gly Leu Cys Gly Leu Val Val Val Ala Leu Ala Glu Ile Phe
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Phe Arg Asp Gly Lys Ser Phe
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<210> 3759

<211> 830

<212> DNA

<213> Homo sapiens

<400> 3759

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420
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480
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540

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720
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<213> Homo sapiens

<400> 3760
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20 25 30
Cys Asp Arg Glu Leu Tyr Pro Gly Glu Pro Arg Leu His Leu Ser Ala
35 40 45
Pro Gly Pro Ala Ser His Gln Asp Gln Pro Glu Trp Gln Glu Asp Met
50 55 60
Gly Arg Thr Gly Gly Gly Gly Cys Gly His Pro Ser Phe Asn Gln Met
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Leu Asp Val Lys Gly Pro Ile Pro Val Lys Arg Gly Gly Gln Ala Leu
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Phe Val Leu Leu
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<210> 3761
<211> 458
<212> DNA
<213> Homo sapiens

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458

<210> 3762
 <211> 75
 <212> PRT
 <213> Homo sapiens

<400> 3762
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 20 25 30
 Arg Pro Pro Pro Glu Gly Leu Gly Lys Gly Gly Arg Pro Ala Ala Ala
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 Gly Gly Gly Pro Pro Gly His Pro Gly Ala Pro Arg Arg Gly Thr Pro
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<210> 3763
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 <212> DNA
 <213> Homo sapiens

<400> 3763
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<210> 3764
 <211> 288
 <212> PRT
 <213> Homo sapiens

<400> 3764
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 35 40 45
 Asn Gly Gly Ala Ser Glu Ala Gly Glu Asp Arg Glu Ala Pro Gly Lys
 50 55 60
 Arg Arg Arg Leu Gly Phe Leu Ala Thr Ala Trp Leu Thr Phe Tyr Asp
 65 70 75 80
 Ile Ala Met Thr Ala Gly Trp Leu Val Leu Ala Ile Ala Met Val Arg
 85 90 95
 Phe Tyr Met Glu Lys Gly Thr His Arg Gly Leu Tyr Lys Ser Ile Gln
 100 105 110
 Lys Thr Leu Lys Phe Phe Gln Thr Phe Ala Leu Leu Glu Ile Val His
 115 120 125
 Cys Leu Ile Gly Ile Val Pro Thr Ser Val Ile Val Thr Gly Val Gln
 130 135 140
 Val Ser Ser Arg Ile Phe Met Val Trp Leu Ile Thr His Ser Ile Lys
 145 150 155 160
 Pro Ile Gln Asn Glu Glu Ser Val Val Leu Phe Leu Val Ala Trp Thr
 165 170 175
 Val Thr Glu Ile Thr Arg Tyr Ser Phe Tyr Thr Phe Ser Leu Leu Asp
 180 185 190
 His Leu Pro Tyr Phe Ile Lys Trp Ala Arg Tyr Asn Phe Phe Ile Ile
 195 200 205
 Leu Tyr Pro Val Gly Val Ala Gly Glu Leu Leu Thr Ile Tyr Ala Ala
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<210> 3765
<211> 2764
<212> DNA
<213> Homo sapiens
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2764

<210> 3766

<211> 464

<212> PRT

<213> Homo sapiens

<400> 3766

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Lys Val Lys Lys Met Gly Leu Gly His Glu Gln Gly Phe Gly Ala Pro
 50           55           60
Cys Leu Lys Cys Lys Glu Lys Cys Glu Gly Phe Glu Leu His Phe Trp
 65           70           75           80
Arg Lys Ile Cys Arg Asn Cys Lys Cys Gly Gln Glu Glu His Asp Val
          85           90           95
Leu Leu Ser Asn Glu Glu Asp Arg Lys Val Gly Lys Leu Phe Glu Asp
          100          105          110
Thr Lys Tyr Thr Thr Leu Ile Ala Lys Leu Lys Ser Asp Gly Ile Pro
          115          120          125
Met Tyr Lys Arg Asn Val Met Ile Leu Thr Asn Pro Val Ala Ala Lys
          130          135          140
Lys Asn Val Ser Ile Asn Thr Val Thr Tyr Glu Trp Ala Pro Pro Val
          145          150          155          160
Gln Asn Gln Ala Leu Ala Arg Gln Tyr Met Gln Met Leu Pro Lys Glu
          165          170          175
Lys Gln Pro Val Ala Gly Ser Glu Gly Ala Gln Tyr Arg Lys Lys Gln
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Leu Ala Lys Gln Leu Pro Ala His Asp Gln Asp Pro Ser Lys Cys His
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Glu Leu Ser Pro Arg Glu Val Lys Glu Met Glu Gln Phe Val Lys Lys
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Tyr Lys Ser Glu Ala Leu Gly Val Gly Asp Val Lys Leu Pro Cys Glu
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Met Asp Ala Gln Gly Pro Lys Gln Met Asn Ile Pro Gly Gly Asp Arg
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Ser Thr Pro Ala Ala Val Gly Ala Met Glu Asp Lys Ser Ala Glu His
          260          265          270
Lys Arg Thr Gln Tyr Ser Cys Tyr Cys Cys Lys Leu Ser Met Lys Glu
          275          280          285
Gly Asp Pro Ala Ile Tyr Ala Glu Arg Ala Gly Tyr Asp Lys Leu Trp
          290          295          300
His Pro Ala Cys Phe Val Cys Ser Thr Cys His Glu Leu Leu Val Asp
          305          310          315          320
Met Ile Tyr Phe Trp Lys Asn Glu Lys Leu Tyr Cys Gly Arg His Tyr
          325          330          335
Cys Asp Ser Glu Lys Pro Arg Cys Ala Gly Cys Asp Glu Leu Ile Phe
          340          345          350
Ser Asn Glu Tyr Thr Gln Ala Glu Asn Gln Asn Trp His Leu Lys His
          355          360          365
Phe Cys Cys Phe Asp Cys Asp Ser Ile Leu Ala Gly Glu Ile Tyr Val
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Met Val Asn Asp Lys Pro Val Cys Lys Pro Cys Tyr Val Lys Asn His

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385              390              395              400
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              420              425              430
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<210> 3767

<211> 2439

<212> DNA

<213> Homo sapiens

<400> 3767

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<211> 379

<212> PRT

<213> Homo sapiens

<400> 3768

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<212> PRT

<213> Homo sapiens

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		260						265					270		
Pro	Ser	Glu	Ser	Thr	Pro	Val	Ser	Cys	Tyr	Pro	Cys	Asn	Arg	Val	Lys
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Ser Tyr Pro Arg Gln Lys Thr Pro Gly Thr Pro Lys Arg Asn Cys Pro
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Pro Val Thr Ala Glu Phe Ser Ser Ser Val Ser Gly Cys Pro Lys Ser
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<213> Homo sapiens

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Gln	Lys	Arg	Pro	Ser	Glu	Ala	Gln	Ser	Val	Ile	Leu	Arg	Arg	Tyr	Phe
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<212> PRT

<213> Homo sapiens

<400> 3774

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			20					25					30		
Val	Arg	Pro	Ala	Gly	Pro	Pro	Asn	Ala	Gly	Ser	Met	Ser	Ala	Gly	Ser
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Ser	Lys	Val	Glu	Leu	Arg	Leu	Ser	Cys	Arg	His	Leu	Leu	Asp	Arg	Asp
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Pro	Leu	Thr	Lys	Ser	Asp	Pro	Ser	Val	Ala	Leu	Leu	Gln	Gln	Ala	Gln
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Val	Gln	Arg	Leu	Arg	Phe	Glu	Val	Tyr	Asp	Thr	His	Gly	Pro	Ser	Gly
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Phe	Ser	Cys	Gln	Glu	Asp	Asp	Phe	Leu	Gly	Gly	Met	Glu	Cys	Thr	Leu
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Cys	Thr	Glu	Ser	Ser	His	Leu	Ala	Arg	Thr	Gly	Pro	Ser	Phe	Leu	Leu
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Arg	Tyr	Asp	Asp	Leu	Cys	Leu	Pro	Trp	Ala	Thr	Ala	Gly	Ala	Val	Arg
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Trp	Trp	Thr	Cys	Arg	Gly	Gly	His	Thr	Gln	Gly	Trp	Gln	Ile	Val	Ala
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Gln	Lys	Lys	Val	Thr	Arg	Pro	Leu	Leu	Leu	Lys	Phe	Gly	Arg	Asn	Ala
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Gly	Lys	Ser	Thr	Ile	Thr	Val	Ile	Ala	Glu	Asp	Ile	Ser	Gly	Asn	Asn
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Ser	Cys	Asp	Val	His	Arg	Pro	Leu	Lys	Phe	Leu	Val	Trp	Asp	Tyr	Asp
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Ser	Ser	Gly	Lys	His	Asp	Phe	Ile	Gly	Glu	Phe	Thr	Ser	Thr	Phe	Gln

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Gly Val Val Val Leu Ala Asp Leu Lys Phe His Arg Val Tyr Ser Phe
      405              410              415
Leu Asp Tyr Ile Met Gly Gly Cys Gln Ile Ser Phe Thr Val Ala Ile
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      435              440              445
Tyr Ile Ser Pro Arg Gln Pro Asn His Tyr Leu Gln Ala Leu Arg Ala
      450              455              460
Val Gly Gly Ile Cys Gln Asp Tyr Asp Ser Asp Lys Arg Phe Pro Ala
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545              550              555              560
Val Leu Thr Asp Gly Val Val Ser Asp Met Ala Glu Thr Arg Thr Ala
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Ile Val Arg Ala Ser Arg Leu Pro Met Ser Ile Ile Ile Val Gly Val
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Gly Asn Ala Asp Phe Ser Asp Met Arg Leu Leu Asp Gly Asp Asp Gly
      595              600              605
Pro Leu Arg Cys Pro Arg Gly Glu Pro Ala Leu Arg Asp Ile Val Gln
      610              615              620
Phe Val Pro Phe Arg Glu Leu Lys Asn Ala Ser Pro Ala Ala Leu Ala
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Lys Cys Val Leu Ala Glu Val Pro Lys Gln Val Val Glu Tyr Tyr Ser
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<210> 3775

<211> 549

<212> DNA

<213> Homo sapiens

<400> 3775

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 35 40 45
 Asp Gln Ser Lys Tyr Pro Ile Arg Glu Ser Glu Met Arg Glu Tyr Ile
 50 55 60
 Val Lys Glu Tyr Arg Asn Gln Phe Pro Glu Ile Leu Arg Arg Ala Ala
 65 70 75 80
 Ala His Leu Glu Cys Ile Phe Arg Phe Glu Leu Arg Glu Leu Asp Pro
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 Glu Ala His Thr Tyr Ile Leu Leu Asn Lys Leu Gly Pro Val Pro Phe
 100 105 110
 Glu Gly Leu Glu Glu Ser Pro Asn Gly Pro Lys Met Gly Leu Leu Met
 115 120 125
 Met Ile Leu Gly Gln Ile Phe Leu Asn Gly Asn Gln Ala Lys Glu Ala
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 <212> PRT
 <213> Homo sapiens

<400> 3778

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			20					25					30		
Glu	Lys	Arg	Asn	Lys	Ile	Glu	Glu	Ala	Pro	Glu	Ala	Thr	Pro	Gln	Pro
		35					40					45			
Ser	Gln	Pro	Gly	Pro	Ser	Ser	Pro	Ile	Ser	Leu	Ser	Ala	Glu	Glu	Glu
	50					55					60				
Asn	Ala	Glu	Gly	Glu	Val	Ser	Arg	Ala	Asn	Thr	Pro	Asp	Ser	Asp	Ile
65					70					75					80
Thr	Glu	Lys	Thr	Glu	Asp	Ser	Ser	Val	Pro	Glu	Thr	Pro	Asp	Asn	Glu
				85					90					95	
Arg	Lys	Ala	Ser	Ile	Ser	Tyr	Phe	Lys	Asn	Gln	Arg	Gly	Ile	Gln	Tyr
			100					105					110		
Ile	Asp	Leu	Ser	Ser	Asp	Ser	Glu	Asp	Val	Val	Ser	Pro	Asn	Cys	Ser
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Asn	Thr	Val	Gln	Glu	Lys	Thr	Phe	Asn	Lys	Asp	Thr	Val	Ile	Ile	Val
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Ser	Glu	Pro	Ser	Glu	Asp	Glu	Glu	Ser	Gln	Gly	Leu	Pro	Thr	Met	Ala
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Arg	Arg	Asn	Asp	Asp	Ile	Ser	Glu	Leu	Glu	Asp	Leu	Ser	Glu	Leu	Glu
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Asp	Leu	Lys	Asp	Ala	Lys	Leu	Gln	Thr	Leu	Lys	Glu	Leu	Phe	Pro	Gln
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Arg	Ser	Asp	Asn	Asp	Leu	Leu	Lys	Leu	Ile	Glu	Ser	Thr	Ser	Thr	Met
		195					200					205			
Asp	Gly	Ala	Ile	Ala	Ala	Ala	Leu	Leu	Met	Phe	Gly	Asp	Ala	Gly	Gly
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Gly	Pro	Arg	Lys	Arg	Lys	Leu	Ser	Ser	Ser	Ser	Glu	Pro	Tyr	Glu	Glu
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Gly	Glu	Glu	Ser	Asn	Glu	Ser	Ala	Glu	Ser	Ser	Ser	Asn	Trp	Glu	Lys
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Tyr	Ala	Ser	Gln	Ser	Glu	Val	Pro	Asn	Gly	Lys	Glu	Val	Ser	Ser	Arg
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Ser	Gln	Asn	Tyr	Pro	Lys	Asn	Ala	Thr	Lys	Thr	Lys	Leu	Lys	Gln	Lys
		340						345					350		
Phe	Ser	Met	Lys	Ala	Gln	Asn	Gly	Phe	Asn	Lys	Lys	Arg	Lys	Lys	Asn
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Val	Phe	Asn	Pro	Lys	Arg	Val	Val	Glu	Asp	Ser	Glu	Tyr	Asp	Ser	Gly

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Ala Gln Lys Ile Thr Glu Leu Arg Pro Phe Asn Ser Trp Glu Ala Leu
      435              440              445
Phe Thr Lys Met Ser Lys Thr Asn Gly Leu Ser Glu Asp Leu Ile Trp
      450              455              460
His Cys Lys Thr Leu Ile Gln Glu Arg Asp Val Val Ile Arg Leu Met
465              470              475              480
Asn Lys Cys Glu Asp Ile Ser Asn Lys Leu Thr Lys Gln Val Thr Met
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Leu Thr Gly Asn Gly Gly Gly Trp Asn Ile Glu Gln Pro Ser Ile Leu
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Asn Gln Ser Leu Ser Leu Lys Pro Tyr Gln Lys Val Gly Leu Asn Trp
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Leu Ala Leu Val His Lys His Gly Leu Asn Gly Ile Leu Ala Asp Glu
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Met Gly Leu Gly Lys Thr Ile Gln Ala Ile Ala Phe Leu Ala Tyr Leu
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Tyr Gln Glu Gly Asn Asn Gly Pro His Leu Ile Val Val Pro Ala Ser
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Thr Ile Asp Asn Trp Leu Arg Glu Val Asn Leu Trp Cys Pro Thr Leu
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Lys Val Leu Cys Tyr Tyr Gly Ser Gln Glu Glu Arg Lys Gln Ile Arg
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Phe Asn Ile His Ser Arg Tyr Glu Asp Tyr Asn Val Ile Val Thr Thr
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Tyr Asn Cys Ala Ile Ser Ser Ser Asp Asp Arg Ser Leu Phe Arg Arg
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Met Gly Ser Ile Arg Tyr Gln His Leu Met Thr Ile Asn Ala Asn Asn
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705              710              715              720
Gln Ser Ile Tyr Glu Lys Glu Arg Ile Ala His Ala Lys Gln Ile Ile
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Lys Pro Phe Ile Leu Arg Arg Val Lys Glu Glu Val Leu Lys Gln Leu
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Pro Pro Lys Lys Asp Arg Ile Glu Leu Cys Ala Met Ser Glu Arg Gln
      755              760              765
Glu Gln Leu Tyr Leu Gly Leu Phe Asn Arg Leu Lys Lys Ser Ile Asn
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<211> 530

<212> PRT

<213> Homo sapiens

<400> 3780

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<212> DNA

<213> Homo sapiens

<400> 3781

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 Cys Thr Gly Gly Asp Ser Tyr His Pro His Glu Gln Ser Ser Pro Pro
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<211> 804

<212> PRT

<213> Homo sapiens

<400> 3784

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Val	Asp	Gly	Gln	Ser	Tyr	Leu	Leu	Leu	Ile	Arg	Asp	Glu	Gly	Gly	Pro	115	120	125	
Pro	Glu	Ala	Gln	Phe	Ala	Met	Trp	Val	Asp	Ala	Val	Ile	Phe	Val	Phe	130	135	140	
Ser	Leu	Glu	Asp	Glu	Ile	Ser	Phe	Gln	Thr	Val	Tyr	His	Tyr	Tyr	Ser	145	150	155	160
Arg	Met	Ala	Asn	Tyr	Arg	Asn	Thr	Ser	Glu	Ile	Pro	Leu	Val	Leu	Val	165	170	175	
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Glu	Thr	Cys	Ala	Thr	Tyr	Gly	Leu	Asn	Val	Glu	Arg	Val	Phe	Gln	Asp	210	215	220	
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2931

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<210> 3785

<211> 1901

<212> DNA¹

<213> Homo sapiens

<400> 3785

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<213> Homo sapiens

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His Phe Ser Arg Leu Pro Leu Gly Gly Trp Ala Glu Asp Gly Gln Ser
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Leu Pro Pro Gln Val His Lys Val
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<210> 3787

<211> 717

<212> DNA

<213> Homo sapiens

<400> 3787

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<210> 3788

<211> 113

<212> PRT

<213> Homo sapiens

<400> 3788

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Cys Ala Ser Ile Lys Leu Arg His Gly Ser Arg Ala Ala Pro Pro Gly
          20          25          30
Pro Trp Gly Ala Lys Cys Ser Trp Arg Gln Val Ala Lys Gly Glu His
          35          40          45
Leu Gly Gln Thr Pro Gly Phe Ser Ser Arg Leu Pro His Leu Pro Ala

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50		55		60	
Ser	Leu	Leu	Ser	Trp	Leu
65		70		75	
Ala	Ala	Val	Ile	Thr	His
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		100		105	
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<210> 3789

<211> 4341

<212> DNA

<213> Homo sapiens

<400> 3789

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1140

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 <211> 1092
 <212> PRT
 <213> Homo sapiens

<400> 3790
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 35 40 45
 Glu Asp Leu His Asn Glu Lys Glu Leu Ile Lys Glu Leu Glu Gln Ser
 50 55 60
 Leu Ala Ser Trp Thr Gln Asn Leu Lys Glu Leu Gln Thr Met Lys Ala
 65 70 75 80
 Asp Leu Thr Arg His Val Leu Val Glu Asp Val Met Val Leu Lys Glu
 85 90 95
 Gln Ile Glu His Leu His Arg Gln Trp Glu Asp Leu Cys Leu Arg Val
 100 105 110
 Ala Ile Arg Lys Gln Glu Ile Glu Asp Arg Leu Asn Thr Trp Val Val
 115 120 125
 Phe Asn Glu Lys Asn Lys Glu Leu Cys Ala Trp Leu Val Gln Met Glu
 130 135 140
 Asn Lys Val Leu Gln Thr Val Asp Ile Ser Ile Glu Glu Met Ile Glu
 145 150 155 160
 Lys Leu Gln Lys Asp Cys Met Glu Glu Ile Asn Leu Phe Ser Glu Asn
 165 170 175
 Lys Leu Gln Leu Lys Gln Met Gly Asp Gln Leu Ile Lys Ala Ser Asn
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 Lys Ser Arg Ala Ala Glu Ile Asp Asp Lys Leu Asn Lys Ile Asn Asp
 195 200 205
 Arg Trp Gln His Leu Phe Asp Val Ile Gly Ser Arg Val Lys Lys Leu
 210 215 220
 Lys Glu Thr Phe Ala Phe Ile Gln Gln Leu Asp Lys Asn Met Ser Asn
 225 230 235 240
 Leu Arg Thr Trp Leu Ala Arg Ile Glu Ser Glu Leu Ser Lys Pro Val
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 Val Tyr Asp Val Cys Asp Asp Gln Glu Ile Gln Lys Arg Leu Ala Glu
 260 265 270
 Gln Gln Asp Leu Gln Arg Asp Ile Glu Gln His Ser Ala Gly Val Glu
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 Ser Val Phe Asn Ile Cys Asp Val Leu Leu His Asp Ser Asp Ala Cys
 290 295 300
 Ala Asn Glu Thr Glu Cys Asp Ser Ile Gln Gln Thr Thr Arg Ser Leu
 305 310 315 320
 Asp Arg Arg Trp Arg Asn Ile Cys Ala Met Ser Met Glu Arg Arg Met
 325 330 335
 Lys Ile Glu Glu Thr Trp Arg Leu Trp Gln Lys Phe Leu Asp Asp Tyr
 340 345 350
 Ser Arg Phe Glu Asp Trp Leu Lys Ser Ala Glu Arg Thr Ala Ala Cys
 355 360 365
 Pro Asn Ser Ser Glu Val Leu Tyr Thr Ser Ala Lys Glu Glu Leu Lys

370		375		380
Arg Phe Glu Ala Phe Gln Arg Gln Ile His Glu Arg Leu Thr Gln Leu				
385		390		395
Glu Leu Ile Asn Lys Gln Tyr Arg Arg Leu Ala Arg Glu Asn Arg Thr				400
	405		410	415
Asp Thr Ala Ser Arg Leu Lys Gln Met Val His Glu Gly Asn Gln Arg				
	420		425	430
Trp Asp Asn Leu Gln Arg Arg Val Thr Ala Val Leu Arg Arg Leu Arg				
	435		440	445
His Phe Thr Asn Gln Arg Glu Glu Phe Glu Gly Thr Arg Glu Ser Ile				
	450		455	460
Leu Val Trp Leu Thr Glu Met Asp Leu Gln Leu Thr Asn Val Glu His				
	465		470	475
Phe Ser Glu Ser Asp Ala Asp Asp Lys Met Arg Gln Leu Asn Gly Phe				
	485		490	495
Gln Gln Glu Ile Thr Leu Asn Thr Asn Lys Ile Asp Gln Leu Ile Val				
	500		505	510
Phe Gly Glu Gln Leu Ile Gln Lys Ser Glu Pro Leu Asp Ala Val Leu				
	515		520	525
Ile Glu Asp Glu Leu Glu Glu Leu His Arg Tyr Cys Gln Glu Val Phe				
	530		535	540
Gly Arg Val Ser Arg Phe His Arg Arg Leu Thr Ser Cys Thr Pro Gly				
	545		550	555
Leu Glu Asp Glu Lys Glu Ala Ser Glu Asn Glu Thr Asp Met Glu Asp				
	565		570	575
Pro Arg Glu Ile Gln Thr Asp Ser Trp Arg Lys Arg Gly Glu Ser Glu				
	580		585	590
Glu Pro Ser Ser Pro Gln Ser Leu Cys His Leu Val Ala Pro Gly His				
	595		600	605
Glu Arg Ser Gly Cys Glu Thr Pro Val Ser Val Asp Ser Ile Pro Leu				
	610		615	620
Glu Trp Asp His Thr Gly Asp Val Gly Gly Ser Ser Ser His Glu Glu				
	625		630	635
Asp Glu Glu Gly Pro Tyr Tyr Ser Ala Leu Ser Gly Lys Ser Ile Ser				
	645		650	655
Asp Gly His Ser Trp His Val Pro Asp Ser Pro Ser Cys Pro Glu His				
	660		665	670
His Tyr Lys Gln Met Glu Gly Asp Arg Asn Val Pro Pro Val Pro Pro				
	675		680	685
Ala Ser Ser Thr Pro Tyr Lys Pro Pro Tyr Gly Lys Leu Leu Leu Pro				
	690		695	700
Pro Gly Thr Asp Gly Gly Lys Glu Gly Pro Arg Val Leu Asn Gly Asn				
	705		710	715
Pro Gln Gln Glu Asp Gly Gly Leu Ala Gly Ile Thr Glu Gln Gln Ser				
	725		730	735
Gly Ala Phe Asp Arg Trp Glu Met Ile Gln Ala Gln Glu Leu His Asn				
	740		745	750
Lys Leu Lys Ile Lys Gln Asn Leu Gln Gln Leu Asn Ser Asp Ile Ser				
	755		760	765
Ala Ile Thr Thr Trp Leu Lys Lys Thr Glu Ala Glu Leu Glu Met Leu				
	770		775	780
Lys Met Ala Lys Pro Pro Ser Asp Ile Gln Glu Ile Glu Leu Arg Val				
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<210> 3791
<211> 1011
<212> DNA
<213> Homo sapiens
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<210> 3792

<211> 288

<212> PRT

<213> Homo sapiens

<400> 3792

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			20					25					30		
Ala	Leu	Ser	Met	Gly	Gly	Lys	Val	Pro	Val	Ser	Glu	Gly	Leu	Glu	His
		35				40						45			
Ser	Asp	Leu	Pro	Asp	Gly	Thr	Gly	Glu	Phe	Leu	Asp	Ala	Trp	Leu	Met
		50				55					60				
Leu	Val	Glu	Lys	Met	Val	Asn	Pro	Thr	Thr	Val	Leu	Glu	Ser	Pro	His
					70					75				80	
Ser	Leu	Pro	Ala	Lys	Leu	Pro	Gly	Gly	Val	Gln	Asn	Phe	Pro	Gln	Phe
				85				90						95	
Ser	Ala	Leu	Arg	Phe	Leu	Val	Val	Thr	Gln	Lys	Ala	Ala	Phe	Thr	Cys
		100						105						110	
Ile	Lys	Asn	Leu	Trp	Asn	Arg	Lys	Pro	Leu	Lys	Val	Tyr	Gly	Gly	Arg
		115					120						125		
Met	Ala	Glu	Ser	Met	Leu	Ala	Ile	Leu	Cys	His	Ile	Leu	Arg	Gly	Glu
		130				135					140				
Pro	Val	Ile	Arg	Glu	Arg	Leu	Ser	Lys	Glu	Lys	Glu	Gly	Ser	Arg	Gly
				145		150				155				160	
Glu	Glu	Asp	Thr	Gly	Gln	Glu	Glu	Gly	Gly	Ser	Arg	Arg	Glu	Pro	Gln
				165				170						175	
Val	Asn	Gln	Gln	Gln	Leu	Gln	Gln	Leu	Met	Asp	Met	Gly	Phe	Thr	Arg

	180		185		190										
Glu	His	Ala	Met	Glu	Ala	Leu	Leu	Asn	Thr	Ser	Thr	Met	Glu	Gln	Ala
	195						200					205			
Thr	Glu	Tyr	Leu	Leu	Thr	His	Pro	Pro	Pro	Ile	Met	Gly	Gly	Val	Val
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Arg	Asp	Leu	Ser	Met	Ser	Glu	Glu	Asp	Gln	Met	Met	Arg	Ala	Ile	Ala
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Met	Ser	Leu	Gly	Gln	Asp	Ile	Pro	Met	Asp	Gln	Arg	Ala	Glu	Ser	Pro
			245						250					255	
Glu	Glu	Val	Ala	Cys	Arg	Lys	Glu	Glu	Glu	Glu	Arg	Lys	Ala	Arg	Glu
			260					265					270		
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<210> 3793
 <211> 360
 <212> DNA
 <213> Homo sapiens

<400> 3793
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<210> 3794
 <211> 96
 <212> PRT
 <213> Homo sapiens

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		20					25					30			
Phe	Val	Pro	Gly	Arg	Asn	Asn	Ser	Phe	Phe	Phe	Ser	Trp	Arg	Gln	Cys
		35				40					45				
Phe	Thr	Leu	Val	Ala	Gln	Ala	Gly	Gly	Gln	Trp	Arg	Asp	Leu	Ser	Ser
	50					55				60					
Leu	Gln	Pro	Pro	Pro	Phe	Gly	Leu	Lys	Arg	Phe	Ser	Cys	Leu	Ser	Leu
65				70					75					80	
Pro	Ser	Ser	Trp	Asp	Tyr	Arg	His	Ala	Ser	Pro	Cys	Thr	Met	Pro	Asp
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<210> 3795
 <211> 1341

<212> DNA

<213> Homo sapiens

<400> 3795

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<210> 3796

<211> 294

<212> PRT

<213> Homo sapiens

<400> 3796

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      35           40           45
Val Asp Arg Glu Arg Phe Cys Arg Trp Ala Gly Leu Pro Arg Gln Gly
      50           55           60
Phe Pro Ile Ile Phe His Gly Val Met Gly Lys Asp Glu Arg Glu Gly
      65           70           75           80
Asn Ser Pro Ser Phe Phe Asn Pro Glu Glu Ala Ala Thr Val Thr Ser
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Tyr Leu Lys Leu Leu Leu Ala Pro Ser Ser Lys Lys Gly Lys Ala Arg
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Leu Ser Pro Arg Ser Val Gly Val Ile Ser Pro Tyr Arg Lys Gln Val
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Glu Lys Ile Arg Tyr Cys Ile Thr Lys Leu Asp Arg Glu Leu Arg Gly
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Leu Asp Asp Ile Lys Asp Leu Lys Val Gly Ser Val Glu Glu Phe Gln
          145          150          155          160
Gly Gln Glu Arg Ser Val Ile Leu Ile Ser Thr Val Arg Ser Ser Gln
          165          170          175
Ser Phe Val Gln Leu Asp Leu Asp Phe Asn Leu Gly Phe Leu Lys Asn
          180          185          190
Pro Lys Arg Phe Asn Val Ala Val Thr Arg Ala Lys Ala Leu Leu Ile
          195          200          205
Ile Val Gly Asn Pro Leu Leu Leu Gly His Asp Pro Asp Trp Lys Val
          210          215          220
Phe Leu Glu Phe Cys Lys Glu Asn Gly Gly Tyr Thr Gly Cys Pro Phe
          225          230          235          240
Pro Ala Lys Leu Asp Leu Gln Gln Gly Gln Asn Leu Leu Gln Gly Leu
          245          250          255
Ser Lys Leu Ser Pro Ser Thr Ser Gly Pro His Ser His Asp Tyr Leu
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Pro Gln Glu Arg Glu Gly Glu Gly Gly Leu Ser Leu Gln Val Glu Pro
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<210> 3797

<211> 1970

<212> DNA

<213> Homo sapiens

<400> 3797

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180

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 1970

<210> 3798

<211> 473

<212> PRT

<213> Homo sapiens

<400> 3798

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		20						25					30		
His	Trp	Trp	Ser	Glu	Arg	Thr	His	Lys	Asn	Leu	Ser	Asp	Met	Glu	Asn
		35					40					45			
Glu	Phe	Tyr	Tyr	Arg	Tyr	Pro	Ser	Phe	Gln	Asp	Val	His	Val	Met	Val
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Phe	Val	Gly	Phe	Gly	Phe	Leu	Met	Thr	Phe	Leu	Gln	Arg	Tyr	Gly	Phe
65					70					75				80	
Ser	Ala	Val	Gly	Phe	Asn	Phe	Leu	Leu	Ala	Ala	Phe	Gly	Ile	Gln	Trp
			85						90					95	
Ala	Leu	Leu	Met	Gln	Gly	Trp	Phe	His	Phe	Leu	Gln	Asp	Arg	Tyr	Ile
			100					105					110		
Val	Val	Gly	Val	Glu	Asn	Leu	Ile	Asn	Ala	Asp	Phe	Cys	Val	Ala	Ser
		115					120					125			
Val	Cys	Val	Ala	Phe	Gly	Ala	Val	Leu	Gly	Lys	Val	Ser	Pro	Ile	Gln
		130				135					140				
Leu	Leu	Ile	Met	Thr	Phe	Phe	Gln	Val	Thr	Leu	Phe	Ala	Val	Asn	Glu
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Phe	Ile	Leu	Leu	Asn	Leu	Leu	Lys	Val	Lys	Asp	Ala	Gly	Gly	Ser	Met
			165						170					175	
Thr	Ile	His	Thr	Phe	Gly	Ala	Tyr	Phe	Gly	Leu	Thr	Val	Thr	Arg	Ile
		180						185					190		
Leu	Tyr	Arg	Arg	Asn	Leu	Glu	Gln	Ser	Lys	Glu	Arg	Gln	Asn	Ser	Val
		195					200					205			
Tyr	Gln	Ser	Asp	Leu	Phe	Ala	Met	Ile	Gly	Thr	Leu	Phe	Leu	Trp	Met
		210				215					220				
Tyr	Trp	Pro	Ser	Phe	Asn	Ser	Ala	Ile	Ser	Tyr	His	Gly	Asp	Ser	Gln
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			245						250					255	
Thr	Ser	Val	Ala	Ile	Ser	Ser	Ala	Leu	His	Lys	Lys	Gly	Lys	Leu	Asp
			260					265					270		
Met	Val	His	Ile	Gln	Asn	Ala	Thr	Leu	Ala	Gly	Gly	Val	Ala	Val	Gly
		275					280					285			
Thr	Ala	Ala	Glu	Met	Met	Leu	Met	Pro	Tyr	Gly	Ala	Leu	Ile	Ile	Gly
		290					295					300			
Phe	Val	Cys	Gly	Ile	Ile	Ser	Thr	Leu	Gly	Phe	Val	Tyr	Leu	Thr	Pro
305					310					315				320	
Phe	Leu	Glu	Ser	Arg	Leu	His	Ile	Gln	Asp	Thr	Cys	Gly	Ile	Asn	Asn

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          325          330          335
Leu His Gly Ile Pro Gly Ile Ile Gly Gly Ile Val Gly Ala Val Thr
          340          345          350
Ala Ala Ser Ala Ser Leu Glu Val Tyr Gly Lys Glu Gly Leu Val His
          355          360          365
Ser Phe Asp Phe Gln Gly Phe Asn Gly Asp Trp Thr Ala Arg Thr Gln
          370          375          380
Gly Lys Phe Gln Ile Tyr Gly Leu Leu Val Thr Leu Ala Met Ala Leu
385          390          395          400
Met Gly Gly Ile Ile Val Gly Leu Ile Leu Arg Leu Pro Phe Trp Gly
          405          410          415
Gln Pro Ser Asp Glu Asn Cys Phe Glu Asp Ala Val Tyr Trp Glu Met
          420          425          430
Pro Glu Gly Asn Ser Thr Val Tyr Ile Pro Glu Asp Pro Thr Phe Lys
          435          440          445
Pro Ser Gly Pro Ser Val Pro Ser Val Pro Met Val Ser Pro Leu Pro
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Met Ala Ser Ser Val Pro Leu Val Pro
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<210> 3799
 <211> 210
 <212> DNA
 <213> Homo sapiens

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<400> 3799
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120
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210

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<210> 3800
 <211> 70
 <212> PRT
 <213> Homo sapiens

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<400> 3800
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20     25     30
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35     40     45
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Lys Asp Lys Arg Arg Lys
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<210> 3801
 <211> 4070

<212> DNA

<213> Homo sapiens

<400> 3801

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 3960
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<210> 3802

<211> 476

<212> PRT

<213> Homo sapiens

<400> 3802

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Pro	Glu	Ile	Gln	Lys	Pro	Glu	Arg	Lys	Ile	Gln	Phe	Lys	Glu	Lys	Val
			20					25					30		
Leu	Trp	Thr	Ala	Ile	Thr	Leu	Phe	Ile	Phe	Leu	Val	Cys	Cys	Gln	Ile
			35					40				45			
Pro	Leu	Phe	Gly	Ile	Met	Ser	Ser	Asp	Ser	Ala	Asp	Pro	Phe	Tyr	Trp
			50			55					60				
Met	Arg	Val	Ile	Leu	Ala	Ser	Asn	Arg	Gly	Thr	Leu	Met	Glu	Leu	Gly
65				70						75				80	
Ile	Ser	Pro	Ile	Val	Thr	Ser	Gly	Leu	Ile	Met	Gln	Leu	Leu	Ala	Gly
				85					90					95	
Ala	Lys	Ile	Ile	Glu	Val	Gly	Asp	Thr	Pro	Lys	Asp	Arg	Ala	Leu	Phe
				100				105					110		
Asn	Gly	Ala	Gln	Lys	Leu	Phe	Gly	Met	Ile	Ile	Thr	Ile	Gly	Gln	Ser

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Ile Val Tyr Val Met Thr Gly Met Tyr Gly Asp Pro Ser Glu Met Gly
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Ala Gly Ile Cys Leu Leu Ile Ile Ile Gln Leu Phe Val Ala Gly Leu
145              150              155              160
Ile Val Leu Leu Leu Asp Glu Leu Leu Gln Lys Gly Tyr Gly Leu Gly
      165              170              175
Ser Gly Ile Ser Leu Phe Ile Ala Thr Asn Ile Cys Glu Thr Ile Val
      180              185              190
Trp Lys Ala Phe Ser Pro Thr Thr Ile Asn Thr Gly Arg Gly Thr Glu
      195              200              205
Phe Glu Gly Ala Val Ile Ala Leu Phe His Leu Leu Ala Thr Arg Thr
      210              215              220
Asp Lys Val Arg Ala Leu Arg Glu Ala Phe Tyr Arg Gln Asn Leu Pro
225              230              235              240
Asn Leu Met Asn Leu Ile Ala Thr Ile Phe Val Phe Ala Val Val Ile
      245              250              255
Tyr Phe Gln Gly Phe Arg Val Asp Leu Pro Ile Lys Ser Ala Arg Tyr
      260              265              270
Arg Gly Gln Tyr Asn Thr Tyr Pro Ile Lys Leu Phe Tyr Thr Ser Asn
      275              280              285
Ile Pro Ile Ile Leu Gln Ser Ala Leu Val Ser Asn Leu Tyr Val Ile
      290              295              300
Ser Gln Met Leu Ser Ala Arg Phe Ser Gly Asn Phe Leu Val Asn Leu
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Leu Gly Gln Trp Ser Asp Thr Ser Ser Gly Gly Pro Ala Arg Ala Tyr
      325              330              335
Pro Val Gly Gly Leu Cys Tyr Tyr Leu Ser Pro Pro Glu Ser Phe Gly
      340              345              350
Ser Val Leu Glu Asp Pro Val His Ala Val Val Tyr Ile Val Phe Met
      355              360              365
Leu Gly Ser Cys Ala Phe Phe Ser Lys Thr Trp Ile Glu Val Ser Gly
      370              375              380
Ser Ser Ala Lys Asp Val Ala Lys Gln Leu Lys Glu Gln Gln Met Val
385              390              395              400
Met Arg Gly His Arg Glu Thr Ser Met Val His Glu Leu Asn Arg Tyr
      405              410              415
Ile Pro Thr Ala Ala Ala Phe Gly Gly Leu Cys Ile Gly Ala Leu Ser
      420              425              430
Val Leu Ala Asp Phe Leu Gly Ala Ile Gly Ser Gly Thr Gly Ile Leu
      435              440              445
Leu Ala Val Thr Ile Ile Tyr Gln Tyr Phe Glu Ile Phe Val Lys Glu
      450              455              460
Gln Ser Glu Val Gly Ser Met Gly Ala Leu Leu Phe
465              470              475

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<210> 3803

<211> 345

<212> DNA

<213> Homo sapiens

<400> 3803

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 gaagcttatt cacgtatgag tcatgcattg gaagagatta aaaaattcct ggttcctgac
 240
 tacaatgatg aaattcgtca ggaacaacta cgtgaattat cttacttaaa tggctcagag
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 345

<210> 3804
 <211> 115
 <212> PRT
 <213> Homo sapiens

<400> 3804
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 Glu Leu Arg Lys Ser Gly Glu Ala Lys Tyr Ala His Leu Ser Asp Glu
 35 40 45
 Leu His Val Leu Ile Glu Val Phe Ala Pro Pro Gly Glu Ala Tyr Ser
 50 55 60
 Arg Met Ser His Ala Leu Glu Glu Ile Lys Lys Phe Leu Val Pro Asp
 65 70 75 80
 Tyr Asn Asp Glu Ile Arg Gln Glu Gln Leu Arg Glu Leu Ser Tyr Leu
 85 90 95
 Asn Gly Ser Glu Asp Ser Gly Arg Gly Arg Gly Ile Arg Gly Arg Gly
 100 105 110
 Ile Arg Ile
 115

<210> 3805
 <211> 1923
 <212> DNA
 <213> Homo sapiens

<400> 3805
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 120
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<211> 280
 <212> PRT
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<400> 3806

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 35 40 45
 Ser Tyr His Pro Ala Pro Ser Gly Arg Gly Ser Ala Pro Ser Pro Arg
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 35 40 45
 Arg Gly Thr Arg Thr Arg Pro Ser Thr Ser Ser Pro Trp Ser Leu Ala
 50 55 60
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<211> 294

<212> PRT

<213> Homo sapiens

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Ser	Pro	Leu	Val	Leu	Leu	Glu	Phe	Gln	Cys	Pro	Thr	Pro	Gln	Ile	Cys
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Ser	Arg	Asp	Phe	Glu	Tyr	Tyr	Lys	Gln	Phe	Cys	Val	Pro	Gly	Phe	Lys
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Val	Leu	Ile	Pro	Ser	Lys	Pro	Leu	Ala	Arg	Arg	Cys	Phe	Pro	Ala	Ile
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His	Ala	Tyr	Lys	Gly	Val	Leu	Met	Val	Gly	Asn	Glu	Thr	Thr	Tyr	Glu
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Tyr	Gly	Gly	Glu	Ser	Gly	Tyr	His	Arg	Ala	Leu	Leu	Gly	Leu	Gln	Ile
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Phe	Asn	Ala	Phe	Met	Phe	Phe	Trp	Leu	Ala	Asn	Phe	Val	Leu	Ala	Leu
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 <212> DNA
 <213> Homo sapiens

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<213> Homo sapiens

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      35             40             45
Ile Arg Lys Leu Arg Gln Asp Ile Leu Leu Met Lys Pro Tyr Phe Ile
      50             55             60
Thr Cys Arg Glu Ala Met Glu Ala Arg Leu Leu Leu Gln Asp Leu Leu
      65             70             75             80
Asp Val His Ala Gly Arg Leu Gly Cys Ser Leu Thr Glu Ile His Thr
      85             90             95
Leu Phe Ala Lys His Ile Lys Leu Asp Cys Glu Arg Cys Gln Ala Lys
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<212> PRT

<213> Homo sapiens

<400> 3820

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			20					25					30		
Tyr	Phe	Phe	Thr	Asn	Cys	Ser	Ile	Ser	Phe	Thr	Ser	Leu	Gly	Asp	Asn
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Ser	Trp	His	Phe	Glu	Gly	Ser	Trp	Ser	Cys	Ala	Gly	Ser	Cys	Phe	Ala
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Ser	Cys	Phe	Phe	Arg	Tyr	Cys	Ala	Pro	Ser	Glu	Pro	Ala	Thr	Gly	Arg
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Arg	Lys	Phe	Asp	Gly	Ala	Gly	Arg	Val	Ala	Val	Glu	Arg	Arg	Arg	Gly
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Ser	Ser	Ala	Gly	Phe	Pro	Cys	Ser	Gln	Arg	Ser	Arg	Arg	Pro	Ala	Glu
			100					105					110		
Pro	Gly	Arg	Gly	Ile	Thr	Asp	Arg	Arg	Arg	Gly	Pro	Ile	Gly	Arg	

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275	280	285
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290	295	300
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Gln Asn Trp His Leu Lys His Phe Cys Cys Phe Asp Cys Asp Ser Ile		
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Leu Ala Gly Glu Ile Tyr Val Met Val Asn Asp Lys Pro Val Cys Lys		
465	470	475
Pro Cys Tyr Val Lys Asn His Ala Val Val Arg Ser Val Leu Arg Ile		
485	490	495
Trp Leu Pro Gln Pro Ala Leu Gly Leu Glu Phe Met Leu Phe Leu Lys		
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<211> 375

<212> PRT

<213> Homo sapiens

<400> 3822

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			35				40					45			
Arg	Ser	Asp	Leu	Val	Leu	Pro	Phe	Leu	Pro	Arg	Ala	Arg	Ala	Glu	Arg
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Thr	Val	Met	Arg	Gln	Asp	Asn	Arg	Asp	Thr	Val	Asp	Asp	Thr	Val	Ser
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Ser	Glu	Ser	Leu	Gln	Ser	Leu	Phe	Ser	Glu	Trp	Asp	Asn	Pro	Val	Phe
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Asp	Ser	Tyr	Glu	Lys	Gln	Gln	Ala	Gln	Gly	Ser	Gly	Arg	Lys	Lys	Leu
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Leu	Ser	Ser	Thr	Leu	Ile	Pro	Pro	Leu	Glu	Ile	Thr	Val	Thr	Glu	Glu
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Gln	Arg	Arg	Leu	Leu	Trp	Cys	Tyr	His	Lys	Asn	Leu	Glu	Asp	Leu	Gly
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Leu	Glu	Phe	Val	Phe	Pro	Asp	Thr	Ser	Asp	Ser	Leu	Val	Leu	Val	Gly
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Lys	Val	Pro	Leu	Cys	Phe	Val	Glu	Arg	Glu	Ala	Asn	Glu	Leu	Arg	Arg

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          260          265          270
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          275          280          285
Lys Phe Asn Asp Gly Leu Ser Leu Gln Glu Ser Cys Arg Leu Ile Glu
          290          295          300
Ala Leu Ser Ser Cys Gln Leu Pro Phe Gln Cys Ala His Gly Arg Pro
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Ser Met Leu Pro Leu Ala Asp Ile Asp His Leu Glu Gln Glu Lys Gln
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<210> 3823

<211> 6280

<212> DNA

<213> Homo sapiens

<400> 3823

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<210> 3829

<211> 5713<212> DNA

<213> Homo sapiens

<400> 3829

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<211> 444

<212> PRT

<213> Homo sapiens

<400> 3830

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			20				25					30			
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Glu Asn Thr Pro Phe Val Pro Asp Met Ile Ala Ser Asn Phe Leu His
      85              90              95
Ala Tyr Ile Val Val Gln Val Glu Thr Pro Gly Thr Glu Thr Pro Ser
      100              105              110
Tyr Lys Val Ser Val Thr Ala Arg Glu Asp Val Pro Thr Phe Gly Pro
      115              120              125
Pro Leu Pro Ser Pro Pro Val Phe Gln Lys Gly Pro Glu Phe Arg Glu
      130              135              140
Phe Leu Leu Thr Lys Leu Thr Asn Ala Glu Asn Ala Cys Cys Lys Ser
  145              150              155              160
Asp Lys Phe Ala Lys Leu Glu Asp Arg Thr Arg Ala Ala Leu Leu Asp
      165              170              175
Asn Leu His Asp Glu Leu His Ala His Thr Gln Ala Met Leu Gly Leu
      180              185              190
Gly Pro Glu Glu Asp Lys Phe Glu Asn Gly Gly His Gly Gly Phe Leu
      195              200              205
Glu Ser Phe Lys Arg Ala Ile Arg Val Arg Ser His Ser Met Glu Thr
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      355              360              365
Glu Glu Gly Asp Ser Gly Gly Ser Gln Pro Ser Thr Thr Ser Pro Phe
      370              375              380
Lys Gln Glu Val Phe Val Tyr Ser Pro Ser Pro Ser Ser Glu Ser Pro
  385              390              395              400
Ser Leu Gly Ala Ala Ala Thr Pro Ile Ile Met Ser Arg Ser Pro Thr
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Asp Lys Leu Ser His Ala Ser Ser Gly Ala Gly His
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<210> 3831

<211> 726

<212> DNA

<213> Homo sapiens

<400> 3831

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<210> 3832

<211> 107

<212> PRT

<213> Homo sapiens

<400> 3832

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Leu Ser Ser Ala Leu Ala Cys Tyr Gly Leu Ser Phe Leu Gln Leu His
35     40     45
Ser Thr Asn Ser His Ile Asp Arg Ile Asn Phe Ser Val Lys Met Val
50     55     60
Ser Ser Ile Leu Gln Ile Pro Lys Leu Ser Tyr Leu Gly Leu Gly Asp
65     70     75     80
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<210> 3833

<211> 1764

<212> DNA

<213> Homo sapiens

<400> 3833

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<210> 3834

<211> 361

<212> PRT

<213> Homo sapiens

<400> 3834

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			20					25					30		
Val	Ser	Val	Cys	Asp	His	Cys	Lys	Gly	Lys	Met	Gln	Leu	Val	Ala	Asp
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			180					185					190		
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		275					280					285			
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<210> 3835

<211> 2366

<212> DNA

<213> Homo sapiens

<400> 3835

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<210> 3836

<211> 479

<212> PRT

<213> Homo sapiens

<400> 3836

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Val Leu Phe Met Val Tyr Gly Asn Val His Val Ser Thr Glu Ser Asn
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Leu Gln Ala Thr Glu Arg Arg Ala Glu Gly Leu Tyr Ser Gln Leu Leu
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Gly Leu Thr Ala Ser Gln Ser Asn Leu Thr Lys Glu Leu Asn Phe Thr
      115      120      125
Thr Arg Ala Lys Asp Ala Ile Met Gln Met Trp Leu Asn Ala Arg Arg
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Asp Leu Asp Arg Ile Asn Ala Ser Phe Arg Gln Cys Gln Gly Asp Arg
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Val Ile Tyr Thr Asn Asn Gln Arg Tyr Met Ala Ala Ile Ile Leu Ser
      165      170      175
Glu Lys Gln Cys Arg Asp Gln Phe Lys Asp Met Asn Lys Ser Cys Asp
      180      185      190
Ala Leu Leu Phe Met Leu Asn Gln Lys Val Lys Thr Leu Glu Val Glu
      195      200      205
Ile Ala Lys Glu Lys Thr Ile Cys Thr Lys Asp Lys Glu Ser Val Leu
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Leu Asn Lys Arg Val Ala Glu Glu Gln Leu Val Glu Cys Val Lys Thr
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Arg Glu Leu Gln His Gln Glu Arg Gln Leu Ala Lys Glu Gln Leu Gln
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Asp Leu Arg Asn Leu Trp Arg Asp Ser Ile Ile Pro Arg Ser Leu Asp
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Asn Leu Gly Tyr Asn Leu Tyr His Pro Leu Gly Ser Glu Leu Ala Ser
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Ile Arg Arg Ala Cys Asp His Met Pro Ser Leu Met Ser Ser Lys Val
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Glu Glu Leu Ala Arg Ser Leu Arg Ala Asp Ile Glu Arg Val Ala Arg
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Glu Asn Ser Asp Leu Gln Arg Gln Lys Leu Glu Ala Gln Gln Gly Leu
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Arg Ala Ser Gln Glu Ala Lys Gln Lys Val Glu Lys Glu Ala Gln Ala
      355      360      365
Arg Glu Ala Lys Leu Gln Ala Glu Cys Ser Arg Gln Thr Gln Leu Ala
      370      375      380
Leu Glu Glu Lys Ala Val Leu Arg Lys Glu Arg Asp Asn Leu Ala Lys
  385      390      395      400
Glu Leu Glu Glu Lys Lys Arg Glu Ala Glu Gln Leu Arg Met Glu Leu
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Ala Ile Arg Asn Ser Ala Leu Asp Thr Cys Ile Lys Thr Lys Ser Gln
      420      425      430
Pro Met Met Pro Val Ser Arg Pro Met Gly Pro Val Pro Asn Pro Gln
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465

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<210> 3837

<211> 2084

<212> DNA

<213> Homo sapiens

<400> 3837

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<210> 3838

<211> 468

<212> PRT

<213> Homo sapiens

<400> 3838

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			20					25					30		
Ser	His	Leu	Pro	Pro	Glu	His	Ser	Asp	Val	Val	Ile	Val	Gly	Gly	Gly
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Val	Leu	Gly	Leu	Ser	Val	Ala	Tyr	Trp	Leu	Lys	Lys	Leu	Glu	Ser	Arg
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Arg	Gly	Ala	Ile	Arg	Val	Leu	Val	Val	Glu	Arg	Asp	His	Thr	Tyr	Ser
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 210 215 220
 Ser Ser Gln Arg Met Leu Thr Thr Asp Asp Lys Ala Val Val Leu Lys
 225 230 235 240
 Arg Ile His Glu Val His Val Lys Met Asp Arg Ser Leu Glu Tyr Gln
 245 250 255
 Pro Val Glu Cys Ala Ile Val Ile Asn Ala Ala Gly Ala Trp Ser Ala
 260 265 270
 Gln Ile Ala Ala Leu Ala Gly Val Gly Glu Gly Pro Pro Gly Thr Leu
 275 280 285
 Gln Gly Thr Lys Leu Pro Val Glu Pro Arg Lys Arg Tyr Val Tyr Val
 290 295 300
 Trp His Cys Pro Gln Gly Pro Gly Leu Glu Thr Pro Leu Val Ala Asp
 305 310 315 320
 Thr Ser Gly Ala Tyr Phe Arg Arg Glu Gly Leu Gly Ser Asn Tyr Leu
 325 330 335
 Gly Gly Arg Ser Pro Thr Glu Gln Glu Glu Pro Asp Pro Ala Asn Leu
 340 345 350
 Glu Val Asp His Asp Phe Phe Gln Asp Lys Val Trp Pro His Leu Ala
 355 360 365
 Leu Arg Val Pro Ala Phe Glu Thr Leu Lys Cys Phe Val His Pro Gln
 370 375 380
 Val Gln Ser Ala Trp Ala Gly Tyr Tyr Asp Tyr Asn Thr Phe Asp Gln
 385 390 395 400
 Asn Gly Val Val Gly Pro His Pro Leu Val Val Asn Met Tyr Phe Ala
 405 410 415
 Thr Gly Phe Ser Gly His Gly Leu Gln Gln Ala Pro Gly Ile Gly Arg
 420 425 430
 Ala Val Ala Glu Met Val Leu Lys Gly Arg Phe Gln Thr Ile Asp Leu
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<210> 3839

<211> 758

<212> DNA

<213> Homo sapiens

<400> 3839

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<211> 252

<212> PRT

<213> Homo sapiens

<400> 3840

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Met	Glu	Tyr	Leu	Asn	Ser	Arg	Cys	Val	Leu	Phe	Thr	Tyr	Phe	Gln	Gly
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Asp	Ile	Gly	Ser	Val	Val	Asp	Glu	His	Phe	Ser	Arg	Ala	Leu	Gly	Gln
50					55					60					
Ala	Ile	Thr	Leu	His	Pro	Glu	Ser	Ala	Ile	Ser	Lys	Ser	Lys	Met	Gly
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Leu	Thr	Pro	Leu	Trp	Arg	Asp	Ser	Ser	Ala	Leu	Ser	Ser	Gln	Arg	Asn
			85					90					95		
Ser	Phe	Pro	Thr	Ser	Phe	Trp	Thr	Ser	Ser	Tyr	Gln	Pro	Pro	Pro	Ala
		100					105					110			
Pro	Cys	Leu	Gly	Gly	Val	His	Pro	Asp	Phe	Gln	Val	Thr	Gly	Pro	Pro
	115					120				125					
Gly	Thr	Phe	Ser	Ala	Ala	Asp	Pro	Ser	Pro	Trp	Pro	Gly	His	Asn	Leu
130					135					140					
His	Gln	Thr	Gly	Pro	Ala	Pro	Pro	Pro	Ala	Val	Ser	Glu	Ser	Trp	Pro
145				150					155					160	
Tyr	Pro	Leu	Thr	Ser	Gln	Val	Ser	Pro	Ser	Tyr	Ser	His	Met	His	Asp
			165				170					175			
Val	Tyr	Met	Arg	His	His	His	Pro	His	Ala	His	Met	His	His	Arg	His
		180					185					190			
Arg	His	His	His	His	His	His	His	Pro	Pro	Ala	Gly	Ser	Ala	Leu	Asp
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Pro	Ser	Tyr	Gly	Pro	Leu	Leu	Met	Pro	Ser	Val	His	Ala	Ala	Arg	Ile
	210				215					220					
Pro	Ala	Pro	Gln	Cys	Asp	Ile	Thr	Lys	Thr	Glu	Pro	Thr	Thr	Val	Thr
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 <211> 367
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 <213> Homo sapiens

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 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Glu His Pro Asn Asp Val Arg Cys Ser Ser Thr Leu Val Thr His Ser
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 Lys Gly Tyr Glu Asn Gly Thr Asn Arg Leu Ser Leu Pro Lys Pro Ile
 65 70 75 80
 Leu Lys Ser Glu Lys Asn Lys Pro Leu Asp Pro Glu Met Gln Cys Leu
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<210> 3843
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 <213> Homo sapiens

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 Ala Pro Gly Ala Glu Ala Ser Pro Ser Pro Cys Ile Thr Glu Arg Ser
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 Lys Gln Lys Ala Arg Arg Thr Arg Ser Ser Ser Ser Ser Ser
 65 70 75 80
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 85 90 95
 Ser Ser Asp Gly Arg Lys Lys Arg Gly Lys Tyr Lys Asp Lys Arg Arg
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<210> 3845
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 <212> DNA
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<400> 3845

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<210> 3846

<211> 197

<212> PRT

<213> Homo sapiens

<400> 3846

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			20					25					30		
Gly	Pro	Ala	Glu	Pro	Arg	Val	Ala	Gly	Ala	Gly	Ala	Ala	Ala	Ala	Glu
		35					40					45			
Gly	Ala	Ala	Ala	Gly	Ala	Cys	Gly	Pro	Ala	Arg	Cys	Ala	Asp	Gln	Gly
		50				55					60				
Gly	Ala	Arg	Glu	Arg	Gly	Gly	Arg	Gly	Gly	Arg	Gly	Ala	Gly	Gly	Gly
65					70					75				80	
Gly	Gly	Ala	His	Gly	His	Phe	Pro	Gln	Arg	Pro	Pro	Gln	Gln	Ala	Gly
			85						90					95	
Gln	Arg	Ala	Ala	Ser	Arg	Ala	Gly	Cys	Gly	His	Arg	Gln	Leu	Gln	Arg
			100					105					110		
Ala	Pro	Ala	Pro	Gly	Leu	Arg	Gln	His	Pro	Cys	Gly	Ser	Gly	Thr	Glu
		115					120					125			
Gly	Leu	Arg	Gly	Gly	His	Leu	Ser	Glu	Thr	Val	Cys	Ala	His	Ala	Glu
	130					135					140				
Arg	Thr	Gln	Ala	Pro	Leu	Gln	Ser	Ala	Leu	Gly	Gln	Pro	Ala	Pro	Arg
145					150					155				160	
Pro	His	Thr	Leu	Gln	Arg	His	Leu	Gly	Pro	His	Ala	Thr	Gly	His	Gly
			165					170					175		
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185

190

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<212> DNA
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 <211> 120
 <212> PRT
 <213> Homo sapiens

<400> 3848
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 35 40 45
 Met Asp Asn Val Cys Ile Ile Cys Arg Glu Glu Met Val Thr Gly Ala
 50 55 60
 Lys Arg Leu Pro Cys Asn His Ile Phe His Thr Arg Trp Glu Gly Pro
 65 70 75 80
 Trp Gly Ala Cys Pro Ala Gly Pro Arg Pro Gln Lys Ala Gly Pro Lys
 85 90 95
 Gly Pro Ala Asp Leu Cys Leu Ala Leu Thr Arg Ser Cys Leu Arg Ser
 100 105 110
 Trp Phe Gln Arg Gln Gln Thr Cys
 115 120

<210> 3849
 <211> 1139
 <212> DNA
 <213> Homo sapiens

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<213> Homo sapiens
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Leu	Cys	Ile	Arg	Val	Phe	Gln	Glu	Thr	Gln	Lys	Leu	Lys	Lys	Arg	Arg
	210					215					220				
Arg	Ala	Leu	Lys	Ala	Ala	Ala	Ala	Gln	Lys	Gln	Ala	Lys	Arg	Arg	
225				230					235				240		
Asn	Pro	Asp	Ser	Pro	Ala	Lys	Ala	Ile	Pro	Lys	Thr	Leu	Lys	Asp	Ser
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<210> 3851

<211> 1183

<212> DNA

<213> Homo sapiens

<400> 3851

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1080

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 1183

<210> 3852

<211> 323

<212> PRT

<213> Homo sapiens

<400> 3852

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Val	Leu	Val	Val	Leu	Leu	Val	Val	Ile	Val	Val	Leu	Ala	Phe	Asn	Tyr
			20					25					30		
Trp	Ser	Ile	Ser	Ser	Arg	His	Val	Leu	Leu	Gln	Glu	Glu	Val	Ala	Glu
		35				40						45			
Leu	Gln	Gly	Gln	Val	Gln	Arg	Thr	Glu	Val	Ala	Arg	Gly	Arg	Leu	Glu
		50				55					60				
Lys	Arg	Asn	Ser	Asp	Leu	Leu	Leu	Val	Asp	Thr	His	Lys	Lys	Gln	
65				70					75					80	
Ile	Asp	Gln	Lys	Glu	Ala	Asp	Tyr	Gly	Arg	Leu	Ser	Ser	Arg	Leu	Gln
			85					90					95		
Ala	Arg	Glu	Gly	Leu	Gly	Lys	Arg	Cys	Glu	Asp	Asp	Lys	Val	Lys	Leu
			100					105					110		
Gln	Asn	Asn	Ile	Ser	Tyr	Gln	Met	Ala	Asp	Ile	His	His	Leu	Lys	Glu
		115					120					125			
Gln	Leu	Ala	Glu	Leu	Arg	Gln	Glu	Phe	Leu	Arg	Gln	Glu	Asp	Gln	Leu
		130				135					140				
Gln	Asp	Tyr	Arg	Lys	Asn	Asn	Thr	Tyr	Leu	Val	Lys	Arg	Leu	Glu	Tyr
145				150					155					160	
Glu	Ser	Phe	Gln	Cys	Gly	Gln	Gln	Met	Lys	Glu	Leu	Arg	Ala	Gln	His
			165					170					175		
Glu	Glu	Asn	Ile	Lys	Lys	Leu	Ala	Asp	Gln	Phe	Leu	Glu	Glu	Gln	Lys
		180						185					190		
Gln	Glu	Thr	Gln	Lys	Ile	Gln	Ser	Asn	Asp	Gly	Lys	Glu	Leu	Asp	Ile
		195				200					205				
Asn	Asn	Gln	Val	Val	Pro	Lys	Asn	Ile	Pro	Lys	Val	Ala	Glu	Asn	Val
		210				215					220				
Ala	Asp	Lys	Asn	Glu	Glu	Pro	Ser	Ser	Asn	His	Ile	Pro	His	Gly	Lys
225				230					235					240	
Glu	Gln	Ile	Lys	Arg	Gly	Gly	Asp	Ala	Gly	Met	Pro	Gly	Ile	Glu	Glu
			245					250					255		
Asn	Asp	Leu	Ala	Lys	Val	Asp	Asp	Leu	Pro	Pro	Ala	Leu	Arg	Lys	Pro
		260						265					270		
Pro	Ile	Ser	Val	Ser	Gln	His	Glu	Ser	His	Gln	Ala	Ile	Ser	His	Leu
		275					280					285			
Pro	Thr	Gly	Gln	Pro	Leu	Ser	Pro	Asn	Met	Pro	Pro	Asp	Ser	His	Ile
		290				295					300				
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 <211> 375
 <212> DNA
 <213> Homo sapiens

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<210> 3854
 <211> 125
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Leu Ser Glu Cys Tyr Arg Gly Phe Ala Asp Ser Glu Arg Lys Val Ile
 50 55 60
 Pro Ile Ile Ser Lys Cys Leu Glu Gly Met Ile Leu Ala Ala Lys Ser
 65 70 75 80
 Val Asp Glu Arg Arg Asp Ser Gln Met Val Val Asp Ser Phe Lys Ser
 85 90 95
 Gly Phe Glu Pro Pro Gly Asp Phe Pro Phe Glu Asp Tyr Ser Gln His
 100 105 110
 Ile Tyr Arg Thr Ile Ser Asp Gly Thr Ile Ser Ala Ser
 115 120 125

<210> 3855
 <211> 1377
 <212> DNA
 <213> Homo sapiens

<400> 3855
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cagaactgtg gctctgggtg ggttgggata gtggactatg gacctagacc caacaagagt
 180
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 360
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 420
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 480
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<210> 3856

<211> 330

<212> PRT

<213> Homo sapiens

<400> 3856

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			20					25					30		
Ala	Tyr	Pro	Thr	Ala	Phe	Ala	Ser	Gln	Asn	Cys	Gly	Ser	Gly	Val	Val

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  65      70      75      80
Tyr Val Gly Asp Gly Phe Ser Cys Ser Gly Asn Leu Leu Gln Val Leu
      85      90      95
Met Ser Phe Pro Ser Leu Thr Asn Phe Leu Thr Glu Val Leu Ala Tyr
      100      105      110
Ser Asn Ser Ser Ala Arg Gly Arg Ala Phe Leu Glu His Leu Thr Asp
      115      120      125
Leu Ser Ile Arg Gly Thr Leu Phe Val Pro Gln Asn Ser Gly Leu Gly
      130      135      140
Glu Asn Glu Thr Leu Ser Gly Arg Asp Ile Glu His His Leu Ala Asn
  145      150      155      160
Val Ser Met Phe Phe Tyr Asn Asp Leu Val Asn Gly Thr Xaa Pro Ala
      165      170      175
Asn Glu Gly Gly Lys Gln Ala Ala His His Cys Gln Pro Gly Pro Thr
      180      185      190
Xaa Gln Pro Thr Glu Thr Arg Phe Val Asp Gly Arg Ala Ile Leu Gln
      195      200      205
Trp Asp Ile Phe Ala Ser Asn Gly Ile Ile His Val Ile Ser Arg Pro
      210      215      220
Leu Lys Ala Pro Pro Ala Pro Val Thr Leu Thr His Thr Gly Leu Gly
  225      230      235      240
Ala Gly Ile Phe Phe Ala Ile Ile Leu Val Thr Gly Ala Val Ala Leu
      245      250      255
Ala Ala Tyr Ser Tyr Phe Arg Ile Asn Arg Arg Thr Ile Gly Phe Gln
      260      265      270
His Phe Glu Ser Glu Glu Asp Ile Asn Val Ala Ala Leu Gly Lys Gln
      275      280      285
Gln Pro Glu Asn Ile Ser Asn Pro Leu Tyr Glu Ser Thr Thr Ser Ala
      290      295      300
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<210> 3857

<211> 797

<212> DNA

<213> Homo sapiens

<400> 3857

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<212> PRT
<213> Homo sapiens
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<210> 3860

<211> 348

<212> PRT

<213> Homo sapiens

<400> 3860

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			20					25					30		
Asp	Cys	Asn	Glu	Thr	Ser	Phe	Phe	Phe	Glu	Ala	Arg	Ser	Lys	Thr	Ala
		35					40					45			
Cys	Lys	His	Leu	Trp	Lys	Cys	Ser	Val	Glu	His	His	Thr	Phe	Phe	Arg
	50					55					60				
Met	Pro	Glu	Asn	Glu	Ser	Asn	Ser	Leu	Ser	Arg	Lys	Leu	Ser	Lys	Phe


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65          70          75          80
Gly Ser Ile Arg Tyr Lys His Arg Tyr Ser Gly Arg Thr Ala Leu Gln
          85          90          95
Met Ser Arg Asp Leu Ser Ile Gln Leu Pro Arg Pro Asp Gln Asn Val
          100          105          110
Thr Arg Ser Arg Ser Lys Thr Tyr Pro Lys Arg Ile Ala Gln Thr Gln
          115          120          125
Pro Ala Glu Ser Asn Thr Ile Ser Arg Ile Thr Ala Asn Met Glu Asn
          130          135          140
Gly Glu Asn Glu Gly Thr Ile Lys Ile Ile Ala Pro Ser Pro Val Lys
145          150          155          160
Ser Phe Lys Lys Ala Lys Asn Glu Asn Ser Pro Asp Thr Gln Arg Ser
          165          170          175
Lys Ser His Ala Pro Trp Glu Glu Asn Gly Pro Gln Ser Gly Leu Tyr
          180          185          190
Asn Ser Pro Ser Asp Arg Thr Lys Ser Pro Lys Phe Pro Tyr Thr Arg
          195          200          205
Arg Arg Asn Pro Ser Cys Gly Ser Asp Asn Asp Ser Val Gln Pro Val
          210          215          220
Arg Arg Arg Lys Ala His Asn Ser Gly Glu Asp Ser Asp Leu Lys Gln
225          230          235          240
Arg Arg Arg Ser Arg Ser Arg Cys Asn Thr Ser Ser Gly Ser Glu Ser
          245          250          255
Glu Asn Ser Asn Arg Glu His Arg Lys Lys Arg Asn Arg Ile Arg Gln
          260          265          270
Glu Asn Asp Met Val Asp Ser Ala Pro Gln Trp Glu Ala Val Leu Arg
          275          280          285
Arg Gln Lys Glu Lys Asn Gln Ala Asp Pro Asn Asn Arg Arg Ser Arg
          290          295          300
His Arg Ser Arg Ser Arg Ser Pro Asp Ile Gln Ala Lys Glu Glu Leu
305          310          315          320
Trp Lys His Ile Gln Lys Glu Leu Val Asp Pro Ser Gly Leu Ser Glu
          325          330          335
Glu Gln Leu Lys Glu Ile Pro Tyr Thr Lys Ile Glu
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<210> 3861

<211> 748

<212> DNA

<213> Homo sapiens

<400> 3861

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240
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360

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caagccgtgc agcgcaacgg gcgcaccccc ggagttcagg cgcgcgacct ctttgcgcag
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 480
 gaaaacgtgc tgctgagccc ggacgagcgc cgcgtcaagc tcaccgactt cggcttcggc
 540
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 600
 acccgagtca tgcatttctt gagcacctac tgtctgcccag gccccagagc tcattggcgaa
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 748

<210> 3862

<211> 210

<212> PRT

<213> Homo sapiens

<400> 3862

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 20 25 30
 Lys Tyr Lys Gly Thr Val Ala Ile Lys Val Val Asp Arg Arg Arg Ala
 35 40 45
 Pro Pro Asp Phe Val Asn Lys Phe Leu Pro Arg Glu Leu Ser Ile Leu
 50 55 60
 Arg Gly Val Arg His Pro His Ile Val His Val Phe Glu Phe Ile Glu
 65 70 75 80
 Val Cys Asn Gly Lys Leu Tyr Ile Val Met Glu Ala Ala Ala Thr Asp
 85 90 95
 Leu Leu Gln Ala Val Gln Arg Asn Gly Arg Ile Pro Gly Val Gln Ala
 100 105 110
 Arg Asp Leu Phe Ala Gln Ile Ala Gly Ala Val Arg Tyr Leu His Asp
 115 120 125
 His His Leu Val His Arg Asp Leu Lys Cys Glu Asn Val Leu Leu Ser
 130 135 140
 Pro Asp Glu Arg Arg Val Lys Leu Thr Asp Phe Gly Phe Gly Arg Gln
 145 150 155 160
 Ala His Gly Tyr Pro Asp Leu Ser Thr Thr Tyr Cys Gly Ser Ala Val
 165 170 175
 Arg Val Thr Arg Val Met His Phe Leu Ser Thr Tyr Cys Leu Pro Gly
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 Pro Arg Ala His Gly Glu Glu Thr Trp Ala His Pro Cys Arg Lys Arg
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 Asp Asn
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<210> 3863

<211> 341

<212> DNA

<213> Homo sapiens

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 240
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<210> 3864
 <211> 108
 <212> PRT
 <213> Homo sapiens

<400> 3864
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 35 40 45
 Lys Asn Leu Val Glu Ile Ser His Thr Val Phe Phe Pro Glu Ser Gln
 50 55 60
 Leu Arg Ala Lys Leu Lys Cys Pro Gly Gly Ser Cys Thr Pro Gly Leu
 65 70 75 80
 Lys Lys Ile Gly Ser Leu Lys Val Ser Cys Glu Glu Phe Leu Leu Met
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 Gly Leu Arg Tyr Gln His Leu Asp Pro Pro Ser Arg
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<210> 3865
 <211> 492
 <212> DNA
 <213> Homo sapiens

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 gagacctatg tgaagccac ttaattttct gaaacttcac atcatgtacc ttcattgtaa
 180
 tattctgaca cttgtttcat gcagccatac cagtcacaac tttaaatttt tagtcagact
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 300
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 360

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<210> 3866

<211> 109

<212> PRT

<213> Homo sapiens

<400> 3866

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Ser	His	Asn	Phe	Lys	Phe	Leu	Val	Arg	Leu	Cys	Ser	Gln	Gly	Phe	Arg
		20						25				30			
Ile	Ile	Asn	Thr	Asn	Gly	Leu	Gly	Gln	Pro	Ser	His	Ser	Ser	Leu	Leu
		35				40					45				
Phe	Thr	Ser	Leu	Gln	Leu	Gln	Leu	Ser	Phe	Phe	Ile	Thr	Leu	Leu	Phe
	50				55					60					
Leu	Ser	Ser	Leu	Gly	Gln	Ile	Val	Gln	Thr	Glu	Tyr	Ser	Leu	Thr	Lys
65				70					75					80	
Met	Leu	Gly	Ser	Arg	Pro	Gly	Ala	Ala	Ala	His	Pro	Cys	Asn	Pro	Ser
				85				90						95	
Ile	Leu	Gly	Gly	Gln	Ser	Arg	Gln	Ile	Thr	Gln	Gly	Gln			
		100					105								

<210> 3867

<211> 1032

<212> DNA

<213> Homo sapiens

<400> 3867

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 240
 agaaagcgag agcgtgaact caccgccctg aaggagagccc tgaaagaaga ggtttccagc
 300
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 600

cgacagtttag aggaggccct tgtgcacgcc agaaaggaag aaaaagaagc tgtgtcagcc
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 720
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 840
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<210> 3868

<211> 344

<212> PRT

<213> Homo sapiens

<400> 3868

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		20						25					30		
Gln	Leu	Ser	Glu	Met	His	Asp	Glu	Leu	Asp	Ser	Ala	Lys	Arg	Ser	Glu
	35						40					45			
Asp	Arg	Glu	Lys	Gly	Ala	Leu	Ile	Glu	Glu	Leu	Leu	Gln	Ala	Lys	Gln
50					55					60					
Asp	Leu	Gln	Asp	Leu	Leu	Ile	Ala	Lys	Glu	Glu	Gln	Glu	Asp	Leu	Leu
65				70					75					80	
Arg	Lys	Arg	Glu	Arg	Glu	Leu	Thr	Ala	Leu	Lys	Gly	Ala	Leu	Lys	Glu
			85					90					95		
Glu	Val	Ser	Ser	His	Asp	Gln	Glu	Met	Asp	Lys	Leu	Lys	Glu	Gln	Tyr
		100						105					110		
Asp	Ala	Glu	Leu	Gln	Ala	Leu	Arg	Glu	Ser	Val	Glu	Glu	Ala	Thr	Lys
	115					120					125				
Asn	Val	Glu	Val	Leu	Ala	Ser	Arg	Ser	Asn	Thr	Ser	Glu	Gln	Asp	Gln
130					135				140						
Ala	Gly	Thr	Glu	Met	Arg	Val	Lys	Leu	Leu	Gln	Glu	Glu	Asn	Glu	Lys
145				150				155						160	
Leu	Gln	Gly	Arg	Ser	Glu	Glu	Leu	Glu	Arg	Arg	Val	Ala	Gln	Leu	Gln
			165					170					175		
Arg	Gln	Ile	Glu	Asp	Leu	Lys	Gly	Asp	Glu	Ala	Lys	Ala	Lys	Glu	Thr
		180						185					190		
Leu	Lys	Lys	Tyr	Glu	Gly	Glu	Ile	Arg	Gln	Leu	Glu	Glu	Ala	Leu	Val
	195					200						205			
His	Ala	Arg	Lys	Glu	Glu	Lys	Glu	Ala	Val	Ser	Ala	Arg	Arg	Ala	Leu
210					215					220					
Glu	Asn	Glu	Leu	Glu	Ala	Ala	Gln	Gly	Asn	Leu	Ser	Gln	Thr	Thr	Gln
225				230					235					240	
Glu	Gln	Lys	Gln	Leu	Ser	Glu	Lys	Leu	Lys	Glu	Glu	Ser	Glu	Gln	Lys

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<211> 1226
<212> DNA
<213> Homo sapiens
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120						
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180						
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240						
cactgataaa	tgccactggg	atcctaggag	aagctgggga	ccatgctga	ggtagtgaag	
300						
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360						
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420						
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900						
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960						
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1020						

gctctcggca gcctgcacgg cccggctcag ggccttggtg agctcctcta ggtcgcccag
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<210> 3870
 <211> 100
 <212> PRT
 <213> Homo sapiens

<400> 3870
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 20 25 30
 Leu Leu Gly Ser Gln Trp His Leu Ser Val Ala Ser Tyr Leu Pro Gly
 35 40 45
 Pro Gly Trp Gly Thr Val Cys Gly His Glu Ala Arg Pro Pro Pro Ala
 50 55 60
 Pro Leu Pro Arg Gly Ser Ser Ile Pro Leu His Phe Trp Asn Val Cys
 65 70 75 80
 Ala Ser Met Met Phe Val Tyr Leu Arg His Leu Lys Ile Tyr Phe Arg
 85 90 95
 Tyr Glu Gly Lys
 100

<210> 3871
 <211> 473
 <212> DNA
 <213> Homo sapiens

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 180
 taggctgagg gaaaatacaa agatgatcct gttgatctcc gccttgatat tgaacgtcgt
 240
 aaaaaacata aggagagaga tcttaaacga ggtaaatcga gagaatcagt ggattcccga
 300
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<210> 3872

<211> 66
 <212> PRT
 <213> Homo sapiens

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 35 40 45
 Ala Glu Lys Thr Glu Lys Thr His Lys Gly Ser Lys Lys Gln Lys Lys
 50 55 60
 Asp Leu
 65

<210> 3873
 <211> 869
 <212> DNA
 <213> Homo sapiens

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<210> 3874

<211> 289

<212> PRT

<213> Homo sapiens

<400> 3874

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          20           25           30
Glu Ala Tyr His Leu Ser Phe Glu Arg Arg Gln Lys Ser Ser Glu Ala
          35           40           45
Pro Val Gln Ser Pro Gln Arg Ser Val Asp Ser Ile Ser Gln Glu Ser
          50           55           60
Ser Thr Ser Ser Phe Ser Ser Met Ser Ala Gly Ser Arg Gln Glu Glu
65           70           75           80
Thr Lys Lys Asp Tyr Arg Glu Val Glu Lys Leu Leu Arg Ala Val Ala
          85           90           95
Asp Gly Asp Leu Glu Met Val Arg Tyr Leu Leu Glu Trp Thr Glu Glu
          100          105          110
Asp Leu Glu Asp Ala Glu Asp Thr Val Ser Ala Ala Asp Pro Glu Phe
          115          120          125
Cys His Pro Leu Cys Gln Cys Pro Lys Cys Ala Pro Ala Gln Lys Arg
          130          135          140
Leu Ala Lys Val Pro Ala Ser Gly Leu Gly Val Asn Val Thr Ser Gln
145          150          155          160
Asp Gly Ser Ser Pro Leu His Val Ala Ala Leu His Gly Arg Ala Asp
          165          170          175
Leu Ile Arg Leu Leu Lys His Gly Ala Asn Ala Gly Ala Arg Asn
          180          185          190
Ala Asp Gln Ala Val Pro Leu His Leu Ala Cys Gln Gln Gly His Phe
          195          200          205
Gln Val Val Lys Cys Leu Leu Asp Ser Asn Ala Lys Pro Asn Lys Lys
          210          215          220
Asp Leu Ser Gly Asn Thr Pro Leu Ile Tyr Ala Cys Ser Gly Gly His
225          230          235          240Glu Leu
Val Ala Leu Leu Leu Gln His Gly Ala Ser Ile Asn Ala
          245          250          255
Leu Thr Ile Arg Gly Asn Thr Ala Leu His Glu Ala Val Ile Glu Lys
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<210> 3875

<211> 2640

<212> DNA

<213> Homo sapiens

<400> 3875

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<211> 824

<212> PRT

<213> Homo sapiens

<400> 3876

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His	Gly	Leu	His	Ser	Val	Leu	Glu	Glu	Trp	Phe	Val	Glu	Val	Leu	Gln
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Gln	Cys	Glu	Asn	Ser	Ala	Asp	Glu	Pro	Gln	Cys	Leu	Leu	Leu	Leu	Leu
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Thr Gly Asp Leu Ala Val Glu Leu Ser Lys Thr Asp Pro Ala Ser Leu		
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	500	505
Asp Leu Phe Ile Asn Glu Tyr Arg Ser Leu Leu Ala Asp Arg Leu Leu		
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His Gln Phe Ser Phe Ser Pro Glu Arg Glu Ile Arg Asn Val Glu Leu		
	530	535
Leu Lys Leu Arg Phe Gly Glu Ala Pro Met His Phe Cys Glu Val Met		
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<210> 3877

<211> 1112

<212> DNA

<213> Homo sapiens

<400> 3877

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<211> 370

<212> PRT

<213> Homo sapiens

<400> 3878

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			20					25					30		
His	Ala	Lys	Lys	Ala	Asn	Gly	Pro	Asn	Tyr	Ile	Gln	Pro	Gln	Lys	Arg
		35					40					45			
Gln	Thr	Thr	Phe	Glu	Ser	Gln	Asp	Arg	Lys	Ala	Val	Ser	Pro	Ser	Ser
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Asp	Ser	Cys	His	Ser	Thr	Thr	Lys	Thr	Glu	Ala	Ser	Gln	Glu	Glu	Arg
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Ser	Asp	Ser	Ser	Gly	Leu	Thr	Ser	Leu	Lys	Lys	Ser	Pro	Lys	Val	Ser
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				165					170					175	
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Glu	Glu	Thr	Ser	Thr	Gln	Glu	Gln	Ser	His	Pro	Gly	Glu	Glu	Trp	Val
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Pro	Gln	Phe	Glu	Gly	Arg	Ala	Gly	Gln	Lys	Leu	Met	Asp	Leu	Gln	Ser
		260						265					270		
His	Phe	Gly	Thr	Asp	Asp	Arg	Phe	Arg	Met	Asp	Ser	Arg	Phe	Leu	Glu
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Gln	Ser	Val	Leu	Gln	Ile	Asn	Leu	Ser	Asn	Ser	Thr	Asn	Arg	Gly	Ser
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<210> 3879

<211> 2769

<212> DNA

<213> Homo sapiens

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<211> 116

<212> PRT

<213> Homo sapiens

<400> 3880

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			20					25					30		
Ala	Ile	Asp	Leu	Ser	Arg	Asn	Gln	Phe	Gln	Asp	Phe	Pro	Glu	Gln	Leu
		35					40					45			
Thr	Ala	Leu	Pro	Ala	Leu	Glu	Thr	Ile	Asn	Leu	Glu	Glu	Asn	Glu	Ile
	50					55					60				
Val	Asp	Val	Pro	Val	Glu	Lys	Leu	Ala	Ala	Met	Pro	Ala	Leu	Arg	Ser
65					70				75					80	
Ile	Asn	Leu	Arg	Phe	Asn	Pro	Leu	Asn	Ala	Glu	Val	Arg	Val	Ile	Ala
			85					90					95		
Pro	Pro	Leu	Ile	Lys	Phe	Asp	Met	Leu	Met	Ser	Pro	Glu	Gly	Ala	Arg
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<210> 3881

<211> 1393

<212> DNA

<213> Homo sapiens

<400> 3881

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<210> 3882

<211> 277

<212> PRT

<213> Homo sapiens

<400> 3882

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 Asn Gly Glu Met Thr Pro Pro Leu Gln Gly Pro Arg Ala Arg Phe Arg
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<212> DNA

<213> Homo sapiens

<400> 3883

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<211> 199

<212> PRT

<213> Homo sapiens

<400> 3884

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<213> Homo sapiens

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<212> DNA

<213> Homo sapiens

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<212> PRT

<213> Homo sapiens

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Ala Leu Asp Ile Leu Ile Lys Asn Tyr Ser Asp Ser Leu Thr Ala Ala		670
	675	680
Met Ile Asp Ala Val Leu Asp Glu Leu Pro Pro Leu Ile Ser Glu Ser		685
	690	695
Asp Met His Val Ser Gln Met Ala Ile Ser Phe Leu Thr Thr Leu Ala		700
705	710	715
Lys Val Tyr Pro Ser Ser Leu Ser Lys Ile Ser Gly Ser Ile Leu Asn		720
	725	730
Glu Leu Ile Gly Leu Val Arg Ser Pro Leu Leu Gln Gly Gly Ala Leu		735
	740	745
Ser Ala Met Leu Asp Phe Phe Gln Ala Leu Val Val Thr Gly Thr Asn		750
	755	760
Asn Leu Gly Tyr Met Asp Leu Leu Arg Met Leu Thr Gly Pro Val Tyr		765
	770	775
Ser Gln Ser Thr Ala Leu Thr His Lys Gln Ser Tyr Tyr Ser Ile Ala		780
785	790	795
Lys Cys Val Ala Ala Leu Thr Arg Ala Cys Pro Lys Glu Gly Pro Ala		800
	805	810
Val Val Gly Gln Phe Ile Gln Asp Val Lys Asn Ser Arg Ser Thr Asp		815
	820	825
Ser Ile Arg Leu Leu Ala Leu Leu Ser Leu Gly Glu Val Gly His His		830
	835	840
Ile Asp Leu Ser Gly Gln Leu Glu Leu Lys Ser Val Ile Leu Glu Ala		845
	850	855
Phe Ser Ser Pro Ser Glu Glu Val Lys Ser Ala Ala Ser Tyr Ala Leu		860
865	870	875
Gly Ser Ile Ser Val Gly Asn Leu Pro Glu Tyr Leu Pro Phe Val Leu		880
	885	890
Gln Glu Ile Thr Ser Gln Pro Lys Arg Gln Tyr Leu Leu Leu His Ser		895
	900	905
Leu Lys Glu Ile Ile Ser Ser Ala Ser Val Val Gly Leu Lys Pro Tyr		910
	915	920
Val Glu Asn Ile Trp Ala Leu Leu Leu Lys His Cys Glu Cys Ala Glu		925
	930	935
Glu Gly Thr Arg Asn Val Val Ala Glu Cys Leu Gly Lys Leu Thr Leu		940
945	950	955
Ile Asp Pro Glu Thr Leu Leu Pro Arg Leu Lys Gly Tyr Leu Ile Ser		960
	965	970
Gly Ser Ser Tyr Ala Arg Ser Ser Val Val Thr Ala Val Lys Phe Thr		975
	980	985
Ile Ser Asp His Pro Gln Pro Ile Asp Pro Leu Leu Lys Asn Cys Ile		990
	995	1000
Gly Asp Phe Leu Lys Thr Leu Glu Asp Pro Asp Leu Asn Val Arg Arg		1005
1010	1015	1020
Val Ala Leu Val Thr Phe Asn Ser Ala Ala His Asn Lys Pro Ser Leu		

1025 1030 1035 1040
 Ile Arg Asp Leu Leu Asp Thr Val Leu Pro His Leu Tyr Asn Glu Thr
 1045 1050 1055
 Lys Val Arg Lys Glu Leu Ile Arg Glu Val Glu Met Gly Pro Phe Lys
 1060 1065 1070
 His Thr Val Asp Asp Gly Leu Asp Ile Arg Lys Ala Ala Phe Glu Cys
 1075 1080 1085
 Met Tyr Thr Leu Leu Asp Ser Cys Leu Asp Arg Leu Asp Ile Phe Glu
 1090 1095 1100
 Phe Leu Asn His Val Glu Asp Gly Leu Lys Asp His Tyr Asp Ile Lys
 1105 1110 1115 1120
 Met Leu Thr Phe Leu Met Leu Val Arg Leu Ser Thr Leu Cys Pro Ser
 1125 1130 1135
 Ala Val Leu Gln Arg Leu Asp Arg Leu Val Glu Pro Leu Arg Ala Thr
 1140 1145 1150
 Cys Thr Thr Lys Val Lys Ala Asn Ser Val Lys Gln Glu Phe Glu Lys
 1155 1160 1165
 Gln Asp Glu Leu Lys Arg Ser Ala Met Arg Ala Val Ala Ala Leu Leu
 1170 1175 1180
 Thr Ile Pro Glu Ala Glu Lys Ser Pro Leu Met Ser Glu Phe Gln Ser
 1185 1190 1195 1200
 Gln Ile Ser Ser Asn Pro Glu Leu Ala Ala Ile Phe Glu Ser Ile Gln
 1205 1210 1215
 Lys Asp Ser Ser Ser Thr Asn Leu Glu Ser Met Asp Thr Ser
 1220 1225 1230

<210> 3889

<211> 556

<212> DNA

<213> Homo sapiens

<400> 3889

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 120
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 180
 cttattaagg gagatggcga ggtcctagag gaaatcgtaa ccaaagaacg acacagagag
 240
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 300
 ccttgagggc ccccgctggc caaggcctgt ggacgacgct ggcgcccag cctgggcagg
 360
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 420
 tctggcccag cccagtctct tctcaggggc agggggtgga ggttggggtc accggcctgc
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 556

<210> 3890

<211> 101
 <212> PRT
 <213> Homo sapiens

<400> 3890
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 Glu Glu Asp Gly Pro Val Leu Thr Asp Glu Gln Val Pro Asn Pro Gly
 20 25 30
 His Glu Ala His Asp Gln Gly Gly Trp Asp Ala Arg Gln Ser Ile Ile
 35 40 45
 Arg Lys Val Val Asp Pro Glu Thr Gly Arg Thr Arg Leu Ile Lys Gly
 50 55 60
 Asp Gly Glu Val Leu Glu Glu Ile Val Thr Lys Glu Arg His Arg Glu
 65 70 75 80
 Ile Asn Lys Gln Ala Thr Arg Gly Asp Cys Leu Ala Phe Gln Met Arg
 85 90 95
 Ala Gly Leu Leu Pro
 100

<210> 3891
 <211> 1687
 <212> DNA
 <213> Homo sapiens

<400> 3891
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 120
 acaggccacg gcactgagag tagtggctct ggcctctttg ccctgtgcac cctggatggg
 180
 aactgaagc tcattggaaga aatggaagaa gcagacaagc tgctgtggtc agtcagagtg
 240
 gatcaccagc tctttgccct ggagaaactg gatgtcaccg gcaacgggca tgaggaggtg
 300
 gttgcatgcg cctgggatgg acagacatat atcattgatc acaaccgcac cgtcgtccgc
 360
 ttccaagtgg atgaaaatat ccgtgccttc tgtgcaggcc tgtacgcctg caaagagggc
 420
 cgcaacagcc cctgcctcgt atatgtcact ttcaaccaga agatctatgt gtactgggag
 480
 gtgcagctgg agcggatgga gtctaccaat ctggtgaaac tgctggagac caagccgagt
 540
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 600
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 660
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 720
 ctacccccta aaggtatctg tggatttggc aggataggga atatgcatta cagaaatgca
 780
 ggatttgact ctgggcatga aagatggcag cagccctagg gtgaccgtga actatagacc
 840

tcgcagtcctt ttcggtgaaa gaagagacaa gttgaccctc tgcccatttc cttatggacc
 900
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 960
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 1020
 ataaggaaaac caggcttttag gcccagggga gcagtggagg taagggtccc accccatctt
 1080
 aagctctgtc ttccgtggca caattccaag ttcttgacgt tagtaattgt taaaggaatg
 1140
 gcaaactgtt ttgttttgaa ggatctttct acagtctggt cttacccatg ttcctagcaa
 1200
 ccctgagatg attttcttcc atttaccaaa gcagccgggt cagtgccttc tcacgttgcc
 1260
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 1320
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 1380
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 1440
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 1560
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 caaatcc
 1687

<210> 3892

<211> 179

<212> PRT

<213> Homo sapiens

<400> 3892

Val	Arg	Val	Leu	Asn	Ile	Trp	Pro	Tyr	Pro	Gln	Gln	Glu	Cys	Leu	His
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Ser	Pro	Asn	Trp	Gln	His	Gln	Thr	Gly	His	Gly	Thr	Glu	Ser	Ser	Gly
			20					25					30		
Ser	Gly	Leu	Phe	Ala	Leu	Cys	Thr	Leu	Asp	Gly	Thr	Leu	Lys	Leu	Met
		35					40					45			
Glu	Glu	Met	Glu	Glu	Ala	Asp	Lys	Leu	Leu	Trp	Ser	Val	Gln	Val	Asp
	50					55				60					
His	Gln	Leu	Phe	Ala	Leu	Glu	Lys	Leu	Asp	Val	Thr	Gly	Asn	Gly	His
65					70					75				80	
Glu	Glu	Val	Val	Ala	Cys	Ala	Trp	Asp	Gly	Gln	Thr	Tyr	Ile	Ile	Asp
			85					90					95		
His	Asn	Arg	Thr	Val	Val	Arg	Phe	Gln	Val	Asp	Glu	Asn	Ile	Arg	Ala
			100					105					110		
Phe	Cys	Ala	Gly	Leu	Tyr	Ala	Cys	Lys	Glu	Gly	Arg	Asn	Ser	Pro	Cys
	115						120					125			
Leu	Val	Tyr	Val	Thr	Phe	Asn	Gln	Lys	Ile	Tyr	Val	Tyr	Trp	Glu	Val

130		135		140
Gln Leu Glu Arg Met Glu Ser Thr Asn Leu Val Lys Leu Leu Glu Thr				
145		150		155
Lys Pro Ser Thr Thr Ala Cys Cys Arg Ser Trp Ala Trp Ile Leu Thr				
	165		170	175
Thr Ser Leu				

<210> 3893

<211> 1591

<212> DNA

<213> Homo sapiens

<400> 3893

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 120
 aagagtaaag aaaattgtgt tgtggataac atcaaagtgt gcagtaatga cactgggagat
 180
 ggaaaattca agtgtgtttg catcactatg agagtgcctc ggaacccaac tatcggagat
 240
 aaatttgcca gtcgccatgg gcagaagggc attttaagca gatttgtggc ggctgaggac
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 360
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 420
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 480
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 660
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 720
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 780
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 840
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 900
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 960
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 1200

tatctttggt caaaaagttc atgtcttctc aaaatatgaa atattgataa atggaagagc
 1260
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 1320
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 1380
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 1440
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 1560
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 1591

<210> 3894

<211> 334

<212> PRT

<213> Homo sapiens

<400> 3894

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Lys	Leu	Gln	Tyr	Gly	Asp	Pro	Tyr	Tyr	Ser	Tyr	Leu	Asn	Leu	Asn	Thr
		20						25					30		
Gly	Glu	Ser	Phe	Val	Met	Tyr	Tyr	Lys	Ser	Lys	Glu	Asn	Cys	Val	Val
		35					40					45			
Asp	Asn	Ile	Lys	Val	Cys	Ser	Asn	Asp	Thr	Gly	Ser	Gly	Lys	Phe	Lys
	50					55					60				
Cys	Val	Cys	Ile	Thr	Met	Arg	Val	Pro	Arg	Asn	Pro	Thr	Ile	Gly	Asp
65					70					75				80	
Lys	Phe	Ala	Ser	Arg	His	Gly	Gln	Lys	Gly	Ile	Leu	Ser	Arg	Leu	Trp
				85					90					95	
Pro	Ala	Glu	Asp	Met	Pro	Phe	Thr	Glu	Ser	Gly	Met	Val	Pro	Asp	Ile
			100					105					110		
Leu	Phe	Asn	Pro	His	Gly	Phe	Pro	Ser	Arg	Met	Thr	Ile	Gly	Met	Leu
		115					120					125			
Ile	Glu	Ser	Met	Ala	Gly	Lys	Ser	Ala	Ala	Leu	His	Gly	Leu	Cys	His
	130					135					140				
Asp	Ala	Thr	Pro	Phe	Ile	Phe	Ser	Glu	Glu	Asn	Ser	Ala	Leu	Glu	Tyr
145					150					155				160	
Phe	Gly	Glu	Met	Leu	Lys	Ala	Ala	Gly	Tyr	Asn	Phe	Tyr	Gly	Thr	Glu
			165						170					175	
Arg	Leu	Tyr	Ser	Gly	Ile	Ser	Gly	Leu	Glu	Leu	Glu	Ala	Asp	Ile	Phe
		180					185						190		
Ile	Gly	Val	Tyr	Tyr	Gln	Arg	Leu	Arg	His	Met	Val	Ser	Asp	Lys	
	195					200						205			
Phe	Gln	Val	Arg	Thr	Thr	Gly	Ala	Arg	Asp	Arg	Val	Thr	Asn	Gln	Pro
	210					215						220			
Ile	Gly	Gly	Arg	Asn	Val	Gln	Gly	Gly	Ile	Arg	Phe	Gly	Glu	Met	Glu
225				230					235					240	
Arg	Asp	Ala	Leu	Leu	Ala	His	Gly	Thr	Ser	Phe	Leu	Leu	His	Asp	Arg
			245						250					255	
Leu	Phe	Asn	Cys	Ser	Asp	Arg	Ser	Val	Ala	His	Val	Cys	Val	Lys	Cys

3042

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 gttcaaaaaa aaaaaaaaaa aaaaaaa
 1227

<210> 3896

<211> 346

<212> PRT

<213> Homo sapiens

<400> 3896

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 Leu Lys Gln His Lys Glu Ala Lys Arg Phe Glu Ile Ala Arg Ser Gln
 20 25 30
 Pro Glu Asp Thr Pro Glu Asn Thr Val Arg Arg Gln Glu Gln Pro Ser
 35 40 45
 Ile Glu Ser Thr Ser Pro Ile Ser Arg Thr Asp Glu Ile Arg Lys Asn
 50 55 60
 Thr Tyr Arg Thr Leu Asp Ser Leu Glu Gln Thr Ile Lys Gln Leu Glu
 65 70 75 80
 Asn Thr Ile Ser Glu Met Ser Pro Lys Ala Leu Val Asp Thr Ser Cys
 85 90 95
 Ser Ser Asn Arg Asp Ser Val Ala Ser Ser Ser His Ile Ala Gln Glu
 100 105 110
 Ala Ser Pro Arg Pro Leu Leu Val Pro Asp Glu Gly Pro Thr Ala Leu
 115 120 125
 Glu Pro Pro Thr Ser Ile Pro Ser Ala Ser Arg Lys Gly Ser Ser Gly
 130 135 140
 Ala Pro Gln Thr Ser Arg Met Pro Val Pro Met Ser Ala Lys Asn Arg
 145 150 155 160
 Pro Gly Thr Leu Asp Lys Pro Gly Lys Gln Ser Lys Leu Gln Asp Pro
 165 170 175
 Arg Gln Tyr Arg Gln Ala Asn Gly Ser Ala Lys Lys Ser Gly Gly Asp
 180 185 190
 Phe Lys Pro Thr Ser Pro Ser Leu Pro Ala Ser Lys Ile Pro Ala Leu
 195 200 205
 Ser Pro Ser Ser Gly Lys Ser Ser Ser Leu Pro Ser Ser Ser Gly Asp
 210 215 220
 Ser Ser Asn Leu Pro Asn Pro Pro Ala Thr Lys Pro Ser Ile Ala Ser
 225 230 235 240
 Asn Pro Leu Ser Pro Gln Thr Gly Pro Pro Ala His Ser Ala Ser Leu
 245 250 255
 Ile Pro Ser Val Ser Asn Gly Ser Leu Lys Phe Gln Ser Leu Thr His
 260 265 270
 Thr Gly Lys Gly His His Leu Ser Phe Ser Pro Gln Ser Gln Asn Gly
 275 280 285
 Arg Ala Pro Pro Pro Leu Ser Phe Ser Ser Ser Pro Pro Ser Pro Ala
 290 295 300
 Ser Ser Val Ser Leu Asn Gln Gly Ala Lys Gly Thr Arg Thr Ile His
 305 310 315 320
 Thr Pro Ser Leu Thr Ser Tyr Lys Ala Gln Asn Gly Ser Ser Ser Lys
 325 330 335
 Ala Thr Pro Ser Thr Ala Lys Glu Thr Ser

340

345

<210> 3897

<211> 366

<212> DNA

<213> Homo sapiens

<400> 3897

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120
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240
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ggtccc
366

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<210> 3898

<211> 111

<212> PRT

<213> Homo sapiens

<400> 3898

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Met Ala Gly Arg Pro Gly Leu Leu His Trp Leu Leu Ala Ser Ser Gly
20           25           30
His Pro Arg Phe Val His Glu Trp Lys Ala Met Leu Thr Ala Ala Gln
35           40           45
Cys Val Gln Asp Val Ser Glu Thr Pro Val Pro Leu Pro Val Pro Leu
50           55           60
Ser Val Pro Leu Ser Thr Ser Val Thr Ser Ser Leu Arg Gly Ser His
65           70           75           80
Pro Thr Leu Cys His Cys His Ile Phe Leu Cys Ala Gln Pro Leu Pro
85           90           95
Pro Pro Glu Thr Phe Leu Glu Ile Ser Lys Cys Asn Ser Arg Ser
100          105          110

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<210> 3899

<211> 1092

<212> DNA

<213> Homo sapiens

<400> 3899

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120

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accttccgga aaatggcggc tgccaggccc agcctgggccc gagtcctccc aggatcctct
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 240
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 420
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 480
 aacacgaccc tggacctcct agaccggggg ctgcagggtcc atgtggtggt ggacgcctgc
 540
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<210> 3900

<211> 249

<212> PRT

<213> Homo sapiens

<400> 3900

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Pro	Ser	Glu	Arg	Arg	Glu	Val	Arg	Val	Pro	Pro	Pro	His	Leu	Gln	Arg
		20						25					30		
Gly	Arg	Ser	Gly	Leu	Glu	Pro	Gly	Thr	Phe	Arg	Lys	Met	Ala	Ala	Ala
		35					40					45			
Arg	Pro	Ser	Leu	Gly	Arg	Val	Leu	Pro	Gly	Ser	Ser	Val	Leu	Phe	Leu
		50				55					60				
Cys	Asp	Met	Gln	Glu	Lys	Phe	Arg	His	Asn	Ile	Ala	Tyr	Phe	Pro	Gln
65				70						75				80	
Ile	Val	Ser	Val	Ala	Ala	Arg	Met	Leu	Lys	Val	Ala	Arg	Leu	Leu	Glu
			85						90					95	
Val	Pro	Val	Met	Leu	Thr	Glu	Gln	Tyr	Pro	Gln	Gly	Leu	Gly	Pro	Thr

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      100      105      110
Val Pro Glu Leu Gly Thr Xaa Gly Pro Ser Ala Ala Gly Gln Asp Leu
      115      120      125
Leu Gln His Gly Ala Cys Leu Gln Gln Glu Leu Asp Ser Arg Pro Gln
      130      135      140
Leu Arg Ser Val Leu Leu Cys Gly Ile Glu Ala Gln Ala Cys Ile Leu
      145      150      155      160
Asn Thr Thr Leu Asp Leu Leu Asp Arg Gly Leu Gln Val His Val Val
      165      170      175
Val Asp Ala Cys Ser Ser Arg Ser Gln Val Asp Arg Leu Val Ala Leu
      180      185      190
Ala Arg Met Arg Gln Ser Gly Ala Phe Leu Ser Thr Ser Glu Gly Leu
      195      200      205
Ile Leu Gln Leu Val Gly Asp Ala Val His Pro Gln Phe Lys Glu Ile
      210      215      220
Gln Lys Leu Ile Lys Glu Pro Ala Pro Asp Ser Gly Leu Leu Gly Leu
      225      230      235      240
Phe Gln Gly Gln Asn Ser Leu Leu His
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<210> 3901

<211> 1287

<212> DNA

<213> Homo sapiens

<400> 3901

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240
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840

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<210> 3902

<211> 312

<212> PRT

<213> Homo sapiens

<400> 3902

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			20				25						30		
Trp	Ala	Ala	Thr	Thr	Ala	Arg	Asn	Ala	Leu	Val	Val	Ser	Phe	Ala	Ala
			35				40					45			
Leu	Val	Ala	Tyr	Ser	Phe	Glu	Val	Thr	Gly	Tyr	Gln	Pro	Phe	Ile	Leu
			50			55					60				
Thr	Gly	Glu	Thr	Ala	Glu	Gly	Leu	Pro	Pro	Val	Arg	Ile	Pro	Pro	Phe
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Ser	Val	Thr	Thr	Ala	Asn	Gly	Thr	Ile	Ser	Phe	Thr	Glu	Met	Val	Gln
				85					90					95	
Asp	Met	Gly	Ala	Gly	Leu	Ala	Val	Val	Pro	Leu	Met	Gly	Leu	Leu	Glu
			100						105				110		
Ser	Ile	Ala	Val	Ala	Lys	Ala	Phe	Ala	Ser	Gln	Asn	Asn	Tyr	Arg	Ile
			115				120						125		
Asp	Ala	Asn	Gln	Glu	Leu	Leu	Ala	Ile	Gly	Leu	Thr	Asn	Met	Leu	Gly
			130				135					140			
Ser	Leu	Val	Ser	Ser	Tyr	Pro	Val	Thr	Gly	Ser	Phe	Gly	Arg	Thr	Ala
145					150					155				160	
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			165						170					175	
Gly	Val	Leu	Val	Leu	Leu	Ser	Leu	Asp	Tyr	Leu	Thr	Ser	Leu	Phe	Tyr
			180					185						190	
Tyr	Ile	Pro	Lys	Ser	Ala	Leu	Ala	Ala	Val	Ile	Ile	Met	Ala	Val	Ala
			195				200						205		
Pro	Leu	Phe	Asp	Thr	Lys	Ile	Phe	Arg	Thr	Leu	Trp	Arg	Val	Lys	Arg
			210				215						220		
Leu	Asp	Leu	Leu	Pro	Leu	Cys	Val	Thr	Phe	Leu	Leu	Cys	Phe	Trp	Glu
225					230					235				240	
Val	Gln	Tyr	Gly	Ile	Leu	Ala	Gly	Ala	Leu	Val	Ser	Leu	Leu	Met	Leu

```

                245                250                255
Leu His Ser Ala Ala Arg Pro Glu Thr Lys Val Ser Glu Gly Pro Val
                260                265                270
Leu Val Leu Gln Pro Ala Ser Gly Leu Ser Phe Pro Val Leu Cys Pro
                275                280                285
Pro Leu Pro Ala Val Gln Asp Pro Lys Thr Leu Ser Pro Thr Leu Ser
                290                295                300
Ser Pro Gln Gly Cys Arg His Leu
305                310

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<210> 3903

<211> 598

<212> DNA

<213> Homo sapiens

<400> 3903

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240
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360
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420
gctgacacta agctggctaa tgtactgttt gcccgaggc tcgccaacca gcttgaggcc
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<210> 3904

<211> 199

<212> PRT

<213> Homo sapiens

<400> 3904

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Ala Arg Arg Gly Ala Arg Val Val Leu Ala Cys Arg Ser Gln Glu Arg
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Gly Glu Ala Ala Phe Asp Leu Arg Gln Glu Ser Gly Asn Asn Glu
20     25     30
Val Ile Phe Met Ala Leu Asp Leu Ala Ser Leu Ala Ser Val Arg Ala
35     40     45
Phe Ala Thr Ala Phe Leu Ser Ser Glu Pro Arg Leu Asp Ile Leu Ile
50     55     60
His Asn Ala Gly Ile Ser Ser Cys Gly Arg Thr Arg Glu Ala Phe Asn
65     70     75     80
Leu Leu Leu Arg Val Asn His Ile Gly Pro Phe Leu Leu Thr His Leu

```



```

      85              90              95
Leu Leu Pro Cys Leu Lys Ala Cys Ala Pro Ser Arg Val Val Val Val
      100              105              110
Ala Ser Ala Ala His Cys Arg Gly Arg Leu Asp Phe Lys Arg Leu Asp
      115              120              125
Arg Pro Val Val Leu Ala Ala Gly Ala Ala Ala Tyr Ala Asp Thr Lys
      130              135              140
Leu Ala Asn Val Leu Phe Ala Arg Glu Leu Ala Asn Gln Leu Glu Ala
      145              150              155              160
Thr Gly Val Thr Cys Tyr Ala Ala His Pro Gly Pro Val Asn Ser Glu
      165              170              175
Leu Phe Leu Arg His Val Pro Gly Trp Leu Arg Pro Leu Leu Arg Pro
      180              185              190
Leu Ala Trp Leu Val Pro Arg
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<210> 3905

<211> 370

<212> DNA

<213> Homo sapiens

<400> 3905

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<210> 3906

<211> 123

<212> PRT

<213> Homo sapiens

<400> 3906

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Gly Ser Ser Glu Leu Arg Ser Ala Phe Ser Ala Ala Arg Thr Thr Pro
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20     25     30
Asn Ile Gly Gly Asp Phe Asp Val Ala Thr Gly Gln Phe Arg Cys Arg
35     40     45
Val Pro Gly Ala Tyr Phe Phe Ser Phe Thr Ala Gly Lys Ala Pro His
50     55     60
Lys Ser Pro Ser Val Met Leu Val Arg Asn Arg Asp Glu Val Gln Ala
65     70     75     80
Leu Ala Phe Asp Glu Gln Arg Arg Pro Gly Ala Arg Arg Ala Ala Ser

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	85		90		95
Gln Ser Ala Met Leu Gln Leu Asp Tyr Gly Asp Thr Val Trp Leu Arg					
	100		105		110
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<210> 3907

<211> 4474

<212> DNA

<213> Homo sapiens

<400> 3907

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 120
 ccacaaagag ctgccaagat agctgggccca ggaagaaagc gccgcagccc tgaccagac
 180
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 360
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<210> 3908

<211> 1373

<212> PRT

<213> Homo sapiens

<400> 3908

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 20 25 30
 Ser Pro Asp Pro Asp Ala Val Ala Asp Pro Gly Ala Leu Trp Leu Ser
 35 40 45
 Thr Lys Arg Leu Lys Met Ser Gly Gly Ala Ser Ala Thr Gly Pro Arg
 50 55 60
 Arg Gly Pro Pro Gly Leu Glu Asp Thr Thr Ser Lys Lys Lys Gln Lys
 65 70 75 80
 Asp Arg Ala Asn Gln Glu Ser Lys Asp Gly Asp Pro Arg Lys Glu Thr
 85 90 95
 Gly Ser Arg Tyr Val Ala Gln Ala Gly Leu Glu Pro Leu Ala Ser Gly
 100 105 110
 Asp Pro Ser Ala Ser Ala Ser His Ala Ala Gly Ile Thr Gly Ser Arg
 115 120 125
 His Arg Thr Arg Leu Phe Phe Pro Ser Ser Ser Gly Ser Ala Ser Thr
 130 135 140
 Pro Gln Glu Glu Gln Thr Lys Glu Gly Ala Cys Glu Asp Pro His Asp
 145 150 155 160
 Leu Leu Ala Thr Pro Thr Pro Glu Leu Leu Leu Asp Trp Arg Gln Ser
 165 170 175
 Ala Glu Glu Val Ile Val Lys Leu Arg Val Gly Val Gly Pro Leu Gln
 180 185 190
 Leu Glu Asp Val Asp Ala Ala Phe Thr Asp Thr Asp Cys Val Val Arg
 195 200 205
 Phe Ala Gly Gly Gln Gln Trp Gly Gly Val Phe Tyr Ala Glu Ile Lys
 210 215 220
 Ser Ser Cys Ala Lys Val Gln Thr Arg Lys Gly Ser Leu Leu His Leu
 225 230 235 240
 Thr Leu Pro Lys Lys Val Pro Met Leu Thr Trp Pro Ser Leu Leu Val
 245 250 255
 Glu Ala Asp Glu Gln Leu Cys Ile Pro Pro Leu Asn Ser Gln Thr Cys
 260 265 270
 Leu Leu Gly Ser Glu Glu Asn Leu Ala Pro Leu Ala Gly Glu Lys Ala
 275 280 285
 Val Pro Pro Gly Asn Asp Pro Val Ser Pro Ala Met Val Arg Ser Arg
 290 295 300
 Asn Pro Gly Lys Asp Asp Cys Ala Lys Glu Glu Met Ala Val Ala Ala
 305 310 315 320
 Asp Ala Ala Thr Leu Val Asp Gly Lys Glu Pro Glu Ser Met Val Asn
 325 330 335
 Leu Ala Phe Val Lys Asn Asp Ser Tyr Glu Lys Gly Pro Asp Ser Val
 340 345 350
 Val Val His Val Tyr Val Lys Glu Ile Cys Arg Asp Thr Ser Arg Val
 355 360 365
 Leu Phe Arg Glu Gln Asp Phe Thr Leu Ile Phe Gln Thr Arg Asp Gly

370		375		380
Asn Phe Leu Arg Leu His	Pro Gly Cys Gly	Pro His Thr Thr	Phe Arg	
385	390	395	400	
Trp Gln Val Lys Leu Arg	Asn Leu Ile Glu	Pro Glu Gln Cys	Thr Phe	
	405	410	415	
Cys Phe Thr Ala Ser Arg	Ile Asp Ile Cys	Leu Arg Lys Arg	Gln Ser	
	420	425	430	
Gln Arg Trp Gly Gly Leu	Glu Ala Pro Ala	Ala Arg Val Gly	Gly Ala	
	435	440	445	
Lys Val Ala Val Pro Thr	Gly Pro Thr Pro	Leu Asp Ser Thr	Pro Pro	
	450	455	460	
Gly Gly Ala Pro His Pro	Leu Thr Gly Gln	Glu Glu Ala Arg	Ala Val	
465	470	475	480	
Glu Lys Asp Lys Ser Lys	Ala Arg Ser Glu	Asp Thr Gly Leu	Asp Ser	
	485	490	495	
Val Ala Thr Arg Thr Pro	Met Glu His Val	Thr Pro Lys Pro	Glu Thr	
	500	505	510	
His Leu Ala Ser Pro Lys	Pro Thr Cys Met	Val Pro Pro Met	Pro His	
	515	520	525	
Ser Pro Val Ser Gly Asp	Ser Val Glu Glu	Glu Glu Glu Glu	Lys	
	530	535	540	
Lys Val Cys Leu Pro Gly	Phe Thr Gly Leu	Val Asn Leu Gly	Asn Thr	
545	550	555	560	
Cys Phe Met Asn Ser Val	Ile Gln Ser Leu	Ser Asn Thr Arg	Glu Leu	
	565	570	575	
Arg Asp Phe Phe His Asp	Arg Ser Phe Glu	Ala Glu Ile Asn	Tyr Asn	
	580	585	590	
Asn Pro Leu Gly Thr Gly	Gly Arg Leu Ala	Ile Gly Phe Ala	Val Leu	
	595	600	605	
Leu Arg Ala Leu Trp Lys	Gly Thr His His	Ala Phe Gln Pro	Ser Lys	
	610	615	620	
Leu Lys Ala Ile Val Ala	Ser Lys Ala Ser	Gln Phe Thr Gly	Tyr Ala	
625	630	635	640	
Gln His Asp Ala Gln Glu	Phe Met Ala Phe	Leu Leu Asp Gly	Leu His	
	645	650	655	
Glu Asp Leu Asn Arg Ile	Gln Asn Lys Pro	Tyr Thr Glu Thr	Val Asp	
	660	665	670	
Ser Asp Gly Arg Pro Asp	Glu Val Val Ala	Glu Glu Ala Trp	Gln Arg	
	675	680	685	
His Lys Met Arg Asn Asp	Ser Phe Ile Val	Asp Leu Phe Gln	Gly Gln	
	690	695	700	
Tyr Lys Ser Lys Leu Val	Cys Pro Val Cys	Ala Lys Val Ser	Ile Thr	
705	710	715	720	
Phe Asp Pro Phe Leu Tyr	Leu Pro Val Pro	Leu Pro Gln Lys	Gln Lys	
	725	730	735	
Val Leu Pro Val Phe Tyr	Phe Ala Arg Glu	Pro His Ser Lys	Pro Ile	
	740	745	750	
Lys Phe Leu Val Ser Val	Ser Lys Glu Asn	Ser Thr Ala Ser	Glu Val	
	755	760	765	
Leu Asp Ser Leu Ser Gln	Ser Val His Val	Lys Pro Glu Asn	Leu Arg	
	770	775	780	
Leu Ala Glu Val Ile Lys	Asn Arg Phe His	Arg Val Phe Leu	Pro Ser	
785	790	795	800	
His Ser Leu Asp Thr Val	Ser Pro Ser Asp	Thr Leu Leu Cys	Phe Glu	

805 810 815
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 Gln Gln Arg Pro Gln Val Pro Ser Val Pro Ile Ser Lys Cys Ala Ala
 835 840 845
 Cys Gln Arg Lys Gln Gln Ser Glu Asp Glu Lys Leu Lys Arg Cys Thr
 850 855 860
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 865 870 875 880
 Trp Pro Asp His Lys Gly Leu Cys Arg Pro Glu Asn Ile Gly Tyr Pro
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 Phe Leu Val Ser Val Pro Ala Ser Arg Leu Thr Tyr Ala Arg Leu Ala
 900 905 910
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 Pro Phe Gln Pro Gly Arg Met Ala Leu Glu Ser Gln Ser Pro Gly Cys
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 1105 1110 1115 1120
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